

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

(without alignments)
17262.293 Million cell updates/sec

Sequence: 1 gcgatgccgcgcgtcccccgcgtgactgatggcacc 3411

Gapor 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 6940544

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

```

1:  GenEmb1.*
2:  gb_ba.*
3:  gb_htg.*
4:  gb_in.*
5:  gb_om.*
6:  gb_ov.*
7:  gb_pat.*
8:  gb_ph.*
9:  gb_pl.*
10: gb_pr.*
11: gb_ro.*
12: gb_sts.*
13: gb_sy.*
14: gb_un.*
15: gb_vi.*
16: em_ba.*
17: em_fun.*
18: em_hum.*
19: em_in.*
20: em_mu.*
21: em_om.*
22: em_or.*
23: em_ov.*
24: em_pat.*
25: em_ph.*
26: em_pl.*
27: em_ro.*
28: em_sts.*
29: em_un.*
30: em_vi.*
31: em_htg_hum.*
32: em_htg_inv.*
33: em_htg_ether.*
34: em_htg_mus.*
35: em_htg_pin.*
36: em_htg_rod.*
37: em_htg_nam.*
38: em_htg_vrt.*
39: em_sy.*
40: em_hngo_hum.*
41: em_hngo_mus.*
42: em_hngo_other.*

```

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB	ID	Description
1	3411	100.0	4015	6	AR104587	Sequence
2	3411	100.0	4015	6	AR175848	Sequence
3	3411	100.0	4015	6	E36793	Human telom
4	3411	100.0	4015	6	AR182221	Sequence
5	3411	100.0	4015	6	AR224455	Sequence
6	3411	100.0	4015	6	AR226390	Sequence
7	3411	100.0	4015	6	AR243328	Sequence
8	3411	100.0	4015	6	AR263555	Sequence
9	3411	100.0	4015	6	AR265996	Sequence
10	3411	100.0	4015	6	AR390470	Sequence
11	3411	100.0	4015	6	AR390470	Sequence
12	3411	100.0	4015	6	AR404030	Sequence
13	3411	100.0	4015	6	AX019310	Sequence
14	3411	100.0	4015	6	AX133979	Sequence
15	3411	100.0	4015	6	AX552695	Sequence
16	3411	100.0	4015	6	AX810036	Sequence
17	3411	100.0	4015	6	BD011044	Human tel
18	3411	100.0	4015	6	BD015832	Quantitat
19	3411	100.0	4015	6	BD082985	Method fo
20	3411	100.0	4015	6	BD131727	Method fo
21	3411	100.0	4015	6	BD218834	Method an
22	3411	100.0	4015	9	AF015950	Method an
23	3411	100.0	4015	6	AX001446	Homo sapi
24	3411	100.0	4042	6	AX003121	Sequence
25	3411	100.0	4042	6	BD136185	Sequence
26	3411	100.0	4070	6	AX391846	Human tel
27	3407.8	99.9	4027	6	BD233924	Sequence
28	3407.8	99.9	4027	6	AF018167	Method an
29	3406.2	99.9	4037	6	E36819	Homo sapi
30	3406.2	99.9	4037	6	AR390496	Human telom
31	3406.2	99.9	4037	6	AR393110	Sequence
32	3406.2	99.9	4037	6	AX810378	Sequence
33	3406.2	99.9	4037	6	BD011070	Human tel
34	3404.8	99.8	33964	6	BD196267	Verterbat
35	3399.9	99.6	13766	6	AX481414	Sequence
36	3397.6	99.6	13766	6	AX553919	Sequence
37	3396.8	99.6	8960	12	AF054379	Synthetic
38	3396	99.6	3396	6	BD091553	Adult bon
39	3396	99.6	3396	6	BD094749	The cell
40	3396	99.6	3396	6	BD096291	Cells cap
41	3392.8	99.5	3396	6	BD196290	Verterbat
42	3385.6	99.3	8742	6	AX553924	Sequence
43	3326	97.5	3918	6	BD196293	Sequence
44	3390.8	96.5	3544	6	AX752636	Verterbat
45	3278.8	96.1	3500	6	BD196299	Verterbat

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
AR104587	AR104587	Sequence 224 from patent US 6093809.	AR104587	AR104587.1	GI:12817295	Unknown.	Unclassified.	1 (bases 1 to 4015)	Cech,T.R. and Lingner,J.	Telomerase	Patent: US 6093809-A 224 25-Jul-2000; Location/Qualifiers
	4015 bp	DNA	linear	6,261,836							

Db 2093 GTGCTGGAGCTGACGATATCAAGGAGCTGGGACCTTGTGCTGCTGTCGAGGCT 2152
 Qy 2101 CAGGACCCGCGCGCTGAGCTGTAATTGTCAGAGTGATGACGAGCGGTAACACAC 2160
 Db 2153 CAGGACCCGCGCGCTGAGCTGTAATTGTCAGAGTGATGACGAGCGGTAACACAC 2212
 Qy 2161 ATCCCCAGAGACAGGCTCAAGAGGTATGCGCAGATCATCAAACCCAGAAACGTAC 2220
 Db 2213 ATCCCCAGAGACAGGCTCAAGAGGTATGCGCAGATCATCAAACCCAGAAACGTAC 2272
 Qy 2221 TGCGTGGCTGGATGCGCTGATCAGAGAGCGCGCATGAGACGTCGCAAGGCTTC 2280
 Db 2273 TGCGTGGCTGGATGCGCTGATCAGAGAGCGCGCATGAGACGTCGCAAGGCTTC 2332
 Qy 2281 AAGAGCAAGCTCTTACCTTGAAGACCTTCAGCGCTTACATGCGACAGTTCTGCTCAC 2340
 Db 2333 AAGAGCAAGCTCTTACCTTGAAGACCTTCAGCGCTTACATGCGACAGTTCTGCTCAC 2392
 Qy 2341 CTGACAGAGACCAAGCCGCTGAGGAGATGCGCTGATCAGAGAGCTCTCCCTGAAT 2400
 Db 2393 CTGACAGAGACCAAGCCGCTGAGGAGATGCGCTGATCAGAGAGCTCTCCCTGAAT 2452
 Qy 2401 GAGGACAGAGTGGCTCTTTCAGAGTCTTCTACAGCTTCACTGCGACCAAGCGCTGCG 2460
 Db 2453 GAGGACAGAGTGGCTCTTTCAGAGTCTTCTACAGCTTCACTGCGACCAAGCGCTGCG 2512
 Qy 2461 ATCAGAGGAGCAAGTCTACCTACAGTGGCAGAGGATCCCGAGAGGCTTCACTCTCCAG 2520
 Db 2513 ATCAGAGGAGCAAGTCTACCTACAGTGGCAGAGGATCCCGAGAGGCTTCACTCTCCAG 2572
 Qy 2521 CTGCTGACAGCTGCTGCTACAGGACATGAGACAGAGCTGTTGCGGAGATTCCGCG 2580
 Db 2573 CTGCTGACAGCTGCTGCTACAGGACATGAGACAGAGCTGTTGCGGAGATTCCGCG 2632
 Qy 2581 GACGAGGCTGCTGCTGCTTGGTGGATGATTTCTTGTGTGACACTTCACTCCACCC 2640
 Db 2633 GACGAGGCTGCTGCTGCTTGGTGGATGATTTCTTGTGTGACACTTCACTCCACCC 2692
 Qy 2641 GCGAAACCTTCTCAAGACCTGATCCAGAGTGTCCCTGAGATGAGCTGCTGAGTGAAC 2700
 Db 2693 GCGAAACCTTCTCAAGACCTGATCCAGAGTGTCCCTGAGATGAGCTGCTGAGTGAAC 2752
 Qy 2701 TTGCGAAAGACAGTGTGAACCTTCTGTAAGAACAGAGGCTCTGAGTGGACAGGCTTTT 2760
 Db 2753 TTGCGAAAGACAGTGTGAACCTTCTGTAAGAACAGAGGCTCTGAGTGGACAGGCTTTT 2812
 Qy 2761 GTTCAGATGCGGCGCCACGCGCTATTCCCTGGGCGGCTGCTGCTGATACCGGAGCC 2820
 Db 2813 GTTCAGATGCGGCGCCACGCGCTATTCCCTGGGCGGCTGCTGCTGATACCGGAGCC 2872
 Qy 2821 CTGAGAGTGAAGAGCACTACCTCCAGTATGCCCGACCTTCATCAGAGCAAGTCTCAC 2880
 Db 2873 CTGAGAGTGAAGAGCACTACCTCCAGTATGCCCGACCTTCATCAGAGCAAGTCTCAC 2932
 Qy 2881 TTGACACGCGGCTTCAAGCTGAGGAGAACATGCGTGGAACTTTTGGGGCTTGGCG 2940
 Db 2933 TTGACACGCGGCTTCAAGCTGAGGAGAACATGCGTGGAACTTTTGGGGCTTGGCG 2992
 Qy 2941 CTGAGAGTGAAGAGCACTGTTTCTGATTTGAGTGAAGACGCTTCAGAGAGTGTGAC 3000
 Db 2993 CTGAGAGTGAAGAGCACTGTTTCTGATTTGAGTGAAGACGCTTCAGAGAGTGTGAC 3052
 Qy 3001 AACATCTACAAAGATCTCTCTGCTGACAGGCTTCAAGGATGATGCTGACGCTC 3060
 Db 3053 AACATCTACAAAGATCTCTCTGCTGACAGGCTTCAAGGATGATGCTGACGCTC 3112
 Qy 3061 CCAATTTCATGACAGAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGACAG 3120
 Db 3113 CCAATTTCATGACAGAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGACAG 3172
 Qy 3121 GCTTCCTCTGCTACTCATCTGAAAGCCAGAGAGATGCTGCGGCGCAAG 3180

Db 3173 GCTTCCTCTGCTACTCCATCTGAAAGCCAGAGACGAGGATGTGCTGCGGCGCAAG 3232
 Qy 3181 GCGCGCGCGCGCGCTTCCCTCCGAGCGCGTGAAGTGTGTGCAACAGACTTCCTG 3240
 Db 3233 GCGCGCGCGCGCGCTTCCCTCCGAGCGCGTGAAGTGTGTGCAACAGACTTCCTG 3292
 Qy 3241 CTCAAGCTGATGACACCGTGTATCACTTACGTGCACTCTCTGGGCTCATCAGAGAGCC 3300
 Db 3293 CTCAAGCTGATGACACCGTGTATCACTTACGTGCACTCTCTGGGCTCATCAGAGAGCC 3352
 Qy 3301 CAGAGCAGCTGATGCGAAGCTCCCGGAGACAGAGCTGACTGCGCTGAGAGCGCGAGCC 3360
 Db 3353 CAGAGCAGCTGATGCGAAGCTCCCGGAGACAGAGCTGACTGCGCGCTGAGAGCGCGAGCC 3412
 Qy 3361 AACCGGACACTGCGCTTCAAGATTCAAGACCACTCTGACTGATGAGCCACCC 3411
 Db 3413 AACCGGACACTGCGCTTCAAGATTCAAGACCACTCTGACTGATGAGCCACCC 3463

RESULT 2

AR175848

LOCUS AR175848 4015 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 224 from patent US 6309867.

ACCESSION AR175848

VERSION AR175848.1 GI:17917147

KEYWORDS

SOURCE

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 4015)

AUTHORS

Cech,T.R. and Nakamura,T.

TITLE

Telomerase

JOURNAL

FEATUDES

source

ORIGIN

Query Match

Best Local Similarity

Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGATGCCGCGGCTGCCCGCTGCGGAGCGCTGCGCTCTGCTGCGACGACTACCGC 60
 Db 53 GCGATGCCGCGGCTGCCCGCTGCGGAGCGCTGCGCTCTGCTGCGACGACTACCGC 112
 Qy 61 GAGGTGCGCGGCTGCGGAGCGCTGCGGAGCGCTGCGGAGCGCTGCGGAGCGCTGCG 120
 Db 113 GAGGTGCGCGGCTGCGGAGCGCTGCGGAGCGCTGCGGAGCGCTGCGGAGCGCTGCG 172
 Qy 121 CAGCGCGGAGACCGCGCGGCTTTCGCGCGGCTGCGGAGCGCTGCGGAGCGCTGCGG 180
 Db 173 CAGCGCGGAGACCGCGCGGCTTTCGCGCGGCTGCGGAGCGCTGCGGAGCGCTGCGG 232
 Qy 181 TGGAGCGACG 240
 Db 233 TGGAGCGACG 292
 Qy 241 CTGAGTGGCCCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 300
 Db 293 CTGAGTGGCCCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 352
 Qy 301 GAGCTTGGCTGCTGAGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 Db 353 GAGCTTGGCTGCTGAGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
 Qy 361 CCGAGCTACTGCGGCAACAGCGTGAACGCGACCTGCGGAGGAGCGCGGCGCTGCGG 420
 Db 413 CCGAGCTACTGCGGCAACAGCGTGAACGCGACCTGCGGAGGAGCGCGGCGCTGCGG 472
 Qy 421 CTGCTGCGCGCGCGTGGGCGAGCAGCTGTGCTTCACTGCTGCGGCGCTCTTT 480

Db	3553	ATTGGGGGAGGTGCTGTGGGAGTAAAACTCGAATATATGATTTTCACTTTGAAA	4012
Qy	3590	AAA 3592	
Db	4013	AAA 4015	

ORIGIN						
Query Match	82.4%	Score 3306.6;	DB 6;	Length 4015;		
Best Local Similarity	89.9%;	Pred. No. 0;				
Matches 3618; Conservative	0;	Mismatches 359;	Indels 46;	Gaps 5		

Qy	B	GCAGCGCTCGTCTCTGCGCACGTGGAAAGCCTTGCCCCCGGCACACCCCGCATGCC	67
Db	1	GCACCGCTGCTCTCTGCGCACGTGGAAAGCCTTGCCCCCGGCACACCCCGCATGCC	60
Qy	68	GCGGCTCCCGGCTGCGGAGCGCGTGGCTCCCTGCTGGCAGGCCATACCGCAGAGTCT	127
Db	61	GCGGCTCCCGGCTGCGGAGCGCGTGGCTCCCTGCTGGCAGGCCATACCGGAGTCT	120
Qy	128	GCCGCTGGCCACGTTCTGTGCGAGCGCTTGAGGAGGCCAGGACTGTGTGCACGCGG	187
Db	121	GCCGCTGGCCACGTTCTGTGCGAGCGCTTGAGGAGGCCAGGACTGTGTGCACGCGG	180
Qy	188	GAACCCCGGCGGCTTTCGCGGCGCTGAGTGGCCCAAGGACCTGAGTGGCGGCTTGAGAGC	247
Db	181	GAACCCCGGCGGCTTTCGCGGCGCTGAGTGGCCCAAGGACTGTGAGTGGCGGCTTGAGAGC	240
Qy	248	ACGCGCGCCCCCGCGCGCCCTCTTCCTTCGCGCCAGGTGTCCTGCTGAAGAGAGTGAGGC	307
Db	241	ACGCGCGCCCCCGCGCGCCCTCTTCCTTCGCGCCAGGTGTCCTGCTGAAGAGAGTGAGGC	300
Qy	308	CCGAGTGTGTGAGAGGCTGTGCGAGCGGCGCGAAGAACGTGCTGAGCTTCGCGTTGCG	367
Db	301	CCGAGTGTGTGAGAGGCTGTGCGAGCGGCGCGAAGAACGTGCTGAGCTTCGCGTTGCG	360
Qy	368	GCTCTGTGACGAGGCGCCGCGGAGGCCCCCGGAGGCTTTCACACACAGCTGCGCAGCTA	427
Db	361	GCTCTGTGACGAGGCGCCGCGGAGGCCCCCGGAGGCTTTCACACACAGCTGCGCAGCTA	420
Qy	428	CCTGCGCCACAACGCTGACCAAGCAGCTGCGGAGGACGAGGCGTGGGAGGCTGCTCTGCG	487
Db	421	CCTGCGCCACAACGCTGACCAAGCAGCTGCGGAGGACGAGGCGTGGGAGGCTGCTCTGCG	480
Qy	488	CCGCGTGGGCGACGAGCTGCTGTGTTCACCTGTGTGCACGCTGCGCGCTCTTTGTGTGCTGT	547
Db	481	CCGCGTGGGCGACGAGCTGCTGTGTTCACCTGTGTGCACGCTGCGCGCTCTTTGTGTGCTGT	540
Qy	548	GAGTCTCCAGTGGCGCTTACAGAGTGTGGGAGCGCGCGCTGACAGAGCTCGGAGGCTGCGAC	607
Db	541	GAGTCTCCAGTGGCGCTTACAGAGTGTGGGAGCGCGCGCTGACAGAGCTCGGAGGCTGCGAC	600
Qy	608	TCAAGGCCGCGCCCGGCACACAGCTTAGTGAACCCGAAAGCGTCTGGAGTGCAGACGCGGC	667

QY 3061 ACATCTACAGAGTCTCTGCTGAGGAGGTA CAGTTTTCACGCACTGCTGAGAGTCC 3120
 Db 3061 ACATCTACAGAGTCTCTGCTGAGGAGGTA CAGTTTTCACGCACTGCTGAGAGTCC 3120
 QY 3121 CATTTCACTGAGCAAGTTTGAAGAACCACCACTTTTCTGCGGCTGCTGACACAG 3180
 Db 3121 CATTTCACTGAGCAAGTTTGAAGAACCACCACTTTTCTGCGGCTGCTGACACAG 3180
 QY 3181 CTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
 Db 3181 CTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
 QY 3241 CAGTGGCAGCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
 Db 3241 CAGTGGCAGCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
 QY 3301 TTAGAAGTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
 Db 3301 TTAGAAGTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
 QY 3361 CGTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
 Db 3361 CGTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
 QY 3421 GGGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
 Db 3421 GGGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
 QY 3481 CCTGTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
 Db 3481 CCTGTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
 QY 3541 ATTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
 Db 3541 ATTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
 QY 3601 AGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3660
 Db 3601 AGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3660
 QY 3661 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3720
 Db 3661 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3720
 QY 3721 GTCCAGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3780
 Db 3721 GTCCAGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3780
 QY 3781 CTGAGCTTAA CAGGCTTCTACTTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTT 3840
 Db 3781 CTGAGCTTAA CAGGCTTCTACTTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTT 3840
 QY 3841 CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3900
 Db 3841 CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3900
 QY 3901 GCACTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3960
 Db 3901 GCACTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3960
 QY 3961 TGAATATATAGTGTTCAGTTTGAAGAAAAA 4012
 Db 3961 TGAATATATAGTGTTCAGTTTGAAGAAAAA 4012

RESULT 2

US-09-424-686f-1
 ; Sequence 1 Application US/09424686f
 ; GENERAL INFORMATION:
 ; APPLICANT: Hagen, Gustav
 ; APPLICANT: Siegmund, Hans-Ulrich
 ; APPLICANT: Weichsel, Walter
 ; APPLICANT: Wick, Maresa

; APPLICANT: Zubov, Dmitry
 ; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and
 ; TITLE OF INVENTION: Therapeutic Use
 ; FILE REFERENCE: Bayer 10, 203
 ; CURRENT APPLICATION NUMBER: US/09/424, 686f
 ; CURRENT FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/EP98/03468
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 1
 ; LENGTH: 4042
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-424-686f-1

Query Match 83.1%; Score 333.6; DB 20; Length 4042;
 Best Local Similarity 90.0%; Pred. No. 0;
 Matches 3645; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 1 GTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
 Db 1 GTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
 QY 61 CGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
 Db 61 CGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
 QY 121 AGGTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
 Db 121 AGGTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
 QY 181 AGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
 Db 181 AGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
 QY 241 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 Db 241 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 QY 301 TGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 Db 301 TGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 QY 361 GCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
 Db 361 GCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
 QY 421 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
 Db 421 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
 QY 481 TGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 Db 481 TGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 QY 541 TGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 Db 541 TGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 QY 601 CTGCACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 Db 601 CTGCACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 QY 661 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 Db 661 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 QY 721 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
 Db 721 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
 QY 781 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840

Db	781	GTGGCGCTCCCTCGAGCCGGAAGCGACGCCGTTGGGAGGGGTCTTGAGGCCACCCGG	840
OY	841	GCAGGACCGGTGAGACCGAATGACCGTGGTCTTGTTGGTGTCACTGCAAGCCGCG	900
Db	841	GCAGGACCGGTGAGACCGAATGACCGTGGTCTTGTTGGTGTCACTGCAAGCCGCG	900
OY	901	AAGAAAGCACTCTTTGGAGGGGTGGCGTCTTGAGACAGCGGCACCTCCACCACTCGTGG	960
Db	901	AAGAAAGCACTCTTTGGAGGGGTGGCGTCTTGAGACAGCGGCACCTCCACCACTCGTGG	960
OY	961	GCCGCCAGACCAACGCGGGGCCCCCATTCACATCGCGGCACACAGTCCCTGGAGCACGC	1020
Db	961	GCCGCCAGACCAACGCGGGGCCCCCATTCACATCGCGGCACACAGTCCCTGGAGCACGC	1020
OY	1021	CTTGTCTCCCGGTGTACGCCGAGCAACAGCATTTCTCTACTCTCAAGGCAACAAGAGC	1080
Db	1021	CTTGTCTCCCGGTGTACGCCGAGCAACAGCATTTCTCTACTCTCAAGGCAACAAGAGC	1080
OY	1081	AGCTGCGGCCTCTTCTTCTACTCAGCTCTCTGAGGCCAGCTGACTGGCGCTGGAGGC	1140
Db	1081	AGCTGCGGCCTCTTCTTCTACTCAGCTCTCTGAGGCCAGCTGACTGGCGCTGGAGGC	1140
OY	1141	TGCTGAGACCACTCTTTCTGGGTTCAAGGCTCTGATGCAAGGAACTCCCGCAAGTTC	1200
Db	1141	TGCTGAGACCACTCTTTCTGGGTTCAAGGCTCTGATGCAAGGAACTCCCGCAAGTTC	1200
OY	1201	CCCGCCTGCCCCAGGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGTGGAAGC	1260
Db	1201	CCCGCCTGCCCCAGGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGTGGAAGC	1260
OY	1261	ACGCCAATGCCCCCTTACGAGGGTGTCTTCAAGACGACTGCCCGCTGGAGCTGCGTCA	1320
Db	1261	ACGCCAATGCCCCCTTACGAGGGTGTCTTCAAGACGACTGCCCGCTGGAGCTGCGTCA	1320
OY	1321	CCCCAGACGCGGTCTGTGCGCCGAGAGAAACCCCAAGGGCTGTGGGCGGCCCCAGAG	1380
Db	1321	CCCCAGACGCGGTCTGTGCGCCGAGAGAAACCCCAAGGGCTGTGGGCGGCCCCAGAG	1380
OY	1381	AGGAGAGACACAGACCCCGGTGCTGTGACGTCTCCCGACAGACAGACGCCCTTGGC	1440
Db	1381	AGGAGAGACACAGACCCCGGTGCTGTGACGTCTCCCGACAGACAGACGCCCTTGGC	1440
OY	1441	AGGTATACGGCTTGTTGGGCGGCTGCTCGCGCGGCTGTGCCCCCAAGGCTCTGGGGCT	1500
Db	1441	AGGTATACGGCTTGTTGGGCGGCTGCTCGCGCGGCTGTGCCCCCAAGGCTCTGGGGCT	1500
OY	1501	CCAGGACACAGACGCGCTTCTCAGAGAACACCAAGAAAGTTCACTCCCTGGAGAGC	1560
Db	1501	CCAGGACACAGACGCGCTTCTCAGAGAACACCAAGAAAGTTCACTCCCTGGAGAGC	1560
OY	1561	ATGCCAATCTCTCGTGTGACAGAGCTGAGAGTGAATGAGCGGTGCGGACTGCGTTGGC	1620
Db	1561	ATGCCAATCTCTCGTGTGACAGAGCTGAGAGTGAATGAGCGGTGCGGACTGCGTTGGC	1620
OY	1621	TGCGCAGAGGCCCAGAGGGTGGCTGTGTTCCGCGCGAGAGAACCGTGTGCGTGAAGAGA	1680
Db	1621	TGCGCAGAGGCCCAGAGGGTGGCTGTGTTCCGCGCGAGAGAACCGTGTGCGTGAAGAGA	1680
OY	1681	TCCTGGCCAAATTCTTGCACTGGCTGATGATGTATAGTGTGAGCTGAGCTCAAGCTTT	1740
Db	1681	TCCTGGCCAAATTCTTGCACTGGCTGATGATGTATAGTGTGAGCTGAGCTCAAGCTTT	1740
OY	1741	TCTTTATGTCAACGAGACCAAGCTTCAAAAGAAAGAGCTCTTTTCTAACCGGAAAGATG	1800
Db	1741	TCTTTATGTCAACGAGACCAAGCTTCAAAAGAAAGAGCTCTTTTCTAACCGGAAAGATG	1800
OY	1801	TCTGAGCAAGTTGCAAGCAATTGGAATCAGACAGCACTTGAAGAAGGTGACGTGCGG	1860
Db	1801	TCTGAGCAAGTTGCAAGCAATTGGAATCAGACAGCACTTGAAGAAGGTGACGTGCGG	1860
OY	1861	AGCTGTGGAAGCAGAGTCAAGCGACGATCGGAGACCAAGGCCCGCTGTGAGTCTCA	1920
Db	1861	AGCTGTGGAAGCAGAGTCAAGCGACGATCGGAGACCAAGGCCCGCTGTGAGTCTCA	1920

Db	1861	AGCTGTGGAGAGCAGAGGTACAGGACGATCGGGAAAGCCAGGCCCGCCCTCTGTGACGTCA	1920
Qy	1921	GACTCCGCTTCATCCCAAGCTTGAACGAGCTGACGGGCTGACGGCCGATTGTGAAACAATGACTACGTGG	1980
Db	1921	GACTCCGCTTCATCCCAAGCTTGAACGAGCTGACGGGCTGACGGCCGATTGTGAAACAATGACTACGTGG	1980
Qy	1981	TGGGAGCCAGAACGTTCCGACAGAGAAAAGAGGAGCCAGGCGCTACAGCTCCAGGGGTGAAAG	2040
Db	1981	TGGGAGCCAGAACGTTCCGACAGAGAAAAGAGGAGCCAGGCGCTACAGCTCCAGGGGTGAAAG	2040
Qy	2041	CATTGTTCAAGGTGCTCAACTACGAGCGGAGCGCGCCCGGCTCTGTGGGCGCTCTG	2100
Db	2041	CATTGTTCAAGGTGCTCAACTACGAGCGGAGCGCGCCCGGCTCTGTGGGCGCTCTG	2100
Qy	2101	TGCTGGGCGCTGGAAGATATCCACAGGGCGCTGGGCGCACTTCGTGCTGCTGTGGGGGCC	2160
Db	2101	TGCTGGGCGCTGGAAGATATCCACAGGGCGCTGGGCGCACTTCGTGCTGCTGTGGGGGCC	2160
Qy	2161	AGGACCCGCGCCCTGAGCTGTACTTTGTGCAAGTGTGATGTGACAGGAGCGGTACACACCA	2220
Db	2161	AGGACCCGCGCCCTGAGCTGTACTTTGTGCAAGTGTGATGTGACAGGAGCGGTACACACCA	2220
Qy	2221	TCCCCCAAGACAGGCTCACAGAGGTCAATGCGACATCATCAAAACCCAGAACGTACT	2280
Db	2221	TCCCCCAAGACAGGCTCACAGAGGTCAATGCGACATCATCAAAACCCAGAACGTACT	2280
Qy	2281	GCGTACGCTCGGTATGCGGTGTGCAGAAAGGCGCGCCCAATGGGCAAGTCGCGAGGCGTTCA	2340
Db	2281	GCGTACGCTCGGTATGCGGTGTGCAGAAAGGCGCGCCCAATGGGCAAGTCGCGAGGCGTTCA	2340
Qy	2341	AGAGCCACGTCCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCAC	2400
Db	2341	AGAGCCACGTCCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCAC	2400
Qy	2401	TGCAGAGAACCCAGGCGCGCTGAGGGATGCGCTGTGCATGAGAGACAGTCCCTCCCTGATG	2460
Db	2401	TGCAGAGAACCCAGGCGCGCTGAGGGATGCGCTGTGCATGAGAGACAGTCCCTCCCTGATG	2460
Qy	2461	AGGCCAGAGTGGCCTCTTCGACGCTCTTCTCAAGCTTCATGTGCGACACAGCCGTGGCA	2520
Db	2461	AGGCCAGAGTGGCCTCTTCGACGCTCTTCTCAAGCTTCATGTGCGACACAGCCGTGGCA	2520
Qy	2521	TCCAGGGGAAATCCTTACGTCCAGTCCAGGGGATCCCGCAGGGGTCCATCTCTCCACGC	2580
Db	2521	TCCAGGGGAAATCCTTACGTCCAGTCCAGGGGATCCCGCAGGGGTCCATCTCTCCACGC	2580
Qy	2581	TGCTCTGACGCTGTGCTACGCGCACATGAGAAACAAGCTTTGGCGGAGATTGGCGGG	2640
Db	2581	TGCTCTGACGCTGTGCTACGCGCACATGAGAAACAAGCTTTGGCGGAGATTGGCGGG	2640
Qy	2641	ACGGGCTGCTCTGCGTTTGGTGTGATATTTCTTGTGTGTGACACCTCACCTCACCAAG	2700
Db	2641	ACGGGCTGCTCTGCGTTTGGTGTGATATTTCTTGTGTGTGACACCTCACCTCACCAAG	2700
Qy	2701	CGAAAAACCTTCTCAGAGACCTGTGCTCGAGGTGCTCTGAGTATGAGTGTGGGTGAACT	2760
Db	2701	CGAAAAACCTTCTCAGAGACCTGTGCTCGAGGTGCTCTGAGTATGAGTGTGGGTGAACT	2760
Qy	2761	TGCGGAAACAAGTGTGAACTTCCCTGTGAGAAACAAGGCGCTGGGTGGAACGAGCTTTTG	2820
Db	2761	TGCGGAAACAAGTGTGAACTTCCCTGTGAGAAACAAGGCGCTGGGTGGAACGAGCTTTTG	2820
Qy	2821	TTTCAGATGCGGCGCCACAGGCGCTATTCCTCGTGTGCGGCGCTGTCTGTGGAATACCCGGAACC	2880
Db	2821	TTTCAGATGCGGCGCCACAGGCGCTATTCCTCGTGTGCGGCGCTGTCTGTGGAATACCCGGAACC	2880
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Db	2881	TGAGAGTGCAGAGGCACTACTCCAGCTATGCCGGAACCTCCATCAGAGCAGCAGTCTCACT	2940
Qy	2941	TCAAACCGCGGCTTCAAAGGCTGGAGAGAAACATGTGTGCGAAACTCTTTGGGGTCTTGTGGCG	3000
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QY	3001	TTGAAGTGTCAACACCTGGTTCTGGAATTGGAGGTGAACAAGCCTCCAGAACGGTGTGACCA	306
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Dp	3181	CTCTCCTCTGTCTACTCATCTCTGAAAAGCCAGAACGACGACAGTATGT-----GCAGG	3240
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Dp	3301	TCAAAGTGTACTGACACCGCTGTACCTTACGTCCACTCTGGGGGTCACTACAGACAGCC	3360
QY	3351	CTGTCAAGGTCTGTCTGTCCCGGCTCTGTGAGGGGTGACAGAGACCTGATGAAAGGACA	3410
Dp	3361	AACCGAGGTGTAGTGTGGAAGTCTCCGGGGAACGACGTACTGTGCTCTGAGGCGCGACCA	3420
QY	3411	GGAGCTGTGTGGAGGTGCACTCTTCCACCTTGTCT-----	3449
Dp	3421	ACCCGCACTGGCCTTCAAGCTTCAAGAACCATCTGACTGATGTGCCACCCGCGCACAGCC	3480
QY	3450	--GCTGTGGAGAGCGCTGAGGGGGCGTGTCTCTGTTTGGCCCATGTGTGGATTGGG	3507
Dp	3481	AGCGCGAAGAGACAGACACAGAGCCCTGTACAGCGGCGCTCTAGTCCCAAGGAGGAGG	3540
QY	3508	GGGCGTGGCTCTCTCTGTTTGTGCTGTGTGTGTGGAATGTGAGCTGTCTCCGTCATGTGCACT	3567
Dp	3541	GGCGGCGCAACCCAGAGCGCGGACCGCTGGAGTGTGAGGCTGATGATGATGTGTGGCG	3600
QY	3568	TAGAGCCCTTGTGCAAAACCCAGGCGCAAG-----GGCTTAGAGAGGAGCGACGCGCAAGCT	3622
Dp	3601	AGGCTGTGATGTCCGGGTGAAGGCTGATGTGTCCGGCTGAGGCTGTAGCGATGTTCACAGCC	3660
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Dp	3661	AAGGCTGTAGTGTCCAGACACCTGTGCTGTCTCACTTCCCAAGGCTGTGCGTCCGCT	3719
QY	3683	CTGCTTCCAGTCAACGTCCTCTGCGCCCTGTGACACTTGTGTCAAGCATCAGGAGAGTTCCT	3742
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Dp	3833	CCACCCCAACCATCAGCTGTGAGAACCTGTAGAGAGACCTGTGAGAGCTCTGGAAATTTTGA	3892
QY	3863	GTGACAAAGGTGTGACCTGTATACACAGGCAAGACCTGTGACCTGTGATGTGGGGTCCCTGT	3922
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[illegible]

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; GENERAL INFORMATION:
; APPLICANT: Hagen, Gustav
; APPLICANT: Siegmund, Hans-Ulrich
; APPLICANT: Weichsel, Walter
; APPLICANT: Nick, Mareisa
; APPLICANT: Zubov, Dmitry

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; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; FILE REFERENCE: Bayer 10.203
; CURRENT APPLICATION NUMBER: US/09/424,686B
; PRIOR FILING DATE: 1998-11-29
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 7
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ACCESSION AX001446
VERSION AX001446.1 GI:7241612
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4042)
AUTHORS Wick, M. and Hagen, G.
TITLE HUMAN CATALYTIC TELOMERASE SUB-UNIT AND ITS DIAGNOSTIC AND
THERAPEUTIC USE
JOURNAL Patent: WO 9859040-A 1 30-DEC-1998;
WICK MARESA (DE); BAYER AG (DE)
FEATURES
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ORIGIN
Query Match 93.8%; Score 3586; DB 6; Length 4042;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 3824; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

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Db 1 GTTTTCAGGACAGCGCTGCTGCTCTGCTGCGCAAGTGGAGAACCTTGGCCCGCCACCCCGC 60
QY 61 CGATGCGCGCGCTGCTGCTGCTGCGAGCGTGTGCTCTGCTGCGAGCACTACCGCG 120
Db 61 CGATGCGCGCGCTGCTGCTGCTGCGAGCGTGTGCTCTGCTGCGAGCACTACCGCG 120
QY 121 AGGTGCTGCGCTGCGCACTGTTGCTGCGCGCGCTGCGAGCGTGTGCTGCGAGCGTGTGCTG 180
Db 121 AGGTGCTGCGCTGCGCACTGTTGCTGCGCGCGCTGCGAGCGTGTGCTGCGAGCGTGTGCTG 180
QY 181 AGCGGCGGAGACCCCGCGCTTTCGCGCGCTGTGTGCGCAAGTGTGCTGTGTGCGTGTGCT 240
Db 181 AGCGGCGGAGACCCCGCGCTTTCGCGCGCTGTGTGCGCAAGTGTGCTGTGTGCGTGTGCT 240
QY 241 GGGACGCAAGCGCGCTGCTGCGCGCGCTGCTGCTGCTGCGCAAGTGTGCTGTGCGTGTGCG 300
Db 241 GGGACGCAAGCGCGCTGCTGCGCGCGCTGCTGCTGCTGCGCAAGTGTGCTGTGCGTGTGCG 300
QY 301 TGGTGGCCCGAGTGTGCGAGCGTGTGCGAGCGCGCGCGCGAGAGAGTGTGCTGTGCGCTTTCG 360
Db 301 TGGTGGCCCGAGTGTGCGAGCGTGTGCGAGCGCGCGCGCGAGAGAGTGTGCTGTGCGCTTTCG 360

QY 361 GCTTGGGCTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 361 GCTTGGGCTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 421 GCACCTACTGCTGCGCAACAGGTGACGACGACGACGACGACGACGACGACGACGACGACGACG 480
Db 421 GCACCTACTGCTGCGCAACAGGTGACGACGACGACGACGACGACGACGACGACGACGACGACG 480
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Db 541 TGTGCGCGCGCTGCGAG 600
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QY 721 GTGCGAG 780
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 1921 CTTATATCCCAAGCTCAGAGGATGCGGAAAGCCAGGCCCGCTCTGATCGTCAAGTCCG 1980
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 3572 CATGCTCAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3631
 3601 CATGCTCAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3660
 3632 GAGTCTCAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3691
 3661 GAGTCTCAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3720
 3692 GGGCAGCTCAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3751
 3721 GGGCAGCTCAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3780
 3752 CAGAGCTCAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3811
 3781 CAGAGCTCAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3840
 3812 AGGTGAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3871
 3841 AGGTGAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3900
 3872 CCGTGTACAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3931
 3901 CCGTGTACAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3960
 3932 GAGTCTCAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 3986
 3961 GAGTCTCAGAGGATGCGGAAAGCCAGAGGATGCGGAAAGCCAGTGT 4015

RESULT 11

[illegible]

PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
xy

PS Disclosure; Fig 20; 387pp; English.

CC The present sequence encodes a human telomerase reverse transcriptase
CC (hTERT) variant from the present invention. The present invention also
CC describes the following methods: (A) determining whether a test compound
CC is a modulator of hTERT, by detecting the change in hTERT recombinant
CC protein or polynucleotide, on administration of the compound; (B)
CC preparation of recombinant telomerase by contacting a protein preparation
CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
CC protein in a sample by binding a relevant probe to the sample and
CC detecting the complex formed or in the case of RNA detection, amplifying
CC the product and correlating the presence of complex or amplification
CC product with presence of hTERT in the sample; and (D) increasing the
CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
CC the use of an agent that causes an increase in cell vertebrate cell
CC proliferation to create a medicament that inhibits ageing. A protein
CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
CC the manufacture of medicaments for inhibiting the effect of ageing or
CC cancer. Inhibitors of telomerase activity can be used to treat conditions
CC that are associated with high telomerase activity. A protein preparation
CC of hTERT can also be used in the new methods

Sequence 3855 BP; 651 A; 1300 C; 1226 G; 678 T; 0 U; 0 Other;

Query Match	98.5%	Score 3767.8;	DB 2;	Length 3855;
Best Local Similarity	100.0%	Score 3855.0;	DB 2;	Length 3855;

Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1,

QY	608	GCAGGCGTGGGCTGCTGCTGCGGACGTCGGGAAAGCCCTGAGCCCGGACACCCCGCGATGCG	67
Db	1	GCAGCGCTGCTGCTGCTGCGGACGTCGGGAAAGCCCTGAGCCCGGACACCCCGCGATGCG	60
QY	68	GCAGCGCTCCCGCTGCGCGAGCGGTGCGCTCCCTGCTGCGAGGACACTACCGACGAGTGT	127
Db	61	GCAGCGCTCCCGCTGCGCGAGCGGTGCGCTCCCTGCTGCGAGGACACTACCGAGGAGTGT	120
QY	128	GCAGCGTGGGCAAGTTCGTGCGGCGGCTGAGGGGCCCAAGGCTGGGCGGTGTGAGGCGG	187
Db	121	GCAGCGTGGGCAAGTTCGTGCGGCGGCTGAGGGGCCCAAGGCGGTGTGAGGCGG	180
QY	188	GCAGCCGCGGCTTTCGCGCGCTGAGTGGCCAGTGTGCTGATGTGCGTCCCGGACGC	247
Db	181	GCAGCCGCGGCTTTCGCGCGCTGAGTGGCCAGTGTGCTGATGTGCGTCCCGGACGC	240
QY	248	ACGCGCGCGCCCGCGCGCCCTCTCTTCGCGAGGTCTCTGCTGAAGAGCTGTGGC	307
Db	241	ACGCGCGCGCCCGCGCGCCCTCTCTTCGCGAGGTCTCTGCTGAAGAGCTGTGGC	300
QY	308	CCGAGGTGTCAGAGGCTGTGCGAGCGGCGGCGGCGAAGAGTGTGCGCTCGGCTTGGC	367
Db	301	CCGAGGTGTCAGAGGCTGTGCGAGCGGCGGCGGCGAAGAGTGTGCGCTTGGCTTGGC	360
QY	368	GCTGCTGGAACGAGGCGCCCGCGGAGCGCCCGCGGAGGCTTTCACCAACGAGTGGACCTA	427
Db	361	GCTGCTGGAACGAGGCGCCCGCGGAGCGCCCGCGGAGGCTTTCACCAACGAGTGGACCTA	420
QY	428	CCGCGCCAAACAGGTGACCGAGACGACCTGCGGAGGAGGCGGAGCGTGGGAGCTGTGTGG	487
Db	421	CCGCGCCAAACAGGTGACCGAGACGACCTGCGGAGGAGGCGGAGCGTGGGAGCTGTGTGG	480
QY	488	CCGCGGTGGGCAAGAGCTGTGTGTTACCTGTGGCAAGCTGCGGCTCTTTGTGTGTGT	547
Db	481	CCGCGGTGGGCAAGAGCTGTGTGTTACCTGTGGCAAGCTGCGGCTCTTTGTGTGTGT	540
QY	548	GGCTCCCAAGTACGAGCTACAGAGTGTGGGGCGCGGCTGTACCACTGGGCGTGGCAC	607
Db	541	GGCTCCCAAGTACGAGCTACAGAGTGTGGGGCGCGGCTGTACCACTGGGCGTGGCAC	600
QY	608	TGAAGCCCGGCGCCCGGCAACGCTTAAGTGAACCCGAAAGGCTGTGAGATGCGAACGGCG	667

Dp	601	TCAGGCCCCGGCCCCCGCCACACACGTAATGAGACCCCGAAGGGGTCTGGGATGCGAAAGGCG	660
Qy	668	CTGGAACCAATAGCGTCAAGGAGAGCCGGGGGTCCCTCTGGGCTTGCCAGCCCCGGGTGGAG	727
Dp	661	CTGGAAACCATAGCGCTCAGAGAGGCGGGGGGTCCCCCTGGGCTCTGCAGGCCCGGGGTGGAG	720
Qy	728	GAGCGCGGGGGAGTAGTGCACGCCGAAGTCTGCGGTGTGCCTCAAGAGAGCCCAAGCGGTGGCG	787
Dp	721	GAGGCGCGGGGGCAATGCGAACCCGAAGTCTGCGGTGTGCCTCAAGAGAGCCCAAGCGGTGGCG	780
Qy	768	TGCCCCCTAGCCCGAGCGGAGCGCCCGTTGGGCAAGGGGTCTTGGGCCACCCGGGCGAGAC	847
Dp	761	TGCCCCCTAGCGCGAGCGGAGCGCCCGTTGGGCAAGGGGTCTTGGGCCACCCGGGCGAGAC	840
Qy	848	GCGTGGACCGAGTAGCGGTGTTTCTGTGGGTGTCACTGCGACAGACCCGCGGAAGAGC	907
Dp	841	GCGTGGACCGAGTAGCACCGTGGTTTCTGTGGGTGTCACTGCGACAGACCCGCGGAAGAGC	900
Qy	908	CACCTCTTTGGAGGGGTGGCTCTCTGGCAGCGCGCACTCCACCCATCTGTTGGCGCGCA	967
Dp	901	CACCTCTTTGGAGGGGTGGCTCTCTGGCAGCGCGCACTCCACCCATCTGTTGGCGCGCGCA	960
Qy	968	GCACCAACGCGGGCCCCCATCCATCATGCGGGGCAACAAGTCCCTGGGGAACAAGCTTGTCC	1027
Dp	961	GCACCAACGCGGGCCCCCATCCATCATGCGGGGCAACAAGTCCCTGGGGAACAAGCTTGTCC	1020
Qy	1028	CCCCGTGTAGGCCGAGACCAAGCACTTCTTACTCTCAGGGGACAAAGAGCAAGCTTGG	1087
Dp	1021	CCCCGTGTAGGCCGAGACCAAGCACTTCTTACTCTCAGGGGACAAAGAGCAAGCTTGGCG	1080
Qy	1088	GCCCTCTTCTACTGACGCTCTGAGAGGCCAGAGCTGACATGCGCGCTGGAGGCTGTGGA	1147
Dp	1081	GCCCTCTTCTACTGACGCTCTGAGAGGCCAGAGCTGACATGCGCGCTGGAGGCTGTGGA	1140
Qy	1148	GACCACTTTTGTGGGTTTCAAGGCCCTGTGATGCCAGGACATCCCCGAGGTTGCCCGGCT	1207
Dp	1141	GACCACTTTTGTGGGTTTCAAGGCCCTGTGATGCCAGGACATCCCCGAGGTTGCCCGGCT	1200
Qy	1208	GCCCCAGCGCTACTGAGAAATGCGGGCCCCGTGTTCTGAGAGCTGTGGGAAACAAGCGCA	1267
Dp	1201	GCCCCAGCGCTACTGAGAAATGCGGGCCCCGTGTTCTGAGAGCTGTGGGAAACAAGCGCA	1260
Qy	1268	GTCGCCCTTACGGGGTGTGCTCTCAGAGAGCACTGCGCGCTCGAGCTCGGCTCACCCAGC	1327
Dp	1261	GTCGCCCTTACGGGGTGTGCTCTCAGAGAGCACTGCGCGCTCGAGCTCGGCTCACCCAGC	1320
Qy	1328	AGCGGATGTCTGTGTCGCCGGAGAAAGCCCAAGGGCTCTGTGAGCGGCCCCCGAGAGAGGA	1387
Dp	1321	AGCGGATGTCTGTGTCGCCGGAGAAAGCCCAAGGGCTCTGTGAGCGGCCCCCGAGAGAGGA	1380
Qy	1388	CACAGACCCCCGTCGCGCTGTGTCGAGCTGTCCGCGACACAGAGACCCCTGTGAGAGGTGA	1447
Dp	1381	CACAGACCCCCGTCGCGCTGTGTCGAGCTGTCCGCGACACAGAGACCCCTGTGAGAGGTGA	1440
Qy	1448	CGGCTTGTGTGGGCGCTGTGTCGCGCGGCTGTGTCGCCCAAGGCGCTCTGGGCTTCAAGCA	1507
Dp	1441	CGGCTTGTGTGGGCGCTGTGTCGCGCGGCTGTGTCGCCCAAGGCGCTCTGGGCTTCAAGCA	1500
Qy	1508	CAAGGAACGCGCGCTCTCTCAGAGAAACAACAAGATTCATCTCCTGTGGGAAGCATGCGAA	1567
Dp	1501	CAAGGAACGCGCGCTCTCTCAGAGAAACAACAAGATTCATCTCCTGTGGGAAGCATGCGAA	1560
Qy	1568	GCTTCGCTCAGAGAGCTGAAGTGAAGATGAGCGTGCAGGGAATGCGCTTGGTCGCGAG	1627
Dp	1561	GCTTCGCTCAGAGAGCTGAAGTGAAGATGAGCGTGCAGGGAATGCGCTTGGTCGCGAG	1620
Qy	1628	GAGGCCAAGGGGTTGGCTGTGTTCCGCGCGGACAGACCGTCTGCGTGAAGAGATCTCGGC	1687
Dp	1621	GAGGCCAAGGGGTTGGCTGTGTTCCGCGCGGACAGACCGTCTGCGTGAAGAGATCTCGGC	1680
Qy	1688	CAAGTTCTGCACTGCTGAATGAAGTGTACGTCGTCAAGCTGCTCAAGTCTTTCTTTTA	1747
Dp	1681	CAAGTTCTGCACTGCTGAATGAAGTGTACGTCGTCAAGCTGCTCAAGTCTTTCTTTTA	1740

OY	1748	GTCACGGAGACCAACGTTTCAAAAAGACAGCTCTTTTTCACCGGAGACATGCTGGAG	1807
Dp	1741	TGTCAAGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGATGCTGGAG	1800
OY	1808	CAAGTTCAAAGCATTTGGAATTCAGACAGCACTTTGAAGGGGTGCAGCTGCGGAGACTGTC	1867
Dp	1801	CAAGTTGCAAAAGCATTTGGAATTCAGACACACTTTGAAGAGGGGTGCAGCTGCGGAGACTGTC	1860
OY	1868	GGAAGCAGAGGTCAAGGCGACATTCGGGAAAGCCAGGCGCGCCCTGCTGACGTCCAGACTCG	1927
Dp	1861	GGAAGCAGAGGTCAAGGCGACATTCGGGAAAGCCAGGCGCGCCCTGCTGACGTCCAGACTCG	1920
OY	1928	CTTCATCCCAAGGCTGACGGGCTGCGGCGCATTTGTGAACATGCACTACGTCGTGGAGC	1987
Dp	1921	CTTCATCCCAAGGCTGACGGGCTGCGGCGCATTTGTGAACATGCACTACGTCGTGGAGC	1980
OY	1988	CAGAACTTCCGACAGAGAAAAGAGGGCCGAGAGGTCTCACTCAAGAGGTGAAGGACATGTT	2047
Dp	1981	CAGAACTTCCGACAGAGAAAAGAGGGCCGAGAGGTCTCACTCACTCAAGAGGTGAAGGACATGTT	2040
OY	2048	CAGCGTCTCACTACGACGCGGCGCGCGCCCTCTGCGGCGCTCTGTGTGTGGG	2107
Dp	2041	CAGCGTCTCACTACGACGCGGCGCGCGCCCTCTGCGGCGCTCTGTGTGTGGG	2100
OY	2108	CCTGGACATATTCACAGAGGCGCTGGCGGACCTTCGTGTGTGTGTGTGGGCGCCAGAGACC	2167
Dp	2101	CCTGGACATATTCACAGAGGCGCTGGCGGACCTTCGTGTGTGTGTGTGGGCGCCAGAGACC	2160
OY	2168	GCCGCTGAGCTGTA-----CATCCCCA	2191
Dp	2161	GCCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGGCGCGTACAGACACATCCCCA	2220
OY	2192	GGAACAGCTCACGAGAGGTCACTCGCAGCATATCAAAACCCAGAAACAATGACTCGGTGCG	2251
Dp	2221	GGAACAGCTCACGAGAGGTCACTCGCAGCATATCAAAACCCAGAAACAATGACTCGGTGCG	2280
OY	2252	TGCGTATGCGGTGTCGAAAGGCCGCCCATGTGGGCAAGCTTCGCAAGGCTTTCAAGAGCA	2311
Dp	2281	TGCGTATGCGGTGTCGAAAGGCCGCCCATGTGGGCAAGCTTCGCAAGGCTTTCAAGAGCA	2340
OY	2312	AGTCCCTAGTCCOAGTGCAGAGGGAGATCCCGCAGGGGCTCATCCTCTCCACGCTGCTGCA	2371
Dp	2341	AGTCCCTAGTCCOAGTGCAGAGGGAGATCCCGCAGGGGCTCATCCTCTCCACGCTGCTGCA	2400
OY	2372	GCTGTGTACGCGCGACATGAGAAACAAGCTGTTGCGGGATTTGCGCGGAGCAGGCTGCG	2431
Dp	2401	GCTGTGTGTACGCGCGACATGAGAAACAAGCTGTTGCGGGATTTGCGCGGAGCAGGCTGCG	2460
OY	2432	TCCGACGTTTGTGGATGATTTCTTGTTGTGTGACACCTCACTCAACCCAGCGAAACCT	2491
Dp	2461	TCCGACGTTTGTGGATGATTTCTTGTTGTGTGACACCTCACTCAACCCAGCGAAACCT	2520
OY	2492	TCTTCAGAACCTTGTCGAGGTGTCCCTGATGTGCTGCTGTGTGAACCTTGCGGAGGA	2551
Dp	2521	TCTTCAGAACCTTGTCGAGGTGTCCCTGATGTGCTGCTGTGTGAACCTTGCGGAGGA	2580
OY	2552	CAGTGTGTAACCTCCCTGTAGAGACAGAGGCCCTGGGTGGACAGGCTTTTGTACAGATGC	2611
Dp	2581	CAGTGTGTAACCTCCCTGTAGAGACAGAGGCCCTGGGTGGACAGGCTTTTGTACAGATGC	2640
OY	2612	CGGCCACAGGCTATTTCCCTGTGTGCGGCTGTGTGTGAATCCCGAACCTTGAGGTGC	2671
Dp	2641	CGGCCACAGGCTATTTCCCTGTGTGCGGCTGTGTGTGAATCCCGAACCTTGAGGTGC	2700
OY	2672	AGAGGCACTATCCAGATATGCCCGGACCTCACTACAGAGCAAGTCTCACTTCAACGCG	2731
Dp	2701	AGAGGCACTATCCAGATATGCCCGGACCTCACTACAGAGCAAGTCTCACTTCAACGCG	2760
OY	2732	GCTTCAGAGCTGGAGAGAAACATGCTGCGCAAACTTTTGGGCTCTTGCGGCTGAAGTGTG	2791
Dp	2761	GCTTCAGAGCTGGAGAGAAACATGCTGCGCAAACTTTTGGGCTCTTGCGGCTGAAGTGTG	2820

QY	2792	ACAGCCGTTTCTGGATTTGCAAGGTGAACAGCCCTCCAGACGGGTGTGACCAAACTTACA	2893
Db	2821	ACAGCCGTTTCTGGATTTGCAAGGTGAACAGCCCTCCAGACGGGTGTGACCAAACTTACA	2880
QY	2852	AGATCCCTCCGCTGACAGCGCTACAGGTTTCAACGATGTGTGTGCAAGCTCCCATTTATC	2911
Db	2881	AGATCCCTCCGCTGACAGCGCTACAGGTTTCAACGATGTGTGTGCAAGCTCCCATTTATC	2940
QY	2912	AGCAAGTTTGGAAAGACCCACATTTTTCCTGGCGGTCATCTGTGACAGCGCCCTCCCT	2971
Db	2941	AGCAAGTTTGGAAAGACCCACATTTTTCCTGGCGGTCATCTGTGACAGCGCCCTCCCT	3000
QY	2972	GCTACCTCCATCTGAAAGCCAGAGACCGAGGAGATGTGCTGTGGGGCCAGAGGCGCCGCG	3031
Db	3001	GCTACCTCCATCTGAAAGCCAGAGACCGAGGAGATGTGCTGTGGGGCCAGAGGCGCCGCG	3060
QY	3032	GCCCTCTGCCCTCCGAGAGCCGTGTGAGTGGGCTGTGTCCACAAAGCATTTCTGTCAAGCTGA	3093
Db	3061	GCCCTCTGCCCTCCGAGAGCCGTGTGAGTGGGCTGTGTCCACAAAGCATTTCTGTCAAGCTGA	3120
QY	3092	CTGCACACCGGTGTCACTTACGTGTCACTCTGTGGGTCACTGAGGACAGCCGACGACGAC	3151
Db	3121	CTGCACACCGGTGTCACTTACGTGTCACTCTGTGGGTCACTGAGGACAGCCGACGACGAC	3180
QY	3152	TGAATCGAAGCTCCGGGGGACAGCGTGACTGTGCTCGAGAGGCGCGACCAACCCGGCAC	3211
Db	3181	TGAATCGAAGCTCCGGGGGACAGCGTGACTGTGCTCGAGAGGCGCGACCAACCCGGCAC	3240
QY	3212	TGCCCTAGACTTGAAGACCATCTGTGACTGATGGCCACCGGCCACAGCCAGGCTCGAGA	3271
Db	3241	TGCCCTAGACTTGAAGACCATCTGTGACTGATGGCCACCGGCCACAGCCAGGCTCGAGA	3300
QY	3272	GCAACACACAGAGCCCTGTTCACGCGGGGCTTACGTCGCCAGAGGAGGAGGGCGGCGCCAC	3331
Db	3301	GCAACACACAGAGCCCTGTTCACGCGGGGCTTACGTCGCCAGAGGAGGAGGGCGGCGCCAC	3360
QY	3332	CACCCAGCCCGCACCGCTGGAGTCTTGAGGCGCTTGAATGATGTTTGGCCGAGGCTGTGCA	3391
Db	3361	CACCCAGCCCGCACCGCTGGAGTCTTGAGGCGCTTGAATGATGTTTGGCCGAGGCTGTGCA	3420
QY	3392	TGTCCGGCTGAAGGCTGATGTCCGGCTGAGAGGCTTGACGAGTGTCCAGCCAAAGGCTGA	3451
Db	3421	TGTCCGGCTGAAGGCTGATGTCCGGCTGAGAGGCTTGACGAGTGTCCAGCCAAAGGCTGA	3480
QY	3452	GTGTCCAGCACACTGCGCTTCTTCACTTCCCCACAGGCTGTGCGCTCGGCTTCCATCCACAG	3511
Db	3481	GTGTCCAGCACACTGCGCTTCTTCACTTCCCCACAGGCTGTGCGCTCGGCTTCCATCCACAG	3540
QY	3512	GCCAGCTTTTCTCACACAGGAGCCCGGCTTCCACTCCCCACATGTGAATATGTCCATCCCC	3571
Db	3541	GCCAGCTTTTCTCACACAGGAGCCCGGCTTCCACTCCCCACATGTGAATATGTCCATCCCC	3600
QY	3572	AGATTTCCGCAATGTTTCAACCCCTGTGCTGCTTCTTGTGCTTCCATCCCCACATCCAG	3631
Db	3601	AGATTTCCGCAATGTTTCAACCCCTGTGCTGCTTCTTGTGCTTCCATCCCCACATCCAG	3660
QY	3632	GTGACAGACCTTGAAAGAGACCTGTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTGCC	3691
Db	3661	GTGACAGACCTTGAAAGAGACCTGTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTGCC	3720
QY	3692	CTGTACACAGGCGAGACCTTGCACTTGATGTGGGGTCCCTGTGGGTCAAAATTTGGGGGGA	3751
Db	3721	CTGTACACAGGCGAGACCTTGCACTTGATGTGGGGTCCCTGTGGGTCAAAATTTGGGGGGA	3780
QY	3752	GGTCTGTGGAGTAAATATCTGAAATATGAGTTTTCACTTTTGAATAAAAAAAAAAAAAA	3811
Db	3781	GGTCTGTGGAGTAAATATCTGAAATATGAGTTTTCACTTTTGAATAAAAAAAAAAAAAA	3840
QY	3812	AAAAAAAAAAAAA 3824	
Db	3841	AAAAAAAAAAAAA 3853	

RESULT 2
AAV72117
ID AAV72117 standard; cDNA; 4042 BP.
XX
AC AAV72117;
XX
DT 24-MAY-1999 (first entry)
XX
DE Human catalytic telomerase sub-unit cDNA.
XX
KW Human; catalytic telomerase subunit; therapy; diagnosis; htc; assay;
KM modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
KM ageing; antisense; neoplastic cell; telomerase-related condition;
KM tumour cell; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 63..3461
FT FT /*tag= a
FT FT /product= "catalytic telomerase subunit"
XX
PN MO859040-A2.
XX
PD 30-DEC-1998.
XX
PF 09-JUN-1998; 98WO-EP003468.
XX
PR 20-JUN-1997; 97DE-01026329.
PR 26-MAR-1998; 98DE-01013274.
PR 14-APR-1998; 98DE-01016496.
XX
PA (FARB) BAYER AG.
XX
PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;
XX
DR MPI; 1999-081216/07.
XX
DR P-PDB; AAW90251.
XX
PT New catalytically active subunit of human telomerase - used in the
PT modulation of telomerase activity, particularly for treating cancer and
PT ageing.
XX
PS Claim 4; Fig 1; 76pp; German.
XX
CC This sequence encodes a novel human catalytic telomerase sub-unit (htc).
CC The encoded protein can be used in screening assays to identify
CC modulators of telomerase and to treat or inhibit cellular disorders,
CC death, defects and/or other pathological processes involving telomerase,
CC particularly cancer and ageing (also suitable for this are agents that
CC stimulate, inhibit or mimic the activity of the subunit). Antisense
CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC and fragments of the protein, used as probes or primers, are used to
CC diagnose telomerase-related conditions (especially neoplasia) by (i)
CC detecting abnormal levels of the subunit protein in body fluids or
CC tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC Expression of the nucleic acid encoding the subunit mRNA is confined to
CC tumour cells, in contrast to the ubiquitous expression of the telomerase
CC RNA subunit
XX
SQ Sequence 4042 BP; 684 A; 1364 C; 1277 G; 717 T; 0 U; 0 Other;
Query Match 93.8%; Score 3586; DB 2; Length 4042;
Best Local Similarity 94.6%; Pred No. 0;
Matches 3824; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

61 CGATGCCGCGCGCTCCCGCTGCCGAGCGGTGCGCTCCCTGCTGCGCAAGCACTACCGCG 120
121 AGGTGCTGCGCGCTGCGCAAGCTTGCGGCGGCTGAGGCGCCCAAGGCTGCGCGCTGTC 180
121 AGGTGCTGCGCGCTGCGCAAGCTTGCGGCGGCTGAGGCGCCCAAGGCTGCGCGCTGTC 180
181 AGCGCGGAGACCCCGCGCGCTTTCGCGCGCTGAGGCGCAAGTGTGCTGAGTGCCTT 240
181 AGCGCGGAGACCCCGCGCGCTTTCGCGCGCTGAGGCGCAAGTGTGCTGAGTGCCTT 240
181 AGCGCGGAGACCCCGCGCGCTTTCGCGCGCTGAGGCGCAAGTGTGCTGAGTGCCTT 240
241 GGGACGACGAGCG 300
241 GGGACGACGAGCG 300
301 TGGTGGCCCGAGTGTGTCAGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 360
301 TGGTGGCCCGAGTGTGTCAGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 360
361 GCTTGGCGCGTGTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
361 GCTTGGCGCGTGTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
421 GCAGCTACCTGCCCAACAGCGTGAACCGCACTGCGGCGGAGCGCGCGCGCGCGCGCG 480
421 GCAGCTACCTGCCCAACAGCGTGAACCGCACTGCGGCGGAGCGCGCGCGCGCGCGCG 480
481 TGGTGGCGCGCGTGTGCGGCGGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTT 540
481 TGGTGGCGCGCGTGTGCGGCGGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTT 540
541 TGGTGGCGCGTGTGCGGCGGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
541 TGGTGGCGCGTGTGCGGCGGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
601 CTGCACTACAGCG 660
601 CTGCACTACAGCG 660
601 CTGCACTACAGCG 660
661 AACGGGCTGGAACCACTACGCTGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
661 AACGGGCTGGAACCACTACGCTGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
721 GTGCGAGAGAGCG 780
721 GTGCGAGAGAGCG 780
781 GTGCGCGTGGCG 840
781 GTGCGCGTGGCG 840
841 GCGAGAGCGGTGAGCGAGTGAACGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
841 GCGAGAGCGGTGAGCGAGTGAACGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
901 AAGAAGCACTCTTGTGAGGAGGCGCTGTGAGACGCGCACTGCCACCATCGATG 960
901 AAGAAGCACTCTTGTGAGGAGGCGCTGTGAGACGCGCACTGCCACCATCGATG 960
901 AAGAAGCACTCTTGTGAGGAGGCGCTGTGAGACGCGCACTGCCACCATCGATG 960
961 GCGCGAGACACACG 1020
961 GCGCGAGACACACG 1020
1021 CTGTGCGCGCGGTGATACGCGGAGACCAAGCACTTCTCTACTCTCTCAAGCGCAAGAG 1080
1021 CTGTGCGCGCGGTGATACGCGGAGACCAAGCACTTCTCTACTCTCTCAAGCGCAAGAG 1080
1081 AGCTGCGCGCTTCTTCTACTACTGAGCTTGTGAGGCGCGCACTGAGCTGCGAGGCG 1140
1081 AGCTGCGCGCTTCTTCTACTACTGAGCTTGTGAGGCGCGCACTGAGCTGCGAGGCG 1140
1141 TCGTGAAGACATCTTCTGAGGCTTCAAGGCGCTGATGCGAGGAGCTCCCGCGAGGTTGC 1200
1141 TCGTGAAGACATCTTCTGAGGCTTCAAGGCGCTGATGCGAGGAGCTCCCGCGAGGTTGC 1200

QY	1201	CCCGGCTGCCCCAGGGCTACTGGCAAAATGCGGCCCTCTGTTTCTGAGCTGCTTGGGAAAC	1260
Db	1201	CCCGGCTGCCCCAGGGCTACTGGCAAAATGCGGCCCTCTGTTTCTGAGCTGCTTGGGAAAC	1260
QY	1261	ACGCGAGTGGCCCTACGGGGTGTCTCTCAAGACACACTGGCCGCTGGAGTGGAGTCA	1320
Db	1261	ACGCGAGTGGCCCTACGGGGTGTCTCTCAAGACACACTGGCCGCTGGAGTGGAGTCA	1320
QY	1321	CCCGAGCAGCCGCTGTCTGTGCCCCGGAGAAACCCCAAGGCTCTTGTGGCGGCCCCGAGG	1380
Db	1321	CCCGAGCAGCCGCTGTCTGTGCCCCGGAGAAACCCCAAGGCTCTTGTGGCGGCCCCGAGG	1380
QY	1381	AGGAGGACACAGACCCCGCTCGCTGATGACAGTCTCTCGCCAGACACAGACCCCTGAC	1440
Db	1381	AGGAGGACACAGACCCCGCTCGCTGATGACAGTCTCTCGCCAGACACAGACCCCTGAC	1440
QY	1441	AGGTGTACGGCTTCTGTGGGGGCTTCTGCTCGCCGCTGTGCTGCCAGGCTCTTGGGGCT	1500
Db	1441	AGGTGTACGGCTTCTGTGGGGGCTTCTGCTCGCCGCTGTGCTGCCAGGCTCTTGGGGCT	1500
QY	1501	CCAGGACACACGACGCGCTTCTCTCAGGAAACACAAAGAATCTCTCCCTGGGGAAAC	1560
Db	1501	CCAGGACACACGACGCGCTTCTCTCAGGAAACACAAAGAATCTCTCCCTGGGGAAAC	1560
QY	1561	ATGCCAAGCTCTCGCTTGCAGAGAGCTGAGTGGAAATGAGCGTGGCGGACCTGGCTTGGC	1620
Db	1561	ATGCCAAGCTCTCGCTTGCAGAGAGCTGAGTGGAAATGAGCGTGGCGGACCTGGCTTGGC	1620
QY	1621	TGCGCAGAGCCCAAGGGTGTGCTGTCTTCGCGCGCAGACACACGCTCTGCGTAGAGGA	1680
Db	1621	TGCGCAGAGCCCAAGGGTGTGCTGTCTTCGCGCGCAGACACACGCTCTGCGTAGAGGA	1680
QY	1681	TCTTGCCCAAGTTCCTGCACAGCGCTGAGATGATGTATGATCGTGAAGTGTCAAGTCTT	1740
Db	1681	TCTTGCCCAAGTTCCTGCACAGCGCTGAGATGATGTATGATCGTGAAGTGTCAAGTCTT	1740
QY	1741	TCTTTATATGTCACGAGACACAGTTTCAAAAGAAACAGGCTCTTTTCTTACCGAGAGATG	1800
Db	1741	TCTTTATATGTCACGAGACACAGTTTCAAAAGAAACAGGCTCTTTTCTTACCGAGAGATG	1800
QY	1801	TCTGAGACAGTGTGGAAAGCAATTGGAAATCAACAAGCACTTGAAGAAGGTGAGTGGGG	1860
Db	1801	TCTGAGACAGTGTGGAAAGCAATTGGAAATCAACAAGCACTTGAAGAAGGTGAGTGGGG	1860
QY	1861	AGCTGTGCGAAGCAGAGGTCAAGGCAATCGGGAAGCCAGGCCCGCTGTGACGTCA	1920
Db	1861	AGCTGTGCGAAGCAGAGGTCAAGGCAATCGGGAAGCCAGGCCCGCTGTGACGTCA	1920
QY	1921	GACTCCGCTTATCATCCCCCAAGCTGACGGGCTGCGGCCGATTGTGAATATGGAATCAAGTGG	1980
Db	1921	GACTCCGCTTATCATCCCCCAAGCTGACGGGCTGCGGCCGATTGTGAATATGGAATCAAGTGG	1980
QY	1981	TGGAGACCAAAAGCTTCCGACAGAAAAAGAGGCGCGAGCGTCACTTCAGAGGGTGAAG	2040
Db	1981	TGGAGACCAAAAGCTTCCGACAGAAAAAGAGGCGCGAGCGTCACTTCAGAGGGTGAAG	2040
QY	2041	CACGTGTTACAGGTGTCAACTACAGAGGGGGCGGGCCGCCGCTCTTGGAGCGCTCTTG	2100
Db	2041	CACGTGTTACAGGTGTCAACTACAGAGGGGGCGGGCCGCCGCTCTTGGAGCGCTCTTG	2100
QY	2101	TGCTGGGCTTGGACGATATCCACAGGGCTTGGCGCACTTGTGCTCGTGTGGGCGCC	2160
Db	2101	TGCTGGGCTTGGACGATATCCACAGGGCTTGGCGCACTTGTGCTCGTGTGGGCGCC	2160
QY	2161	AGGACCGGCGCTGAGCTGTA-----CA	2184
Db	2161	AGGACCGGCGCTGAGCTGTA-----CA	2184
QY	2185	TCCCCCAGAACAGGCTCAACGAGAGTCACTCGCAGACATCATMAACCCCAAGACAGCTACT	2244
Db	2221	TCCCCCAGAACAGGCTCAACGAGAGTCACTCGCAGACATCATMAACCCCAAGACAGCTACT	2280

QY	2245	GGGTGGTGGGATATCCCGGTGTCAGAAAGCCGCAATGGGCAAGTCCGCAAGGCTTCA	2300
Db	2281	GGGTGGTGGGATATCCCGGTGTCAGAAAGCCGCAATGGGCAAGTCCGCAAGGCTTCA	2340
QY	2305	AAA-----	2307
Db	2341	AGAGCGACGTCTTCACTTGAACAGACTCAAGCCGTATGTCAGAGTTCTGTGCTCAC	2400
QY	2308	-----	2307
Db	2401	TGCAGAGAACAGCCCGGTGAGGAGTGCCTGCTCATGAGCAGAGCTCTCCCTGAATG	2460
QY	2308	-----	2307
Db	2461	AGGCGAGATGGCTCTTTCAGACTCTTTCACGCTTCATGTGCAACACGCCGTGCGCA	2520
QY	2348	-----GGCAAGCTCAACGTCAGAGTCCAGGGGATCCCGCAGGGCTCCATCCGCTCACGC	2360
Db	2521	TCAAGGGGGAATGCTCAAGCTCAGTGTCCAGGGGATCCCGCAGGGCTCCATCCCTTCACGC	2580
QY	2363	TGCTTTCAGACTGTGTCTACCGGCAATGAGAAACAAGCTTTTGGCGGGAATTGGCCGG	2422
Db	2581	TGCTTTCAGACTGTGTCTACCGGCAATGAGAAACAAGCTTTTGGCGGGAATTGGCCGG	2644
QY	2423	ACGGCTCTCTGTGGTTGGTGGATGATTTCTTGTGTGACACTCAACCTCACCCAG	2480
Db	2641	ACGGCTCTCTGTGGTTGGTGGATGATTTCTTGTGTGACACTCAACCTCACCCAG	2700
QY	2483	CGAAACCTTCTCTCAGAACCTTGTCGAGGTGTCCTGAGTATGGCTGCGTGTGAACCT	2542
Db	2701	CGAAACCTTCTCTCAGAACCTTGTCGAGGTGTCCTGAGTATGGCTGCGTGTGAACCT	2760
QY	2543	TGCGGAACAGAGTGGTGAATTCCTCTGTAAGAAAGAGAGCCCTGAGTGGACAGGCTTTTG	2602
Db	2761	TGCGGAACAGAGTGGTGAATTCCTCTGTAAGAAAGAGAGCCCTGAGTGGACAGGCTTTTG	2820
QY	2603	TTTCAGATCCGGCCCAACGGCTTATTCCTCTGTGTGGCTCTGTGTGTGATACCCGAGCC	2662
Db	2821	TTTCAGATCCGGCCCAACGGCTTATTCCTCTGTGTGGCTCTGTGTGTGATACCCGAGCC	2880
QY	2663	TGAGAGTTCAGAGCACTACTCCAGCTATGCCCCGACCTGCATCAGAGCAAGCTCTCACCT	2722
Db	2881	TGAGAGTTCAGAGCACTACTCCAGCTATGCCCCGACCTGCATCAGAGCAAGCTCTCACCT	2940
QY	2723	TCAACCCGCGCTTCAAGCTTGGAGGAATGCTGTGCAACTCTTTGGGGTCTTGGCGC	2782
Db	2941	TCAACCCGCGCTTCAAGCTTGGAGGAATGCTGTGCAACTCTTTGGGGTCTTGGCGC	3000
QY	2783	TGAAGTTCACAGCTGTCTGTGATTTGACAGTGGACAGCTCTCAACGGTGTGCACCA	2842
Db	3001	TGAAGTTCACAGCTGTCTGTGATTTGACAGTGGACAGCTCTCAACGGTGTGCACCA	3060
QY	2843	ACATCTACAGATCTCTCTGTGTGACGGCGTACAGCTTCAACGATGTGTGTGACGCTCC	2902
Db	3061	ACATCTACAGATCTCTCTGTGTGACGGCGTACAGCTTCAACGATGTGTGTGACGCTCC	3120
QY	2903	CATTTCATTCAGCAAGTTTGAAGAACCCCACTTTTCTGCGCGGTATCTCTGACACGG	2962
Db	3121	CATTTCATTCAGCAAGTTTGAAGAACCCCACTTTTCTGCGCGGTATCTCTGACACGG	3180
QY	2963	CTCTCCCTCTGTATCTCATCTCTGAAGCAAGACGAGGATGTGCTGTGGGGCCAAAG	3022
Db	3181	CTCTCCCTCTGTATCTCATCTCTGAAGCAAGACGAGGATGTGCTGTGGGGCCAAAG	3240
QY	3023	GGCGCGCGCCCTCTGCTCCCTCCAGGCGGTGACAGTGGCTGTGACCAAGACTTCTGCG	3082
Db	3241	GGCGCGCGCCCTCTGCTCCCTCCAGGCGGTGACAGTGGCTGTGACCAAGACTTCTGCG	3300
QY	3083	TCAAGCTGATCCGACACCGGTGTCAACCTTACGTGACACTCTGTGGGGTCACTGAGCAGACC	3142
Db	3301	TCAAGCTGATCCGACACCGGTGTCAACCTTACGTGACACTCTGTGGGGTCACTGAGCAGACC	3360
QY	3143	AGAGCGAGCTGAGTCGAAAGCTCCCGGGACGAGCTGATGCTGCTGGAAGCCGCAACCA	3202

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Db 3361 AGACGACACTGATGCGAAGCTCCCGGGGACGAGCTGACTGCGCTTGGAGCCCGACGCCA 3420
QY 3203 ACCGGGCACTGCGCTCCCTCAGACCTTCAAGACATCTCTGAGTATGACCCCGCCACAGCC 3262
Db 3421 ACCGGGCACTGCGCTCCCTCAGACCTTCAAGACATCTCTGAGTATGACCCCGCCACAGCC 3480
QY 3263 AGGCGGAGAGAGACACACGAGAGCGCTCTGACGCGCGCTCTGAGTATGAGTATGAGGAGG 3322
Db 3481 AGGCGGAGAGAGACACACGAGAGCGCTCTGACGCGCGCTCTGAGTATGAGTATGAGGAGG 3540
QY 3323 GGGGGCCCAACACACGAGCGCCGACCGCTGGAGTCTGAGGCTGAGTATGAGTATGAGGAGG 3382
Db 3541 GGGGGCCCAACACACGAGCGCCGACCGCTGGAGTCTGAGGCTGAGTATGAGTATGAGGAGG 3600
QY 3383 AGGCGTGTATGCTGCGCTGAGAGGCTGAGTATGCGGCTGAGGCGCTGAGGCGAGTATGAGG 3442
Db 3601 AGGCGTGTATGCTGCGCTGAGAGGCTGAGTATGCGGCTGAGGCGCTGAGGCGAGTATGAGG 3660
QY 3443 AAGGCTGTATGCTGCGCTGAGAGGCTGAGTATGCGGCTGAGGCGCTGAGGCGAGTATGAGG 3502
Db 3661 AAGGCTGTATGCTGCGCTGAGAGGCTGAGTATGCGGCTGAGGCGCTGAGGCGAGTATGAGG 3720
QY 3503 CAGCCGAGAGGAGCTTTCTCTGACAGAGCGCGCTTCACTCCCGCAGATAGGAGATAG 3562
Db 3721 CAGCCGAGAGGAGCTTTCTCTGACAGAGCGCGCTTCACTCCCGCAGATAGGAGATAG 3780
QY 3563 TCCATCCCGCAGATTGCGCATTTGTTACCCCTGCGCTTCCCTTCCCTTCCACCCCG 3622
Db 3781 TCCATCCCGCAGATTGCGCATTTGTTACCCCTGCGCTTCCCTTCCCTTCCACCCCG 3840
QY 3623 ACCATCCAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3682
Db 3841 ACCATCCAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
QY 3683 AGGTGTGCGCTGTATGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3742
Db 3901 AGGTGTGCGCTGTATGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3960
QY 3743 TTGGGGGAGAGTGTGCTGTGAGAGTAAATACGAAATATAGATTTTCACTTTTGAAGAA 3802
Db 3961 TTGGGGGAGAGTGTGCTGTGAGAGTAAATACGAAATATAGATTTTCACTTTTGAAGAA 4020
QY 3803 AAAAAAAAAAAAAAAAAAAAAA 3824
Db 4021 AAAAAAAAAAAAAAAAAAAAAA 4042

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RESULT 3
 AAV22428
 ID AAV22428 standard; cDNA; 4037 BP.
 XX AAV22428;
 AC 13-AUG-1998 (first entry)
 DT
 XX Human telomerase reverse transcriptase encoding cDNA refined sequence.
 DE
 XX Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;
 KW cell proliferation; cancer; ageing; ribonucleoprotein; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 56..3454
 FT /*tag= a
 FT /product= "telomerase reverse transcriptase"
 FT /note= "refined sequence"
 XX
 XX GB2317891-A.
 XX 08-APR-1998.
 PD

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PF 01-OCT-1997; 97GB-00020890.
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
XX Andrews WH;
XX WPI, 1998-171633/16.
XX P-PDB; AAM56113.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variance - are useful in the diagnosis, prognosis and treatment of cell
XX proliferation conditions especially cancer and ageing.
XX
XX Example 1; Fig 74; 387bp; English.
XX
XX The present sequence encodes human telomerase reverse transcriptase
XX (hTERT), which is a ribonucleoprotein. The present invention also
XX describes the following methods: (A) determining whether a test compound
XX is a modulator of hTERT by detecting the change in hTERT recombinant
XX protein or polynucleotide, on administration of the compound; (B)
XX preparation of recombinant telomerase by contacting a protein preparation
XX of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
XX protein in a sample by binding a relevant probe to the sample and
XX detecting the complex formed or in the case of RNA detection, amplifying
XX the product and correlating the presence of complex or amplification
XX product with presence of hTERT in the sample; and (D) increasing the
XX proliferation of a vertebrate cell by increasing hTERT expression; and (E)
XX the use of an agent that causes an increase in cell vertebrate cell
XX proliferation to create a medicament that inhibits ageing. A protein
XX preparation of hTERT and the polynucleotide encoding hTERT can be used in
XX the manufacture of medicaments for inhibiting the effect of ageing or
XX cancer. Inhibitors of telomerase activity can be used to treat conditions
XX that are associated with high telomerase activity. A protein preparation
XX of hTERT can also be used in the new methods
XX
XX SQ Sequence 4037 BP; 682 A; 1362 C; 1275 G; 714 T; 0 U; 4 Other;
XX
XX Query Match 93.4%; Score 3571; DB 2; Length 4037;
XX Best Local Similarity 94.4%; Pred. No. 0;
XX Matches 3809; Conservative 4; Mismatches 4; Indels 218; Gaps 2;
XX
QY 8 GAGGCGTGTGCTCTGCTGCGGACAGTGGGAAGCCCTGGCCCGCCAGCCCGGATGCC 67
Db 1 GAGGCGTGTGCTCTGCTGCGGACAGTGGGAAGCCCTGGCCCGCCAGCCCGGATGCC 60
QY 68 GCGGCTCCCGCTGCGGACAGCGGTGCGCTCCCTGCTGCGGACAGTGGGAAGCCCTGGCC 127
Db 61 GCGGCTCCCGCTGCGGACAGCGGTGCGCTCCCTGCTGCGGACAGTGGGAAGCCCTGGCC 120
QY 128 GCGGCTGCGGACAGTGTGCGGCGCGCTGGGGCCCGCAGGGCTGGGCTGGTGCAGCGCG 187
Db 121 GCGGCTGCGGACAGTGTGCGGCGCGCTGGGGCCCGCAGGGCTGGGCTGGTGCAGCGCG 180
QY 188 GAGCCCGGCGCTTTCGCGCGGTGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
Db 181 GAGCCCGGCGCTTTCGCGCGGTGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 248 ACGGCGCGCGCGCGCGCGCGCGCTCTCTTCCGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCT 307
Db 241 ACGGCGCGCGCGCGCGCGCGCGCTCTCTTCCGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 308 CCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGAGAGAGAGTGTGCTGCTGCTGCTGCTGCT 367

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Db	301	CCGAGTGTCTGCAGAGGCTGTGCAGAGGCGCGCCGAAAGACGTGTGGCTTGTGGCTTTCGC	360
QY	368	GCTGTGTGACCGGAGCCCGCGGGAGCCCCCGAGAGCTTTCACACACAGCGTGCAGACTA	427
Db	361	GCTGTGTGACCGGAGCCCGCGGGAGCCCCCGAGGCTTTCACACACAGGTGCAGACTA	420
QY	428	CCTGGCCCAACAGGTTGACCGACGACTGTGGGGAGCGGGGCGTGGGGCTGTCTGTGCG	487
Db	421	CTTGGCCCAACAGGTTGACCGACGACTGTGGGGAGCGGGGCGTGGGGCTGTCTGTGCG	480
QY	488	CCGCGTGGCGACGACGTGTCTGTTTCACTGTGTGGACGCTGTGCGGCTTTTGTGTGT	547
Db	481	CCGCGTGGCGACGACGTGTCTGTTTCACTGTGTGGACGCTGTGCGGCTTTTGTGTGT	540
QY	548	GCGTCCCAAGCTGCGCTTACAGGTGTGCGGACCGCGCTGTACCAAGTTGGCGCTGCAC	607
Db	541	GCGTCCCAAGCTGCGCTTACAGGTGTGCGGACCGCGCTGTACCAAGTTGGCGCTGCAC	600
QY	608	TGAGGCGCGGCCCCCGCCACACGCTAGTGTGACCCCGAAGGCGCTGTGGATGTGGAACGGGCG	667
Db	601	TGAGGCGCGGCCCCCGCCACACGCTAGTGTGACCCCGAAGGCGCTGTGGATGTGGAACGGGCG	660
QY	668	CTGGAACCAATAGCGTTCAGGAGAGCGGAGTCCCTGTGGGCTTGCAGCGCCCGGTTGCGAG	727
Db	661	CTGGAACCAATAGCGTTCAGGAGAGCGGAGTCCCTGTGGGCTTGCAGCGCCCGGTTGCGAG	720
QY	728	GAGGGGCGGGGCGCAATGTCCAGCCGAAGTGTGCGCTTGTGCTTGCACAGAGGCCCAAGCGCGT	787
Db	721	GAGGGGCGGGGCGCAATGTCCAGCCGAAGTGTGCGCTTGTGCTTGCACAGAGGCCCAAGCGCGT	780
QY	788	TGCCCCCTGAGCCGAGACGCGCCGTTGGAGCAGGGGTTCTTGGGCGCACCCCGGACAGAC	847
Db	781	TGCCCCCTGAGCCGAGACGCGCCGTTGGAGCAGGGGTTCTTGGGCGCACCCCGGACAGAC	840
QY	848	GCGTGGACCGAGTACCGTGGTTTCTGTGTGTGTCTACTGTGCACACCCGCGGAAGAAC	907
Db	841	GCGTGGACCGAGTACCGTGGTTTCTGTGTGTGTCTACTGTGCACACCCGCGGAAGAAC	900
QY	908	CACCTCTTTGAGAGGATGACCTCTGTGGACAGCGGCCACTCCACCGATCCGTGGGCGCGACA	967
Db	901	CACCTCTTTGAGAGGATGACCTCTGTGGACAGCGGCCACTCCACCGATCCGTGGGCGCGACA	960
QY	968	GCACCAACGCGGAGCCCCCAATCCACATCGGAGCACACGTCCTTGGAGACAGCGCTTGTCC	1027
Db	961	GCACCAACGCGGAGCCCCCAATCCACATCGGAGCACACGTCCTTGGAGACAGCGCTTGTCC	1020
QY	1028	CCCGGTGTACGCGCGAGACCAAGCACTTCTCTCACTCTCAAGCGGACAGAGAGCGAGCTGCG	1087
Db	1021	CCCGGTGTACGCGCGAGACCAAGCACTTCTCTCACTCTCAAGCGGACAGAGAGCGAGCTGCG	1080
QY	1088	GCCCTCTCTCTCACTCAAGCTCTCTGAGGCCACAGCTTGAATGCGGCTTGGAGAGCTTGTGA	1147
Db	1081	GCCCTCTCTCTCACTCAAGCTCTCTGAGGCCACAGCTTGAATGCGGCTTGGAGAGCTTGTGA	1140
QY	1148	GACCACTTTTCTGGGTTTCCAGGCCCTTGAATGTCCAGAGACTCCCGCAGATTGCCCGGCT	1207
Db	1141	GACCACTTTTCTGGGTTTCCAGGCCCTTGAATGTCCAGAGACTCCCGCAGATTGCCCGGCT	1200
QY	1208	GCCCCAGCGCTACTGTGCAATGTGCGCCCTGTGTTTGTGAGCTGTGTTGGAAACACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGTGCAATGTGCGCCCTGTGTTTGTGAGCTGTGTTGGAAACACGCGCA	1260
QY	1268	GTCGCCCTTACGGGGGTCTCTCAAGCGACTGCGCGCTGCGAGGTGGGTGTACCCCAAGC	1327
Db	1261	GTCGCCCTTACGGGGGTCTCTCAAGCGACTGCGCGCTGCGAGGTGGGTGTACCCCAAGC	1320
QY	1328	AGCGCGTCTGTGCGCCGAGAAACCCCAAGGCTCTGTGCGGCGCCCCCAAGAGAGAGAA	1387
Db	1321	AGCGCGTCTGTGCGCCGAGAAACCCCAAGGCTCTGTGCGGCGCCCCCAAGAGAGAGAA	1380
QY	1388	CACAGACCCCGTCCGCTGTGTGACACTGTCCGCGACACAGACCCCTTGGACAGTTGA	1447

[illegible]

QY	2310	CAAGCTCTAACGCTCCAGGTGTCAGAGGGATCCCGAGGGGCTCCATCCCTCTCCAGCTGCTCG	2365
Db	2521	CAAGTCTTAACGTCCAGTGCAGAGGGATCCCGAGGGGCTCCATCCCTCTCCAGCTGCTCG	2580
QY	2370	CAGCTCTGTGCTACGGCGCATATGGAAGACAAGTCTTTGGGGGGATTTGGCGGGACGGGCT	2423
Db	2581	CAGCTGTGTGCTACGGCGCATATGGAAGACAAGTCTTTGGGGGGATTTGGCGGGACGGGCT	2640
QY	2430	GCTCCTGTGCTTTGTGTGATGATTTCTGTGTGTGACACTCTCACTCCACCCACGCGAAAC	2485
Db	2641	GCTCCTGTGCTTTGTGTGATGATTTCTGTGTGTGACACTCTCACTCCACCCACGCGAAAC	2700
QY	2480	CTTCTCTCAGAGACCTCTGTGTCGAGGTGTCCCTGATATGCTGTGCTGCTGTGAACTTGGGAA	2549
Db	2701	CTTCTCTCAGAGACCTCTGTGTCGAGGTGTCCCTGATATGCTGTGCTGCTGTGAACTTGGGAA	2768
QY	2550	GACAGTGTGTAACCTCCCTGTATGAAGACGAGGCGCTGTGTGTGACAGGCTTTTGTTCAGAT	2609
Db	2761	GACAGTGTGTAACCTCCCTGTATGAAGACGAGGCGCTGTGTGTGACAGGCTTTTGTTCAGAT	2820
QY	2610	GCGGCGCCACGGGCTTATTCCTCTGTGTGGGCTGTCTGTGATACCGGACCTGTGAGGT	2665
Db	2821	GCGGCGCCACGGGCTTATTCCTCTGTGTGGGCTGTCTGTGATACCGGACCTGTGAGGT	2880
QY	2670	GCAGAGGCACATCTACAGCTATAGCCGGAGCTCCATCAGAGCGAGTCCACCTTCAACG	2729
Db	2881	GCAGAGGCACATCTACAGCTATAGCCGGAGCTCCATCAGAGCGAGTCCACCTTCAACG	2940
QY	2730	GCGCTTCAAAGCTGGGAGGAACATGCTGTGCAAACTCTTTGGGGTCTTGGCGCTGAAAGT	2789
Db	2941	GCGCTTCAAAGCTGGGAGGAACATGCTGTGCAAACTCTTTGGGGTCTTGGCGCTGAAAGT	3000
QY	2790	TCACAGCGCTGTTCTGATATTTGCAGGTTCAGGTCAACAGCTCCAGACGGGTGTGACCAACATTA	2849
Db	3001	TCACAGCGCTGTTCTGATATTTGCAGGTTCAGGTTCAGGTTCAGACGCTCCAGACGGGTGTGACCAACATTA	3060
QY	2850	CAGATCTCTCTGTGTCGACGGGTACAGGTTTACGCAATGTGCTGTGACGCTTCCATTTC	2909
Db	3061	CAGATCTCTCTGTGTCGACGGGTACAGGTTTACGCAATGTGCTGTGACGCTTCCATTTC	3120
QY	2910	TCAGCAATTTGGAAGAACCCACATTTTCTGTGGGCTCATCTCTGTGACAGGCTCCCT	2969
Db	3121	TCAGCAATTTGGAAGAACCCACATTTTCTGTGGGCTCATCTCTGTGACAGGCTCCCT	3180
QY	2970	CTGTACTCTCCATCTTGAAAGCCACAGAACGCAAGGATGTGCTGTGGGGGCTCAAGGGCGCCG	3029
Db	3181	CTGTACTCTCCATCTTGAAAGCCACAGAACGCAAGGATGTGCTGTGGGGGCTCAAGGGCGCCG	3240
QY	3030	CGGCGCTGTGCCCTCCGAGGCGGTGCACTGTGCTGTGCAACAGCATTCCTGTCAAGCT	3089
Db	3241	CGGCGCTGTGCCCTCCGAGGCGGTGCACTGTGCTGTGCAACAGCATTCCTGTCAAGCT	3300
QY	3090	GACTTCGACCCGTGTACCTTACGTCACCTTCTGGGGTCACTTCAGAGACGCCAGCGCA	3149
Db	3301	GACTTCGACCCGTGTACCTTACGTCACCTTCTGGGGTCACTTCAGAGACGCCAGCGCA	3360
QY	3150	GCTGAGTGGAAAGTCCCGGGAGACGACCTGACTGTCCCTGTGAGGCGCGAGCCAACCCGGC	3209
Db	3361	GCTGAGTGGAAAGTCCCGGGAGACGACCTGACTGTCCCTGTGAGGCGCGAGCCAACCCGGC	3420
QY	3210	ACTGGCTCTAATCTTCAAGACCATCTCTGAGTGTGCTCACCCGCTCCACAGCTAGCGCGA	3269
Db	3421	ACTGGCTCTAATCTTCAAGACCATCTCTGAGTGTGCTCACCCGCTCCACAGCTAGCGCGA	3480
QY	3270	GAGCAGACACGACGAGCCCTGTCAAGCCGGGCTCTTACGTCCAGGAGGAGGGAGCGGCT	3329
Db	3481	GAGCAGACACGACGAGCCCTGTCAAGCCGGGCTCTTACGTCCAGGAGGAGGGAGCGGCT	3540
QY	3330	CACACCCAGGGCCGACCGCTGTGGAGTGTGAGGCTGTGATGATGATTTGGCGAGAGGCTGT	3389
Db	3541	CACACCCAGGGCCGACCGCTGTGGAGTGTGAGGCTGTGATGATGATTTGGCGAGAGGCTGT	3600

QY	3330	CATCTCCGGCTGAAGGCTGATGTCCGAGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT	3449
Db	3601	CATGTCCGGCTGAAGGCTGATGTCTCCGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT	3660
QY	3450	GAGTGTCCAGCACCTGCGGTCTTCACTTCCACAGGCTGAGGCTCGACTCCACCCCA	3509
Db	3661	GAGGTGTCCAGCACCTGCGGTCTTCACTTCCACAGGCTGAGGCTCGACTCCACCCCA	3720
QY	3510	GGGCGAGCTTTCCTCACAGGAGCCCGGACTCCACATCCCACTAGAGAAATGTCATCC	3569
Db	3721	GGGCGAGCTTTCCTCACAGGAGCCCGGACTCCACATCCCACTAGAGAAATGTCATCC	3780
QY	3570	CCAGATTGCACTTGTTCACCCCTCGGCTTGCCCTCTTTGCTTCCACCCCAACATCC	3629
Db	3781	CCAGATTGCACTTGTTCACCCCTCGGCTTGCCCTCTTTGCTTCCACCCCAACATCC	3840
QY	3630	AGGTGGAGACCCCTGAGAGAACCTGTGGACTCTGGGAATTTGGANGTGACCAAGAGTGTG	3689
Db	3841	AGGTGGAGACCCCTGAGAGAACCTGTGGACTCTGGGAATTTGGANGTGACCAAGAGTGTG	3900
QY	3680	CCCTGTACACAGCGGAGAGCCCTGTGACCTGTGAGATGGGGGTCCCTGTGTGCTCAAAATTTGGGGG	3749
Db	3901	CCCTGTACACAGCGGAGAGCCCTGTGACCTGTGAGATGGGGGTCCCTGTGTGCTCAAAATTTGGGGG	3960
QY	3750	GAGGTGCTGTGGAGCTAAATACTGAATATATGAGTTTTCAGTTTGGAAAAAATTTGAAAAA	3809
Db	3961	GAGGTGCTGTGGAGCTAAATACTGAATATATGAGTTTTCAGTTTGGAAAAAATTTGAAAAA	4020
QY	3810	AAAAAAAAAAAAAAAA 3824	
Db	4021	AAAAAAAAAAAAAAAA 4035	

RESULT 4
AAV60320

ID	AAV60320 standard; cDNA; 4023 BP.
XX	
AC	AAV60320;
XX	
DT	04-DEC-1998 (first entry)
XX	

XX	Human telomerase gene referred to as hEST2.
DE	
XX	
KW	Catalytic subunit; human; telomerase; telomere maintenance; diagnosis,
KW	treatment; cancer; ss.
XX	
XX	
OS	Homo sapiens.

	Key	Location/Qualifiers
XX		
FH		
FT	CDS	59. .3458
FT		/*tag= a
VV		

PN WO9837181-A2

AA 27-AUG-1998
PD
VX

AA	20-FEB-1998;	98WO-US003404
PF		
XX		

AA	20-FEB-1997;	97US-0038750P
PR	20-MAY-1997;	97US-0047151P
DP		

PR	01-AUG-1997;	97US-0054549P
PR	14-AUG-1997	97US-0055763P

41-608-1997; 97US-0055702F
PR 30-OCT-1997; 97US-0064322P
XX

(WHED) WHITEHEAD INST BIOMEDICAL RES

PI Counter CM, Meyerson M, Weinberg RA, XX

DR WPI; 1998-495367/42.
DR P-PSDB; AAW71376.

XX New isolated human telomerase catalytic sub-unit gene - used to develop
PT

[illegible]

Db	2941	CCGGCGCTTACAGGCTGGAGGAAACAAGCGCGAAACTCTTTGGGGCTTGGCGGCTGAA	3000
QY	2787	GTGTCAACAGCTGTTTCTGGATTTGCAAGGTGAACAGCTCTCCAGACGGTGTGCACCAACAT	2846
Db	3001	GTGTCAACAGCTGTTTCTGGATTTGCAAGGTGAACAGCTCTCCAGACGGTGTGCACCAACAT	3060
QY	2847	CTACAGATCTCTCGCTGCAGGCGGTACAGTTTCAAGCATGTGTGCAGCTCCCATY	2906
Db	3061	CTACAGATCTCTCGCTGCAGGCGGTACAGTTTCAAGCATGTGTGCAGCTCCCATY	3120
QY	2907	TCATCAGCAATTTGGAAAGAACCCCAATTTTCTCGCGGTCACTCTTCAACAGGCTC	2966
Db	3121	TCATCAGCAATTTGGAAAGAACCCCAATTTTCTCGCGGTCACTCTTCAACAGGCTC	3180
QY	2967	CCTCTGCTACTCCATCTGAAAGCCAAAGACGACGAGATGTGCTGGGGGCGCAAGGGCGC	3026
Db	3181	CCTCTGCTACTCCATCTGAAAGCCAAAGACGACGAGATGTGCTGGGGGCGCAAGGGCGC	3240
QY	3027	CGCGGGCCCTTGGCCCTCCAGAGCCGTCAGTGGCTGTGCCACCAAGCATTCCTGTCCAA	3086
Db	3241	CGCGGGCCCTTGGCCCTCCAGAGCCGTCAGTGGCTGTGCCACCAAGCATTCCTGTCCAA	3300
QY	3087	GCTGACTTCGACACCGTGTCCACTTACGTGTCCACTCTGGGGTCACTCAGACCGCCAGAC	3146
Db	3301	GCTGACTTCGACACCGTGTCCACTTACGTGTCCACTCTGGGGTCACTCAGACCGCCAGAC	3360
QY	3147	GCACTGATGTGGGAAGCTCCCGGGGAGAGACGTACATGCCCCCTGGAGGCGCGGCAACCC	3206
Db	3361	GCACTGATGTGGGAAGCTCCCGGGGAGAGACGTACATGCCCCCTGGAGGCGCGGCAACCC	3420
QY	3207	GGCACTGGCCCTCAGACTTCAAGACCATCTTGATGTGACATGTGCACCGGCCACAGCCAGGC	3266
Db	3421	GGCACTGGCCCTCAGACTTCAAGACCATCTTGATGTGACATGTGCACCGGCCACAGCCAGGC	3480
QY	3267	CGAAGACGACACCAAGACGCCCTGTCAAGCCCGGGCTCTAGCTCCCAAGGAGAGAGGGCG	3326
Db	3481	CGAAGACGACACCAAGACGCCCTGTCAAGCCCGGGCTCTAGCTCCCAAGGAGAGAGGGCG	3540
QY	3327	GCCCAACACCAAGGCCCGCACCGCTGGAGTCTGAGGCTTGAGTGTGTTGGCCGAGGC	3386
Db	3541	GCCCAACACCAAGGCCCGCACCGCTGGAGTCTGAGGCTTGAGTGTGTTGGCCGAGGC	3600
QY	3387	CTGCATGTCCGGCTGAAGGCTGAAGTGTCCGCTGAGGCTTGAGTGTGTTGGCCGAGGC	3446
Db	3601	CTGCATGTCCGGCTGAAGGCTGAAGTGTGTCCGCTGAGGCTTGAGTGTGTTGGCCGAGGC	3666
QY	3447	GCTGAGTGTCCAGACCAACCTGCGGTCTTCACTTCCCAAGAGCTGGCGCTCGCTCCAC	3506
Db	3661	GCTGAGTGTCCAGACCAACCTGCGGTCTTCACTTCCCAAGAGCTGGCGCTCGCTCCAC	3720
QY	3507	CCAGGGCCAGCTTTTCTCAACCAAGAGCCGGCTCCACTCCCACTTGAAGATATGTCCA	3566
Db	3721	CCAGGGCCAGCTTTTCTCAACCAAGAGCCGGCTCCACTCCCACTTGAAGATATGTCCA	3780
QY	3567	TCCCCAATTTGCCAATGTTTCAACCCCTGCGCTGECCTCTTGGCTTCCACCCCCACCA	3626
Db	3781	TCCCCAATTTGCCAATGTTTCAACCCCTGCGCTGECCTCTTGGCTTCCACCCCCACCA	3840
QY	3627	TCCAGGTGAGACCCCTGAGAGAGACCTGGAGCTGTGGAAATTTGAGTGAACCAAGGT	3686
Db	3841	TCCAGGTGAGACCCCTGAGAGAGACCCCTGGAGCTGTGGAAATTTGAGTGAACCAAGGT	3900
QY	3687	GTGCCCTGTACACAGGCGAGACCTCTGCACTTGGATGGGGTCCCTGTGGGTCAAAATTTG	3746
Db	3901	GTGCCCTGTGTACACAGGCGAGACCTCTGCACTTGGATGGGGTCCCTGTGGGTCAAAATTTG	3960
QY	3747	GGGAGGTGTGTGTGGAGTAAATATCTGAATATATGATGTTTTCAGTTTGGAAAAAAA	3806
Db	3961	GGGAGGTGTGTGTGGAGTAAATATCTGAATATATGATGTTTTCAGTTTGGAAAAAAA	4020
QY	3807	AAA 3809	

Db	1279	CAGTGCCTTACGGGGTGCTCTCAAGAGCACTGCGCGTGGAGCTGCGGTCAACCCCA	1338
QY	1326	GGAGCCGGGTGTCTGTGTCCTCCGGGAGAAAGCCCAAGGCTCTGTGTGGCGGCCCCCGAGAGAGAG	1385
Db	1339	GGAGCCGGGTGTCTGTGTCCTCCGGGAGAAAGCCCAAGGCTCTGTGTGGCGGCCCCCGAGAGAGAG	1398
QY	1386	GAACACAGACCCCGGTTCGCTGTGTGACGTCTCCGACAGCAAGACGCCCTGTGTGACAGGTG	1445
Db	1399	GAACACAGACCCCGGTTCGCTGTGTGACGTCTCCGACAGCAAGACGCCCTGTGTGACAGGTG	1458
QY	1446	TAGGGTTGTGTGCGGGGCTTCGCTGTGTGACGTCTCCGACAGCAAGACGCCCTGTGTGACAGGTG	1505
Db	1459	TAGGGTTGTGTGCGGGGCTTCGCTGTGTGACGTCTCCGACAGCAAGACGCCCTGTGTGACAGGTG	1518
QY	1506	CAACAAGAAACGCGCGCTTCTCTCAAGAAACAACAAGAAATTCATCTCCCTGGGAGAGATATGC	1565
Db	1519	CAACAAGAAACGCGCGCTTCTCTCAAGAAACAACAAGAAATTCATCTCCCTGGGAGAGATATGC	1578
QY	1566	AAGCTCTGCGCTGACAGAGCTGACGTGTGAGAAAGTGAACGTCGTGGGAACTGTGGCTGTGGC	1625
Db	1579	AAGCTCTGCGCTGACAGAGCTGACGTGTGAGAAAGTGAACGTCGTGGGAACTGTGGCTGTGGC	1638
QY	1626	AGAGAGCCCAAGGGGTGTGCTGTGTTCGCGCCGACAGACAACGTGTGCTGTGAGAGAGATCTGT	1685
Db	1639	AGAGAGCCCAAGGGGTGTGCTGTGTTCGCGCCGACAGACAACGTGTGCTGTGAGAGAGATCTGT	1698
QY	1686	GGCAAGTTCTGTCACTGCGCTGTGTGAGTGTGTACGTGTGTGAGCTGTCAAGTCTTTCTTT	1745
Db	1699	GGCAAGTTCTGTCACTGCGCTGTGTGAGTGTGTACGTGTGTGAGCTGTCTTTCTTT	1758
QY	1746	TATGTCAACGAGACCAACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGTGTCTGG	1805
Db	1759	TATGTCAACGAGACCAACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGTGTCTGG	1818
QY	1806	AGCAAGTTTGAAGATTTGAATTCAGACAGCACTTGAAGAGGTGTGACCTCGGAGAGCTG	1865
Db	1819	AGCAAGTTTGAAGATTTGAATTCAGACAGCACTTGAAGAGGTGTGACCTCGGAGAGCTG	1878
QY	1866	TGGGAAGCAAGAGTCAAGGACGATCGGGAAGCCAGGCCCCGCTTCGTGACGTCCAGATC	1925
Db	1879	TGGGAAGCAAGAGTCAAGGACGATCGGGAAGCCAGGCCCCGCTTCGTGACGTCCAGATC	1938
QY	1926	CGCTTCATCTCCCAAGCTGTGACGGGCTGGGCGCGAATTGTGAACATGATTAAGTGTGGGA	1985
Db	1939	CGCTTCATCTCCCAAGCTGTGACGGGCTGGGCGCGAATTGTGAACATGATTAAGTGTGGGA	1998
QY	1986	GCCAGAACGTTTCGACAGAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAGGCACTG	2045
Db	1999	GCCAGAACGTTTCGACAGAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAGGCACTG	2058
QY	2046	TTTACAGTGTCTCAATTACAGAGGGGCGGGGCGCCCCGCGCTTCCTGGGGGACCTGTGTCTG	2105
Db	2059	TTTACAGTGTCTCAATTACAGAGGGGCGGGGCGCCCCGCGCTTCCTGGGGGACCTGTGTCTG	2118
QY	2106	GAGCTGTGACGATTCACAGGGGCTGTGCGACCTTTCGTGTGCTGTGTGTGGGCGCCAGAGAC	2165
Db	2119	GAGCTGTGACGATTCACAGGGGCTGTGCGACCTTTCGTGTGCTGTGTGTGGGCGCCAGAGAC	2178
QY	2166	CGCGCGCTGTGAGCTGTAT-----CATCCCC	2189
Db	2179	CGCGCGCTGTGAGCTGTATCTTTGTCAAGTGTGATGTGACGGGCGGGGTACGACATCCCC	2238
QY	2190	CAGACACAGGCTTCAGGAGGTCAATGCGCAGCATCAATCAAAACCCCAAGAACGTAATGCGTGTG	2249
Db	2239	CAGACACAGGCTTCAGGAGGTCAATGCGCAGCATCAATCAAAACCCCAAGAACGTAATGCGTGTG	2298
QY	2250	CGTCGGTATGCGGTGTGTACAGAGGCGGCCCATGTGGGACGTCCGCAAGGCGCTTCAAGAA--	2307
Db	2299	CGTCGGTATGCGGTGTGTCAAGAGGCGGCCCATGTGGGACGTCCGCAAGGCGCTTCAAGAGC	2358
QY	2308	-----	2307
Db	2359	CACGTCTTACTTGAACAGACCTTCACGCGGTACATGCGACAGTTGTGTGCTCACTTGCAG	2418

QY	2308	-----	2307
Db	2419	GAGACCAACCCGCTGAGGAGATGCCGTGTCATCGAGCAGAGCTCTCCCTGAATGAGGCC	2478
QY	2308	-----	2307
Db	2479	AGCAGTGGCTCTTCGACGTCCTTCCTACGTTCTATGTGACCAACGCGCGTGCATCAG	2538
QY	2308	GGCAGAGTCTTAAGTCCAGTGGCAGAGGGATCCCGAGAGGCTCACTCTCCACGCTGCTC	2367
Db	2539	GCGAAGTCTTAAGTCCAGTGGCAGAGGGATCCCGAGAGGCTCACTCTCCACGCTGCTC	2598
QY	2368	TGCAGCTCTGTCTACGCGCAGCATGGAGAACAGCTGTTTGGCGGGATTTCCGCGGAGCGG	2427
Db	2599	TGCAGCTCTGTCTACGCGCAGCATGGAGAACAGCTGTTTGGCGGGATTTCCGCGGAGCGG	2658
QY	2428	CTGCTCTGCGCTTGTGTGATGATTTCTTGTGTGTGACACTCACTCAACCCAGCGGAAA	2487
Db	2659	CTGCTCTGCGCTTGTGTGATGATTTCTTGTGTGTGACACTCACTCAACCCAGCGGAAA	2718
QY	2488	ACCTTCTCAGAGACCTGTGTCCAGAGTGTCTCTGATATGAGCTGCTGTGAACCTTGCGG	2547
Db	2719	ACCTTCTCAGAGACCTGTGTCCAGAGTGTCTCTGATATGAGCTGCTGTGAACCTTGCGG	2778
QY	2548	AAGACAGTGTGATCTTCCCTGTGAGAGACGAGGCGCTGGGGTGGCAGGCTTTTGTTCAG	2607
Db	2779	AAGACAGTGTGATCTTCCCTGTGAGAGACGAGGCGCTGGGGTGGCAGGCTTTTGTTCAG	2838
QY	2608	ATGCCGCGCCACGCGCTTATTCCTGTGTGGGCTGTGCTGTGATATCCCGAGCCCTTGAG	2667
Db	2839	ATGCCGCGCCACGCGCTTATTCCTGTGTGGGCTGTGCTGTGATATCCCGAGCCCTTGAG	2898
QY	2668	GTGCAGAGCGCACTACTCAGCTATGCGCCGAGACCTCCATCAGAGGCACTCTCACTTCAAC	2727
Db	2899	GTGCAGAGCGCACTACTCAGCTATGCGCCGAGACCTCCATCAGAGGCACTCTCACTTCAAC	2958
QY	2728	CGCGGCTTCAAGGTGTGGAGAGAACATCGTTCGCAACTCTTTGGGGTCTTGGCGCTGAG	2787
Db	2959	CGCGGCTTCAAGGTGTGGAGAGAACATCGTTCGCAACTCTTTGGGGTCTTGGCGCTGAG	3018
QY	2788	TGTCAAGAGCTGTTTCTGGAATTTTGCAGGTGAACAGCTTCACAGCGGTGTGACCAACATC	2847
Db	3019	TGTCAAGAGCTGTTTCTGGAATTTTGCAGGTGAACAGCTTCACAGCGGTGTGACCAACATC	3078
QY	2848	TACAAAGTCTCTCTGCTGTCAGGGGTACAGGTTTACGCAATGTGTCTGACGCTCCATT	2907
Db	3079	TACAAAGTCTCTCTGCTGTCAGGGGTACAGGTTTACGCAATGTGTCTGACGCTCCATT	3138
QY	2908	CATCAGAGAGTTTGAAGAACCCCACTTTTTCTGTGCGCTCATCTCTGACAGGCTCC	2967
Db	3139	CATCAGAGAGTTTGAAGAACCCCACTTTTTCTGTGCGCTCATCTCTGACAGGCTCC	3198
QY	2968	CTCTGCTACTTCATCTCTGGAAGCCAAAGACGAGGATGTCTGGGGGCTGACAGGGCGCC	3027
Db	3199	CTCTGCTACTTCATCTCTGGAAGCCAAAGAGGAGATGTCTGGGGGCTGACAGGGCGCC	3258
QY	3028	GCCGCGCCCTGTGCGCTTCGAGGCGGTGACAGTGTGCTGTGACCAACCACTTCTGTCAAG	3087
Db	3259	GCCGCGCCCTGTGCGCTTCGAGGCGGTGACAGTGTGCTGTGACCAACCACTTCTGTCAAG	3318
QY	3088	CTTACCTGACACGCTGTGACCTTAAGTGCACCTCTGGGGTCACTCAAGGACAGGCCAGAG	3147
Db	3319	CTTACCTGACACGCTGTGACCTTAAGTGCACCTCTGGGGTCACTCAAGGACAGGCCAGAG	3378
QY	3148	CAGCTGATGCGAAGCTCCCGGGAGACAGCTGACTCTCTGTGAGGCGCGAGCAACCCG	3207
Db	3379	CAGCTGATGCGAAGCTCCCGGGAGACAGCTGACTCTCTGTGAGGCGCGAGCAACCCG	3438
QY	3208	GCACTGCGCCCAACTTCAAGACCACTCTGACTAATGTGCACCCGCGCCACACGCAAGGCC	3267
Db	3439	GCACTGCGCCCAACTTCAAGACCACTCTGACTAATGTGCACCCGCGCCACACGCAAGGCC	3498


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Db 841 GCGTGAACGAGTGAACGTGTTTCTGTGTGTGTCACTGCAACACCGCGGAAGAGC 900
Qy 908 CACCTCTTTGGAGGGGTGCGCTCTCTGAGCAGCGGCCAATCCCACTCCGTGGGCGCA 967
Db 901 CACCTTTTGGAGGGGTGCGCTCTCTGAGCAGCGGCCAATCCCACTCCGTGGGCGCA 960
Qy 968 GCAACAGCGGGGCCCCCAATCCACATCGCGGCCACCAAGTCCCTGGGACAAGCCTTGTCC 1027
Db 961 GCAACAGCGGGGCCCCCAATCCACATCGCGGCCAATCCCTGGGACAAGCCTTGTCC 1020
Qy 1028 CCGGCTGTATGCGCGAACAAGCACTTCTTACTTCTTACGGGCAAGAGAGAGCTGCG 1087
Db 1021 CCGGCTGTATGCGCGAACAAGCACTTCTTACTTCTTACGGGCAAGAGAGAGCTGCG 1080
Qy 1088 GCGCTCTTCTTACTGAGCTCTCTGAGCGCCAGCTGAGCTGCGGAGGCTGTGGA 1147
Db 1081 GCGCTCTTCTTACTGAGCTCTCTGAGCGCCAGCTGAGCTGCGGAGGCTGTGGA 1140
Qy 1148 GACCATCTTTCTGGGTTCCAGGCGCTGATGCGAGGACTCCCGCAGGTTGCCCGCT 1207
Db 1141 GACCATCTTTCTGGGTTCCAGGCGCTGATGCGAGGACTCCCGCAGGTTGCCCGCT 1200
Qy 1208 GCGCCAGCGCTACTGCAATGAGGCGCCCTGTTTCTGAGAGCTGTTGGAAACAAGGCA 1267
Db 1201 GCGCCAGCGCTACTGCAATGAGGCGCCCTGTTTCTGAGAGCTGTTGGAAACAAGGCA 1260
Qy 1268 GTGCCCCCTTACGAGGAGTCTCTTAAGACGACATCCCGCTGAGCTGCGTCAACCCAGC 1327
Db 1261 GTGCCCCCTTACGAGGAGTCTCTCTTAAGACGACATCCCGCTGAGCTGCGTCAACCCAGC 1320
Qy 1328 AGCGGCTGTCTGTGCGCGGAGAAAGCGCCAGGAGCTGTGAGGCGCGCCCGAGAGAGGA 1387
Db 1321 AGCGGCTGTCTGTGCGCGGAGAAAGCGCCAGGAGCTGTGAGGCGCGCCCGAGAGAGGA 1380
Qy 1388 CACAGACCCCGCTGCTGCTGAGAGACGACATCCCGCTGAGAGCAACAGACCCCTGCAAGTGA 1447
Db 1381 CACAGACCCCGCTGCTGCTGAGAGACGACATCCCGCTGAGAGCAACAGACCCCTGCAAGTGA 1440
Qy 1448 CGGCTTCTGTGCGGCGCTGCTGCGCGGAGTGTGCGCCCAAGGCTCTTGGGGCTCCAGCA 1507
Db 1441 CGGCTTCTGTGCGGCGCTGCTGCGCGGAGTGTGCGCCCAAGGCTCTTGGGGCTCCAGCA 1500
Qy 1508 CAAAGAGCGCGCTTCTCTAGAGAACCAAGAAATGTAATCTCTGAGGAAAGCATGCCAA 1567
Db 1501 CAAAGAGCGCGCTTCTCTAGAGAACCAAGAAATGTAATCTCTGAGGAAAGCATGCCAA 1560
Qy 1568 GCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1627
Db 1561 GCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
Qy 1628 GAGCCAGAGGGTGTGCTGTGTTCCGCGCCAGAGACCGTGTGCTGAGAGATCTGGC 1687
Db 1621 GAGCCAGAGGGTGTGCTGTGTTCCGCGCGCAGAGACCGTGTGAGAGATCTGGC 1680
Qy 1688 CAAAGTCTGCACTGCTGATGAGTGTGATGCTGCTGAGCTGCTCAAGCTCTTTCTTTA 1747
Db 1681 CAAAGTCTGCACTGCTGATGAGTGTGATGCTGCTGAGCTGCTCAAGCTCTTTCTTTA 1740
Qy 1748 TGTCAAGAGACCACTTTCAAAAGAACAGGCTCTTTTCTTCAACGGAAGAGTGTGAG 1807
Db 1741 TGTCAAGAGACCACTTTCAAAAGAACAGGCTCTTTTCTTCAACGGAAGAGTGTGAG 1800
Qy 1808 CAAAGTGAAGAGTGTGAATCAAGACAGACTTTGAAGAGGTTGACGTGCGAGAGCTGTC 1867
Db 1801 CAAAGTGAAGAGTGTGAATCAAGACAGACTTTGAAGAGGTTGACGTGCGAGAGCTGTC 1860
Qy 1868 GGAAGCAGAGTGAAGCAGACATCGGGAAGCAGAGCCCGCTGAGAGTCAAGACTCG 1927
Db 1861 GGAAGCAGAGTGAAGCAGACATCGGGAAGCAGAGCCCGCTGAGAGTCAAGACTCG 1920
Qy 1928 CTTCAATCCCAAGCTGAGCGGCTGCGGCGGATTTGTGAACATGACATGCTGTGGAGC 1987
Db 1921 CTTCAATCCCAAGCTGAGCGGCTGCGGCGGATTTGTGAACATGACATGACATGCTGTGGAGC 1980
Qy 1988 CAGAACGTTCCGAGAGAAAGAGAGCCGAGAGTCTACACTGAGAGGTGAAGCATGTT 2047
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Qy 2048 CAGCGTCTCAACTAGAGGAGGCGCGAGCCCGGCTCTTGGAGCGCTGTGTGGG 2107
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Qy 2108 CTTGAGAGATATCAAGAGGCTGTGGGCACTTTGCTGCTGCTGTGTGGGAGCCAGAGACC 2167
Db 2101 CTTGAGAGATATCAAGAGGCTGTGGGCACTTTGCTGCTGCTGTGTGGGAGCCAGAGACC 2160
Qy 2168 GCGGCTGAGCTGTA-----CATCCCCA 2191
Db 2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGAGAGGCGGCTAGACACCATCCCCA 2220
Qy 2192 GGAAGGCTTACGAGAGTCAATGCGCAGATCATCAAAACCCAGAGACGTACTGCGTGG 2251
Db 2221 GGAAGGCTTACGAGAGTCAATGCGCAGATCATCAAAACCCAGAGACGTACTGCGTGG 2280
Qy 2252 TCGGTATGCGGTGTCAGAGAGCGCGCCATGAGGACGTCCGCAAGGCTTCAAGA---- 2307
Db 2281 TCGGTATGCGGTGTCAGAGAGCGCGCCATGAGGACGTCCGCAAGGCTTCAAGAGCCA 2340
Qy 2308 -----CATCCCCA 2307
Db 2341 CGTCTTACCTTGAACAGACTCCAGCCGTATGAGAGAGTTCGTGCTCACCTGAGAGA 2400
Qy 2308 ----- 2307
Db 2401 GACCAAGCGGCTGAGGAGTGCCTGCTCATCAAGCAGAGCTCTCCCTGAATAGGCCAG 2460
Qy 2308 -----G 2309
Db 2461 CAGTGCCTCTTGAAGTCTCTTACGCTTCAATGTGCACACAGCGGCTGACATCAGGGG 2520
Qy 2510 CAAAGTCTTACGTCAGAGTCAAGGAGATCCGAGAGGCTCAATCTCTGACAGTGTGCTG 2369
Db 2521 CAAAGTCTTACGTCAGAGTCAAGGAGATCCGAGAGGCTCAATCTCTGACAGTGTGCTG 2580
Qy 2370 CAGCTGTGCTACGAGGACATGAGAGAACAGCTGTTGCGGAGATTGCGCGGACGAGGCT 2429
Db 2581 CAGCTGTGCTACGAGGACATGAGAGAACAGCTGTTGCGGAGATTGCGCGGACGAGGCT 2640
Qy 2430 GCTCCTGCGGTTGGTGGATGATTTCTTGTGTGAGACCTCACTCAACCGCGGAAAC 2489
Db 2641 GCTCCTGCGGTTGGTGGATGATTTCTTGTGTGAGACCTCACTCAACCGCGGAAAC 2700
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Qy 2550 GACAGTGTGAATTTTCCCTGTGAGAAAGAGGCGCTGTGGTGGACAGGCTTTTGTGAGAT 2609
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Db 3001 TCAAGGCTGTTTCTGAGTTTGAAGTGAACAGCTTCAAGAGGTTGACCAATCTTA 3060
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QY 2850 CAAGATCTCTCTGCTGCAAGGCTTACAGTTCAGCATGTGTGTGAGCTCCCATTTCA 2309
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QY 2910 TCAGCAAGTTTGAAGAAGACCCCACTTTTCTGTGGGCTATCTCTGACACGGCTCCCT 2369
DB 3121 TCAGCAAGTTTGAAGAAGACCCCACTTTTCTGTGGGCTATCTCTGACACGGCTCCCT 3180
QY 2970 CTGCTACTTCATCTCTGAAAGCCAGACGAGGATGTGTGTGGGGCCAAAGGGCCGCG 3029
DB 3181 CTGCTACTTCATCTCTGAAAGCCAGACGAGGATGTGTGTGGGGCCAAAGGGCCGCG 3240
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DB 3841 AGGTGAGACCTTGAAGAAGACCTTGGAGCTCTGGAATTTGAGTGAACAAAGGTGTG 3900
QY 3690 CCCGTGACACAGAGGAGAGACCTTGCACCTGAGTGGGCTGCGCTGAGTGAATTTGGGGG 3749
DB 3901 CCCGTGACACAGAGGAGAGACCTTGCACCTGAGTGGGCTGCGCTGAGTGAATTTGGGGG 3960
QY 3750 GAGGTGTGTGTGAGTAAATATGATATATGATATATGATATATGATATATGATATAT 3804
DB 3961 GAGGTGTGTGTGAGTAAATATGATATATGATATATGATATATGATATATGATATAT 4015

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RESULT 7
AA220279
ID AA220279 standard; cDNA; 4015 BP.
XX
AC AA220279;
XX
DT 17-JAN-2000 (first entry)

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XX DE Human telomerase reverse transcriptase (hTERT) cDNA.
XX KM Telomerase reverse transcriptase; human; hTERT; cell proliferation;
XX KM cancer; ss.
XX OS Homo sapiens.
XX FH Key
XX FT Location/Qualifiers
XX FT CDS
XX FT 56..3454
XX FT /tag=a
XX PN MO9950386-A2.
XX PD 07-OCT-1999.
XX PF 31-MAR-1999; 99WO-US007097.
XX PR 31-MAR-1998; 98US-00052864.
XX PR 03-AUG-1998; 98US-00128354.
XX PA (GERO-) GERON CORP.
XX PI Morin GB;
XX DR MPI; 1999-610842/52.
XX DR P-PSDB; AAY32090.
XX PT New catalytic polypeptide and polynucleotide, useful for increasing
XX PT catalytic activity in a cell.
XX PS Disclosure; Fig 2; 24pp; English.
XX XX
CC This is the nucleotide sequence of cDNA encoding human telomerase reverse
CC transcriptase (hTERT, see AAY32090). Human telomerase is a target for
CC diagnosing and treating diseases relating to cell proliferation and
CC senescence, such as cancer, or for increasing the proliferative capacity
CC of a cell. A claimed method for increasing the proliferative capacity of
CC a vertebrate cell, especially a human or other mammalian cell, involves
CC introducing into the cell a recombinant hTERT polynucleotide encoding an
CC hTERT variant in which residues 192-323, 192-271, 200-271, 222-
CC 240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A
CC claimed method for reducing telomerase activity in a cell involves
CC introducing a recombinant polynucleotide encoding an hTERT variant having
CC a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or
CC 1055-1071. The polynucleotides are obtained by mutagenesis of the hTERT
CC coding sequence
CC XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
Query Match 93.1%; Score 3559; DB 2; Length 4015;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;
QY 8 GCAGGCTGCGCTGCTGCTGCGACGAGTGAAGCCCTGAGCCCGGCGCAACCCCGGAGTCC 67
DB 1 GCAGGCTGCGCTGCTGCTGCGACGAGTGAAGCCCTGAGCCCGGCGCAACCCCGGAGTCC 60
QY 68 GGGGCTTCCCGCTGCGCGAGCGCTGCGCTGCTGCTGCGAGCACTACCGGAGTGTCT 127
DB 61 GCGGCTTCCCGCTGCGCGAGCGCTGCGCTGCTGCTGCTGCGAGCACTACCGGAGTGTCT 120
QY 128 GCGGCTGCGCGAGTGTGCGAGGCGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCG 187
DB 121 GCGGCTGCGCGAGTGTGCGAGGCGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 188 GAGCCCGGCGCTTTCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 247
DB 181 GAGCCCGGCGCTTTCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 248 ACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
DB 241 ACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

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Db 2461 CAGTGGCTCTTCGAGCTCTTCTACGCTTCACTGTGCGACCCAGCGCTGGCATCAGGG 2520
Qy 2310 CAGTCTTCAAGTCCAGTGTCCAGGGGATCCGCAAGGCTCCATCTCTCCACGCTGTCTG 2369
Db 2521 CAGGCTTCAAGTGTCCAGGGGATCCGCAAGGCTCCATCTCTCCACGCTGTCTG 2580
Qy 2370 CAGGCTTCAAGTGTCCAGGGGATCCGCAAGGCTCCATCTCTCCACGCTGTCTG 2429
Db 2581 CAGGCTTCAAGTGTCCAGGGGATCCGCAAGGCTCCATCTCTCCACGCTGTCTG 2640
Qy 2430 GCTCTCTGAGTGTGAGTGTGATTTCTTGTGTGACACTCTCACTCCACCGGAAAC 2489
Db 2641 GCTCTCTGAGTGTGAGTGTGATTTCTTGTGTGACACTCTCACTCCACCGGAAAC 2700
Qy 2490 CTCTCTCAAGGACCTGTGAGTGTGATTTCTTGTGTGACACTCTCACTCCACCGGAAAC 2549
Db 2701 CTCTCTCAAGGACCTGTGAGTGTGATTTCTTGTGTGACACTCTCACTCCACCGGAAAC 2760
Qy 2550 GACAGTGTGAACTTCCCTGTAGAAAGAGAGGCTGTGAGTGTGAGTGTGAGTGTGAGT 2609
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Qy 2610 GCGGCGCCACGAGCTTATCCCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2669
Db 2821 GCGGCGCCACGAGCTTATCCCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2880
Qy 2670 GCAGAGCACTACTCAGCTATGCGCGGACCTCCATGAGAGCCAGTCTCACTTCAACCG 2729
Db 2881 GCAGAGCACTACTCAGCTATGCGCGGACCTCCATGAGAGCCAGTCTCACTTCAACCG 2840
Qy 2730 CCGCTTCAAGGCTGTGAGGAAACATGCTGCGAACTCTTTGGGGTCTTTGGGCTGAAAGT 2789
Db 2941 CCGCTTCAAGGCTGTGAGGAAACATGCTGCGAACTCTTTGGGGTCTTTGGGCTGAAAGT 3000
Qy 2790 TCACAGCTGTGTTGATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2849
Db 3001 TCACAGCTGTGTTGATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3060
Qy 2850 CAGAGTCTCTCTGCTGCGAGGCTGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2909
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Qy 2910 TCAGAGTGTGAGGAAACCCCAATTTTCTGCGGCTATCTCTGAGACGAGCTCTCTCT 2969
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Qy 3150 GCTGTGTGAGGAAAGTCTCCGAGGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3209
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Qy 3210 ACTGCTCTCAAGCTTCAAGACCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3269
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Db 3481 GAGCAGAGACAGAGAGCTCTGTCAAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3380
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Db 3541 CACACCCAGGCGCGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3600
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Db 3601 CATGTCCGCTGAGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3660
Qy 3450 GAGTGTGAGCAGACCTGCGCTTCACTTCCCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3509
Db 3661 GAGTGTGAGCAGACCTGCGCTTCACTTCCCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3720
Qy 3510 GGGCGAGCTTTTCTTCAACGAGAGCGCGCTTCACTTCCCAAGAGTGTGAGTGTGAGTGTGAGT 3569
Db 3721 GGGCGAGCTTTTCTTCAACGAGAGCGCGCTTCACTTCCCAAGAGTGTGAGTGTGAGTGTGAGT 3780
Qy 3570 CCAGATTTGCGATTTGTTACACCTGAGAGCGCGCTTCACTTCCCAAGAGTGTGAGTGTGAGT 3629
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Qy 3750 GAGTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3804
Db 3961 GAGTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 4015

RESULT 8
AAZ30154
ID AAZ30154 standard; cDNA; 4015 BP.
XX
AC AAZ30154;
XX
DT 26-JUN-2000 (first entry)
XX
DE cDNA encoding a human telomerase reverse transcriptase (TRT).
XX
KW Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
KW dendritic cell; telomerase activity; cancer cell; proliferating cell;
KW immunological destruction; telomerase; cancer; proliferation disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "telomerase reverse transcriptase"
XX
PN MO9950392-A1.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99W0-US006838.
XX
PR 31-MAR-1998; 98US-01120067.
XX
PA (GERO-) GERON CORP.
XX
PI Gaeta FCA;
XX
XX MPI; 1999-610845/52.
XX DR P-PDB; AAY43621.
XX
XX Eliciting an in vivo immune response for prevention and treatment of
XX cancers.
XX Disclosure; Fig 2; 26pp; English.
XX
XX The present sequence encodes a human telomerase reverse transcriptase

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XX AAH45901;
XX 06-SEP-2001 (first entry)
XX Human hTERT gene.
XX Human hTERT gene.
XX Human: hTERT; telomerase; catalytic subunit; mRNA quantitation;
XX detection; beta-region; diagnosis; cancer; ds.
XX Homo sapiens.
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XX Key
XX Location/Qualifiers
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XX 275..1628
XX /tag= b
XX /number= 2
XX 1629..1824
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XX 1825..2005
XX /tag= d
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XX /number= 11
XX 2899..3025
XX /tag= s
XX /number= 12

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FT /number= 13
FT exon
FT /tag= u
FT /number= 14
FT exon
FT /tag= v
FT /number= 15
FT exon
FT /tag= w
FT /number= 16
XX
XX EPI108789-A2.
XX
XX 20-JUN-2001.
XX
XX 15-DEC-2000; 2000EP-00127228.
XX
XX 16-DEC-1999; 99US-00465491.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Chang SP, Santini CD;
XX
XX WPI; 2001-376930/40.
XX
XX Quantitating expression of mRNA encoding hTERT, the catalytic subunit of
XX telomerase, as an indicator of cancer, by amplifying RNA using primers
XX complementary to hTERT gene sequence and quantitating amplified products.
XX
XX Claim 1; Page 5-7; 29pp; English.
XX
XX The present sequence is that of the hTERT gene encoding the catalytic
XX subunit of the human telomerase, comprising 16 exons, which is useful in
XX a method for quantitating hTERT mRNA. The method is useful for detecting
XX the presence of beta-region (a 182 nucleotide region consisting of exons
XX 7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis
XX of cancer. The method provides an accurate measure of telomerase activity
XX by selectively measuring mRNA that encodes an active hTERT protein
XX
XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
XX
XX Query Match 93.1%; Score 3559; DB 4; Length 4015;
XX Best Local Similarity 94.6%; Pred. No. 0;
XX Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;
XX
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XX 1 GCAGCGCTGCTCTCTCTCTGCGACGAGGAGCCCTGCGCCCGGACCCCGCGATGCC 60
XX
XX 68 GCGCGCTCCCGCTGCGCGAGCGCTGCTCTCTCTGCGCGACCACTACCGAGGTCT 127
XX 61 GCGCGCTCCCGCTGCGCGAGCGCTGCTCTCTCTGCGCGACCACTACCGAGGTCT 120
XX
XX 128 GCGCGTGGCCAGCTTGTGTCGCGGCTGCGGCGCCCGAGGCTGAGGCTGTCAGGCGG 187
XX 121 GCGCGTGGCCAGCTTGTGTCGCGGCTGCGGCGCCCGAGGCTGAGGCTGTCAGGCGG 180
XX
XX 188 GAGCCCGGCGGCTTTCGCGCGCTGTCGCGGCTGTCGCTGTCGCTGTCGCTGTCG 247
XX 181 GAGCCCGGCGGCTTTCGCGCGCTGTCGCGGCTGTCGCGGCTGTCGCTGTCGCTGTCG 240
XX
XX 248 AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
XX 241 AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
XX
XX 308 CCGAGTGTGCAAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
XX 301 CCGAGTGTGCAAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
XX
XX 368 GCTGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427

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Db 361 GCTGCTGAGACGGGGGCCCCGGGGGCCCCCGGAGGCTTACACACAGCTGCGAGCTA 420
QY 428 CTTGCCCAACAGTGTGACCGAGCGACTGCGGGGGAGCGGGGGCGTGGGGGCTGCTGGCG 487
Db 421 CTTGCCCAACAGTGTGACCGAGCGACTGCGGGGGAGCGGGGGCGTGGGGGCTGCTGGCG 480
QY 488 CCGCGTGGGCGAGCGAGTGTGGTTTCACTGTGGCAAGCTGCGGCTTTTGTGTGGT 547
Db 481 CCGCGTGGGCGAGCGAGTGTGGTTTCACTGTGGCAAGCTGCGGCTTTTGTGTGGT 540
QY 548 GCGTCCCAAGTGTGCGCTTACAGTGTGGGGCGCGCGCTGTACAGAGTCTGGCGCTGCA 607
Db 541 GCGTCCCAAGTGTGCGCTTACAGTGTGGGGCGCGCGCTGTACAGAGTCTGGCGCTGCA 600
QY 608 TCAGGCG 667
Db 601 TCAGGCG 660
QY 668 CTGGAACCATAGCGCTGAGGAGGCGCGGGGTCCTTGGGCTGCGCAAGCTGGGGTGGAG 727
Db 661 CTGGAACCATAGCGCTGAGGAGGCGCGGGGTCCTTGGGCTGCGCAAGCTGGGGTGGAG 720
QY 728 GAGGCGCGGCGGCGAGTGTGCGAGCGCGAGTGTGCGGTCGCGCAAGGCGCGGCGG 787
Db 721 GAGGCGCGGCGGCGAGTGTGCGAGCGCGAGTGTGCGGTCGCGCAAGGCGCGGCGG 780
QY 788 TGCCCTTGAAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db 781 TGCCCTTGAAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 848 GCGTGAACGAGTGTGCGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
Db 841 GCGTGAACGAGTGTGCGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACTCTTTTGAAGGCGT 967
Db 901 CACTCTTTTGAAGGCGT 960
QY 968 GCACCAAGCGGCG 1027
Db 961 GCACCAAGCGGCG 1020
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Db 1021 CCGCGTGTAGCGCGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1088 GCGCT 1147
Db 1081 GCGCT 1140
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QY 1208 GCGCGAAGCGTACGAGGAAATGCGGGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 1267
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Db 1321 AGCGCGT 1380
QY 1388 CACAGACCCCGCGT 1447
Db 1381 CACAGACCCCGCGT 1440
QY 1448 CCGGCTTGT 1507
Db 1441 CCGGCTTGT 1500

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Db 1621 GAGCCAGGCGTTGCTGT 1680
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QY 1748 TGTCAAGAGACAGCTTCAAGAAAGAGCTTCTTCTTCAAGGAAAGTGTGTGAG 1807
Db 1741 TGTCAAGAGACAGCTTCAAGAAAGAGCTTCTTCTTCAAGGAAAGTGTGTGAG 1800
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Db 1801 CAAGTGTGAAGCATTTGGAATGACAAGACCTTGAAGAGGCTGAGCTGGGAGCTGTC 1860
QY 1868 GGAAGAGAGGTCAAGGACAGATCGGGAAGCGAGCGCGCGCGCGCGCGCGCGCGCG 1927
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QY 1928 CTTTATCCCCAAGCGTGTGAGCGGCTGCGGCGGCTTGTGAACATGTGATGTGTGTGT 1987
Db 1921 CTTTATCCCCAAGCGTGTGAGCGGCTGCGGCGGCTTGTGAACATGTGATGTGTGTGT 1980
QY 1988 CAGAACGTTTCGACAGAAAGAGGCGCGAGCGTCTCACTTGAAGGTTGAAGGCACTG 2047
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QY 2048 CAGCGTGTCAATCAATGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2107
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QY 2168 GCGCGCTGAGCTGT-----CATCCCCA 2191
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 QY 3210 ACTGCGCTCAGACTTCAAGACCATCTGAGTGTGACACCCCGCAAGCCAGCCAGC 3269
 Db 3421 ACTGCGCTCAGACTTCAAGACCATCTGAGTGTGACACCCCGCAAGCCAGCCAGC 3480
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 Db 3541 CACACCCAGGCGCGGACCGCTGAGTGTGAGGCTGAGTGTGAGTGTGCGGAGCGCTG 3600
 QY 3390 CATGTCCGCTGAGAGGCTGAGTGTCCGCTAGGCTGAGGCTGAGTGTCCAGCCAGGCT 3449
 Db 3601 CATGTCCGCTGAGAGGCTGAGTGTCCGCTAGGCTGAGGCTGAGTGTCCAGCCAGGCT 3660
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 Db 3961 GAGTGTGAGGAGTAAATATGAAATATGATGATTTTCAAGTTTGAAGAAAAA 4015

RESULT 10
 AAD46821
 ID AAD46821 standard; cDNA, 4015 BP.
 XX
 AC AAD46821.
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human telomerase reverse transcriptase (TERT) cDNA.
 XX
 KW Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
 XX transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
 KW telomerase reverse transcriptase; gene; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 56..3454
 FT /tag= a
 FT /product= "Human telomerase reverse transcriptase"
 XX
 PN WO200274948-A2.
 PD 26-SEP-2002.
 XX
 PF 21-MAR-2002; 2002WO-CA000378.
 XX
 PR 21-MAR-2001; 2001US-0277811P.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Denning C, Clark AJ, Schiff JM;
 XX WPI; 2002-759895/82.
 DR P-PDB; AAE29226.
 XX
 PT Mammalian cells, useful for producing animal tissues with carbohydrate
 PT antigens that are compatible for transplantation into human patients.
 XX
 PS Disclosure; Page 33-34; 71pp; English.
 CC The invention relates to animal tissues with carbohydrate antigens that
 CC are compatible for transplantation into human patients. The mammalian
 CC cell is inactivated homocytously for expression of alpha(1,3)galactosyl-
 CC transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
 CC fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
 CC with carbohydrate antigens that are compatible for transplantation into
 CC human patients. The present sequence is human telomerase reverse
 CC transcriptase (TERT) cDNA used in the invention

XX	Sequence	4015 BP, 663 A, 1363 C, 1275 G, 714 T, 0 U, 0 Other;
SQL	Query Match	93.1%; Score 3559; DB 6; Length 4015;
	Best Local Similarity	94.6%; Pred. No. 0;
	Matches 3797; Conservative	0; Mismatches 0; Indels 218; Gaps 2
QY	8	GGAGGGCTGGGCTGCTGGCTGGGAGACCTTGGGCCCCGGGCACTCCCGGCATGCC 67
DB	1	GCAGGGCTGGCTGCTGGCTGGGAGACCTTGGGCCCCGGGCACTCCCGGCATGCC 60
QY	68	GCGCGCTCCCGCTGCGCCGAGCCGCTGCTCCCTGCTGGCAGCACCTACCGGAGTGTCT 127
DB	61	GCGCGCTCCCGCTGCGCCGAGCCGCTGCTCCCTGCTGGCAGCACCTACCGGAGTGTCT 120
QY	128	GCGCGTGGGCAGTTCGTGTGTGGGCGCTTGGGAGCCCAAGGCTGTGGCGCTGTGTACGCGCG 187
DB	121	GCGCGTGGGCAGTTCGTGTGTGGGCGCTTGGGAGCCCAAGGCTGTGGCGCTGTGTACGCGCG 180
QY	188	GGAGCCGGGCGGCTTCCGCGCGCTGTGGGCGCAGTGGCTGGGTGGTGGTGGCCCTGGGAGCG 247
DB	181	GGAGCCGGGCGGCTTCCGCGCGCTGTGGGCGCAGTGGCTGGGTGGTGGTGGCCCTGGGAGCG 240
QY	248	ACGCGCGCCCGCCCGCGCCCTCTCTTCGCGAGTGTCTTGGCTGAAGAGCTGTGTGAC 307
DB	241	ACGCGCGCCCGCCCGCGCCCTCTCTTCGCGAGTGTCTTGGCTGAAGAGCTGTGTGAC 300
QY	308	CCGAGTGTGCGAGAGCTGTGGGAGCGGGGCGGAGAAAGTGTGGGCTTCGGCTTGGC 367
DB	301	CCGAGTGTGCGAGAGCTGTGGGAGCGGGGCGGAGAAAGTGTGGGCTTCGGCTTGGC 360
QY	368	GCTGCTGAGCGGGGCGCGCGGGGCGCCCGAGGAGCTTTCACCAAGAGCTGGCAGCTA 427
DB	361	GCTGCTGAGCGGGGCGCGCGGGGCGCCCGAGGAGCTTTCACCAAGAGCTGGCAGCTA 420
QY	428	CCTGGCCCAACAGGTGACCAAGCACTGTGGGGAGAGCGGGGCTGTGGGCTGTGTGCG 487
DB	421	CCTGGCCCAACAGGTGACCAAGCACTGTGGGGAGAGCGGGGCTGTGGGCTGTGTGCG 480
QY	488	CCGCGTGGGCGACGACGTGTGTGTTCACCTCTGTGGCAGCTGTGGCGCTCTTGTGTGTGT 547
DB	481	CCGCGTGGGCGACGACGTGTGTGTTCACCTCTGTGGCAGCTGTGGCGCTCTTGTGTGTGT 540
QY	548	GCGTCCCAAGCTGTGGCTTACAGAGTGTGTGGGCGCGCGCTGTACCAAGCTGTGGCGTGTCCAC 607
DB	541	GCGTCCCAAGCTGTGGCTTACAGAGTGTGTGGGCGCGCGCGCTGTACCAAGCTGTGGCGTGTCCAC 600
QY	608	TCAAGCCCGGCGCCCGGCGCACAGCTGATGTGACCCCGAAGGCGTGTGGATGTGCAACCGCG 667
DB	601	TCAAGCCCGGCGCCCGGCGCACAGCTGATGTGACCCCGAAGGCGTGTGGATGTGCAACCGCG 660
QY	668	CTGGAACCATATGCGTCAAGGAGGCGCGGGGTCCTGTGGGCTGTGCACGCGCGGAGTGGAG 727
DB	661	CTGGAACCATATGCGTCAAGGAGGCGCGGGGTCCTGTGGGCTGTGCACGCGCGGAGTGGAG 720
QY	728	GAGGCGGGGGGGGCGAGTGTCAAGCCGCAAGTGTGCTGCTGCAAGAGGCGCCAGGCGTGTGCGCG 787
DB	721	GAGGCGGGGGGGGCGAGTGTCAAGCCGCAAGTGTGCTGCTGCAAGAGGCGCCAGGCGTGTGCGCG 780
QY	788	TGCGCCCTGAGCGGAGCGGAGCGCCGTTGTGGGCAAGGGTCTTGAGCCCAAGCGGAGAGAG 847
DB	781	TGCGCCCTGAGCGGAGCGGAGCGCCGTTGTGGGCAAGGGTCTTGAGCCCAAGCGGAGAGAG 840
QY	848	GCGTGGACCGAGTACCGTGTGTTCTGTGTGTGTGTCACTGTGCAGAGCCCGCGCAAGAGC 907
DB	841	GCGTGGACCGAGTACCGTGTGTTCTGTGTGTGTGTCACTGTGCAGAGCCCGCGCAAGAGC 900
QY	908	CACCTCTTTGGAGGAGTGCCTCTGTGGCAGCGGCACTCCCAACCATCTCGTGGGCGCGCA 967
DB	901	CACCTCTTTGGAGGAGTGCCTCTGTGGCAGCGGCACTCCCAACCATCTCGTGGGCGCGCA 960
QY	968	GCACCAAGCGGGCCCCCATTCACATGTGGGCGACCAAGTTCCTTGGAGACAGCTTGTGC 1027

Db	961	GGACACAGGGGGCCCCCATCACAATCGGGGCAACAAGTCCCTGGGACAGGCTTGCC	1020
Qy	1028	CCGGGTGTAACGCCGAGACCAAGCACTTCTCTAATCTCAAGGCAACAAGAGCACTGCG	1087
Db	1021	CCGGGTGTAACGCCGAGACCAAGCACTTCTCTAATCTCTCAAGGCAACAAGAGCACTGCG	1080
Qy	1088	GCCCTCTTCTTCACTCAAGCTCTCTAGAGCCAGACTGACTGGCGCTGGAGGCTGTGGA	1147
Db	1081	GCCCTCTTCTTCACTCAAGCTCTCTAGAGCCAGACTGACTGGCGCTGGAGGCTGTGGA	1140
Qy	1148	GACCACTCTTCTGAGGTTCCAGGCTCTGATGECAGGGACTTCCCGCAAGTTGCCCCGCT	1207
Db	1141	GACCACTCTTCTGAGGTTCCAGGCTCTGATGECAGGGACTTCCCGCAAGTTGCCCCGCT	1200
Qy	1208	GCCCCAGGCTACTGGCAAAATGCGGCCCTGTTCCTGGAGTGTCTGGAGAACACAGCGCA	1267
Db	1201	GCCCCAGGCTACTGGCAAAATGCGGCCCTGTTCCTGGAGTGTCTGGAGAACACAGCGCA	1260
Qy	1268	GTGCCCCCTACGGGGGTGCTCTCAAGAGCAATGCCCGCTGTGAGACTGAGTCAATCCAGC	1327
Db	1261	GTGCCCCCTACGGGGGTGCTCTCAAGAGCAATGCCCGCTGTGAGACTGAGTCAATCCAGC	1320
Qy	1328	AGCCGAGTCTGTGTGCCCGGAGAAAGCCCAAGGCTCTGTGGCGGCCCCCGAGAGAGAGA	1387
Db	1321	AGCCGAGTCTGTGTGCCCGGAGAAAGCCCAAGGCTCTGTGGCGGCCCCCGAGAGAGAGA	1380
Qy	1388	CACAGAACCCCGCTGACCTGTGTGACGTGCTTCCGCAAGACAGCAAGCCCTTGGCAGGTGA	1447
Db	1381	CACAGAACCCCGCTGACCTGTGTGACGTGCTTCCGCAAGACAGCAAGCCCTTGGCAGGTGA	1440
Qy	1448	CGGCTCTGTGGGGGCTTGCCCTGCAGCGGCTGTGGTCCGCCAGGCTCTGTGGGCTCAAGCA	1507
Db	1441	CGGCTCTGTGGGGGCTTGCCCTGCAGCGGCTGTGGTCCGCCAGGCTCTGTGGGCTCAAGCA	1500
Qy	1508	CAAGGAAGCCGCTTCTCTCAGGAACACCAAGAGTTATCTCTTGGGGAAGCATGCCAA	1567
Db	1501	CAAGGAAGCCGCTTCTCTCAGGAACACCAAGAGTTATCTCTTGGGGAAGCATGCCAA	1560
Qy	1568	GCTCTGCTGACGAGAGCTGAAGTGAAGATGAGCGTGCAGGACTGCTTGGCTGCAG	1627
Db	1561	GCTCTGCTGACGAGAGCTGAAGTGAAGATGAGCGTGCAGGACTGCTTGGCTGCAG	1620
Qy	1628	GAGCCCAAGGGTTGGCTGTGTTCCGGCCGACAGACACGTTGTCGTGAGAGATCTTGCC	1687
Db	1621	GAGCCCAAGGGTTGGCTGTGTTCCGGCCGACAGACACGTTGTCGTGAGAGATCTTGCC	1680
Qy	1688	CAAGTTCCTGACGTGCTGAATGATGTATCGATGTCAGACTGCTCAGTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGACGTGCTGAATGATGTATCGATGTCAGACTGCTCAGTCTTCTTTTA	1740
Qy	1748	TGTACAGGAACCAACGTTTCAAAAGAACAGGCTTTTCTTACCCGAAGAGTGTGAGAG	1807
Db	1741	TGTACAGGAAGCACGTTTCAAAAGAACAGGCTTTTCTTACCCGAAGAGTGTGAGAG	1800
Qy	1808	CAAGTTTCAAAAGCATTGAATTCAGACAGCATTTGAAGAGGTTGCACTGCGAGACTGTC	1867
Db	1801	CAAGTTTCAAAAGCATTGAATTCAGACAGCATTTGAAGAGGTTGCACTGCGAGACTGTC	1860
Qy	1868	GGAAGCAGAGGTACAGGAGATATGGGAAAGCAGGCCCGCTGCTACAGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTACAGGAGATATGGGAAAGCAGGCCCGCTGCTACAGTCCAGACTCCG	1920
Qy	1928	CTTCAATCCCAAGCTTGAAGGGGTGCGCCGATTTGTGAACATGAGCTACGTCTGGAGAG	1987
Db	1921	CTTCAATCCCAAGCTTGAAGGGGTGCGCCGATTTGTGAACATGAGCTACGTCTGGAGAG	1980
Qy	1988	CAGAAAGCTTCCGAGAGAAAGAGGGCCAGAGGCTCACCTGAGAGGTTAAAGCATGTT	2047
Db	1981	CAGAAAGCTTCCGAGAGAAAGAGGGCCAGAGGCTCACCTGAGAGGTTAAAGCATGTT	2040
Qy	2048	CAGCGTCTCAACTACAGAGCGGCGCGAGCCCGGCTCTTGTGGCGCTTGTGTGTGGG	2107
Db	2041	CAGCGTCTCAACTACAGAGCGGCGCGAGCCCGGCTCTTGTGGCGCTTGTGTGTGGG	2100

OY	2108	CCTGGACGATATCCACAGGCGCTGGGCGACCTTCGTGCCTGGCTGGCGGGGCCAGAAACC	2167
Dp	2101	CCTGGACGATATCCACAGGCGCTGGGCGACCTTCGTGCCTGGCTGGCGGGGCCAGAAACC	2166
OY	2168	GCCGCGTGAAGCTA-----CATCCCCCA	2191
Dp	2161	GCGCGCTGAGCGTGACTTTGTCAAGTAGATGTGACGGGCGGTAACAACATATCCC	2228
OY	2192	GGACAGGCTCACGAGAGTCATCGCAGCATATCAAACCCAGAAACAATACTGGATGCG	2251
Dp	2221	GGACAGGCTCACGAGAGTCATCGCAGCATATCAAACCCAGAAACAATACTGGATGCG	2280
OY	2252	TGGGTATGCCGTGGTTCAGAAAGCCGCCATGGGCAAGTCCGCAAGGCTTTCAAGA---	2307
Dp	2281	TGGGTATGCCGTGGTTCAGAAAGCCGCCATGGGCAAGTCCGCAAGGCTTTCAAGAGCCA	2340
OY	2308	-----	2307
Dp	2341	CGTCTTAACCTTGACAGAACCTTCACAGCGTACATGGCAAGTTCGGCTCACCTGCAGAA	2400
OY	2308	-----	2307
Dp	2401	GACAGCCCGCTGAGGAGATGCCGTGCATCGACAGAGCTCTCTCGTAATGAGCCAG	2460
OY	2308	-----	gg 2309
Dp	2461	CAGTGGCTCTTCAGACGTCTTCAAGCTTCATGTGCCACACACGCCCGGCGCATCAAGGG	2520
OY	2310	CAAGTCTTAAGTCCAGTGCACAGGGGATCCCGAGGGCTCAATCCTTCACAGCTGTG	2369
Dp	2521	CAAGTCTTAAGTCCAGTGCACAGGGGATCCCGAGGGCTCAATCCTTCACAGCTGTG	2580
OY	2370	CAGCCTGTGCACGGCGCATATGAGAAACAAGCTTTGCGGGAGATTGGGCGGACGGGCT	2429
Dp	2581	CAGCCTGTGTACGGCGCATATGAGAAACAAGCTTTGCGGGAGATTGGGCGGACGGGCT	2640
OY	2440	GCTCTCGGCTTTGTGTGATGATTTCTTGTGTGTGACACTCACTCACCCACGGAAAC	2489
Dp	2641	GCTCTCGGCTTTGTGTGATGATTTCTTGTGTGTGACACTCACTCACCCACGGAAAC	2700
OY	2490	CTTCTCTCAGAACCTTGATCCAGAGTGTCCCTGAGATAGGCTGCTGTGAACTTGCAGAA	2549
Dp	2701	CTTCTCTCAGAACCTTGATCCAGAGTGTCCCTGAGATAGGCTGCTGTGAACTTGCAGAA	2760
OY	2550	GACAGTGTGAATTCCTCTGTAGAAAGACAGAGCCCTGGGTGGCACGGCTTTGTCAAT	2609
Dp	2761	GACAGTGTGAATTCCTCTGTAGAAAGAGAGCCCTGGGTGGCACGGCTTTGTCAAT	2820
OY	2610	GCCGCGCCACAGGCTAATCCCTGGTGGGCGCTGCTGTGTGATACCGGAACTCGAAGGT	2669
Dp	2821	GCCGCGCCACAGGCTAATCCCTGGTGGGCGCTGCTGTGTGATACCGGAACTCGAAGGT	2880
OY	2670	GCAAGAGGACATACTCCAGCTATGCCCGGACCTCATACAGACCAAGTCTACACTTCAACG	2729
Dp	2881	GCAAGAGGACATACTCCAGCTATGCCCGGACCTCATACAGACCAAGTCTACACTTCAACG	2940
OY	2730	CGGCTTCAAGGCTGGAGAAACATAGCGTCCAAAACCTTTGGGGTCTTGGGGCTGAAGTG	2789
Dp	2941	CGGCTTCAAGGCTGGAGAAACATAGCGTCCAAAACCTTTGGGGTCTTGGGGCTGAAGTG	3000
OY	2790	TCAACAGCTGTTTTCTGATTTTGCAGGTGAAACAGCTTCACAGCGTGTGGACCAACATCTA	2849
Dp	3001	TCAACAGCTGTTTTCTGATTTTGCAGGTGAAACAGCTTCACAGCGTGTGGACCAACATCTA	3060
OY	2850	CAAGATCTCTCTGTGCAGGCGGTACAGATTTCAACGCAATGTGTGTGACAGCTCCCAATTCA	2909
Dp	3061	CAAGATCTCTCTGTGCAGGCGGTACAGATTTCAACGCAATGTGTGTGACAGCTCCCAATTCA	3120
OY	2910	TCACACAGTTTGGAGAAACCCCAATTTTTCGTGGCGGTATCTCTTACACAGGCTTCCCT	2969
Dp	3121	TCACACAGTTTGGAGAAACCCCAATTTTTCGTGGCGGTATCTCTTACACAGGCTTCCCT	3180

QY	2970	CTGCTACTCCATCCTGAAAAGCCAAAGAAACGACGGAGATGTCGTGGGGGCGCAAGGGGCGCCG	3022
Db	3151	CTGCTACTCCATCCTGAAAAGCCAAAGAAACGACGGAGATGTCGTGGGGGCGCAAGGGGCGCCG	3240
QY	3030	CGGCCCTCTGCGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT	3089
Db	3241	CGGCCCTCTGCGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT	3300
QY	3090	GACTCGACACCGGTGTACCTTACGTGSCACTCTCTGGGTGCACTCAGGACAGGCCAGACGA	3145
Db	3301	GACTCGACACCGGTGTACCTTACGTGSCACTCTCTGGGTGCACTCAGGACAGGCCAGACGA	3360
QY	3150	GCTGAGTCCGAAAGCTCCCGGGGAGAGAGCTGACCTGACCTTGAGAGCCGACGCAACCCGGC	3209
Db	3351	GCTGAGTCCGAAAGCTCCCGGGGAGAGAGCTGACCTGACCTTGAGAGCCGACGCAACCCGGC	3420
QY	3210	ACTGCGCTCAGACTTCAAGACCATCTGTGACTGTATGGCCACCCCGCCACAGCCAGCCGGA	3259
Db	3421	ACTGCGCTCAGACTTCAAGACCATCTGTGACTGTATGGCCACCCCGCCACAGCCAGCCGGA	3480
QY	3270	GAGCGAGACACCGAGAGCCCTGTACACGCCGGGCTTACGTCCAGGAGGAGGGGCGGCC	3329
Db	3481	GAGCGAGACACCGAGAGCCCTGTGTACACGCCGGGCTTACGTCCAGGAGGAGGGGCGGCC	3540
QY	3330	CACACCCAGGCGCCGCAACCGCTGGAGAGCTGAGGCGCTGAGTGAAGTGTGGCCAGGCGTG	3389
Db	3541	CACACCCAGGCGCCGCAACCGCTGGAGAGCTGAGTGAAGTGTGGCCAGGCGTG	3600
QY	3390	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT	3449
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT	3650
QY	3450	GAGTGTCCAGACACACTGCGCGTCTTCACTTCCCAACAGCGTGGCGCTCGGCTCCACCCCA	3509
Db	3651	GAGTGTCCAGACACACTGCGCGTCTTCACTTCCCAACAGCGTGGCGCTCGGCTCCACCCCA	3720
QY	3510	GGGCGACGCTTTTCTCTACACAGAGCGCGGCTTGCATCTCCCAATAGAAATATGTCAATCC	3559
Db	3721	GGGCGACGCTTTTCTCTACACAGAGCGCGGCTTGCATCTCCCAATAGAAATATGTCAATCC	3780
QY	3570	CCAGATTCCGCATTTGTCAACCCCTCGGCGCTGCGCTCTTGTGCTTCCACCCCAACATCC	3629
Db	3781	CCAGATTCCGCATTTGTCAACCCCTCGGCGCTGCGCTCTTGTGCTTCCACCCCAACATCC	3840
QY	3530	AGGTGGAGACCCCTGAGAAAGACCTCTGGAGCTCTGGAAATTTGGAGTGAACCAAAGTGTG	3689
Db	3841	AGGTGGAGACCCCTGAGAAAGACCTCTGGAGCTCTGGAAATTTGGAGTGAACCAAAGTGTG	3900
QY	3590	CCCTGTACACAGGCGAGAGACCTCTGCACCTGATGCGGGGTCCCTGTGGGTCAAAATGGGGG	3749
Db	3901	CCCTGTACACAGGCGAGAGACCTCTGCACCTGATGCGGGGTCCCTGTGGGTCAAAATGGGGG	3960
QY	3750	GAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTTTTCACTTTGAAAAAAA	3804
Db	3951	GAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTTTTCACTTTGAAAAAAA	4015
RESULT 11			
ABA97534 standard; DNA; 4015 BP.			
XX	ABA97534;		
XX	05-APR-2002 (first entry)		
XX	Cancer cell discrimination method related human DNA.		
XX	Human; telomerase; enzyme; cancer cell discrimination; gene;		
XX	reverse transcriptase; ds.		
XX	Homo sapiens.		
XX	JP2001309791-A.		

XX 06-NOV-2001.
 PD 02-MAY-2000; 2000JP-00138250.
 PF 02-MAY-2000; 2000JP-00138250.
 RR 02-MAY-2000; 2000JP-00138250.
 XX (KANE/) KANEUCHI H.
 PA (KANE/) KANEUCHI M.
 XX WPI; 2002-134853/18.

PT Discrimination of a cancer cell in a sample tissue, comprises determining
 the expression level of a reverse transcriptase component of telomerase
 using a hybridization assay.

PS Claim 2; Page 9-10; 16pp; Japanese.

CC The present invention relates to a method for the discrimination of a
 CC cancer cell in a sample tissue, which involves determining the expression
 CC level of a reverse transcriptase component of telomerase in a cell
 CC constituting the sample tissue by an in situ hybridization of the mRNA of
 CC the enzyme, and judging a cell showing a higher expression level than
 CC that of the reverse transcriptase component of telomerase in a normal
 CC cell to be a cancer cell. The present sequence is a human DNA used in the
 CC exemplification of the invention

Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 93.1%; Score 3559; DB 6; Length 4015;
 Best Local Similarity 94.6%; Pred. No. 0;
 Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

QY 8 GCAAGCGTGGTCTCTGTCGACAGTGGAAAGCCCTGCCCCGACACCCCGCATGCCC 67
 DB 1 GCAAGCGTGGTCTCTGTCGACAGTGGAAAGCCCTGCCCCGACACCCCGCATGCCC 60
 QY 68 GCGGCGTCCCCGCGTCCGAGCGGCGTCCCTGTCGACGACGACATCCGAGAGTGGT 127
 DB 61 GCGGCGTCCCCGCGTCCGAGCGGCGTCCCTGTCGACGACGACATCCGAGAGTGGT 120
 QY 128 GCGGCGTCCCCGCGTCCGAGCGGCGTCCCTGTCGACGACGACATCCGAGAGTGGT 187
 DB 121 GCGGCGTCCCCGCGTCCGAGCGGCGTCCCTGTCGACGACGACATCCGAGAGTGGT 180
 QY 188 GGAAGCGGCGGCTTCCGCGCGTGGTGGCCAGTGGTGGTGGTGGTGGTGGTGGTGGT 247
 DB 181 GGAAGCGGCGGCTTCCGCGCGTGGTGGCCAGTGGTGGTGGTGGTGGTGGTGGTGGT 240
 QY 248 ACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 307
 DB 241 ACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 QY 308 CCGAGTGGTCTGAGAGGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
 DB 301 CCGAGTGGTCTGAGAGGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
 QY 368 GCTGCTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 427
 DB 361 GCTGCTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 QY 428 CTTGCGGCAACAGGTGACCGACGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
 DB 421 CTTGCGGCAACAGGTGACCGACGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
 QY 488 CCGGCGTGGCGAGCGAGCTGTGCTTCACTGTGCGACGCTGTGCGGCGGCGGCGGCGGCGG 547
 DB 481 CCGGCGTGGCGAGCGAGCTGTGCTTCACTGTGCGACGCTGTGCGGCGGCGGCGGCGGCGG 540
 QY 548 GCGTCCAGAGCTGGCGCTTACAGAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607
 DB 541 GCGTCCAGAGCTGGCGCTTACAGAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600

QY 608 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 667
 DB 601 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
 QY 668 CTGGAACCATAGCTCAGGAGAGCCCGGCGGCTCCCTGCGGCTGCGAGCCCGGCGGCGG 727
 DB 661 CTGGAACCATAGCTCAGGAGAGCCCGGCGGCTCCCTGCGGCTGCGAGCCCGGCGGCGG 720
 QY 728 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 787
 DB 721 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
 QY 788 TGCCCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 847
 DB 781 TGCCCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
 QY 848 GCGTGGACCGAGTGAACGCTGGTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 907
 DB 841 GCGTGGACCGAGTGAACGCTGGTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 900
 QY 908 CACCTCTTTGAGAGGCTGCGCTCTGTCGACGCGCACTCCACCATCTCGTGGCGCGCA 967
 DB 901 CACCTCTTTGAGAGGCTGCGCTCTGTCGACGCGCACTCCACCATCTCGTGGCGCGCA 960
 QY 968 GCAACCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1027
 DB 961 GCAACCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
 QY 1028 CCGGCTGACCGCGGAGACCAAGCACTTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1087
 DB 1021 CCGGCTGACCGCGGAGACCAAGCACTTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1080
 QY 1088 GCGCTCTTTCTACTGAGCTCTTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1147
 DB 1081 GCGCTCTTTCTACTGAGCTCTTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
 QY 1148 GACCATCTTTCTGAGGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1207
 DB 1141 GACCATCTTTCTGAGGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1200
 QY 1208 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1267
 DB 1201 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1260
 QY 1268 GTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1327
 DB 1261 GTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1320
 QY 1328 AGCGGCTGTCTGTGCGGCGGAGAGCCCGAGGCTGTGTCGCGGCGGCGGCGGCGGCGG 1387
 DB 1321 AGCGGCTGTCTGTGCGGCGGAGAGCCCGAGGCTGTGTCGCGGCGGCGGCGGCGGCGG 1380
 QY 1388 CACAGACCCCGGCTGCGCTGTGTCGAGCTGTCTGCGGCGGCGGCGGCGGCGGCGGCGG 1447
 DB 1381 CACAGACCCCGGCTGCGCTGTGTCGAGCTGTCTGCGGCGGCGGCGGCGGCGGCGGCGG 1440
 QY 1448 CCGGCTGTGTCGAGGCTGTGTCGAGCTGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1507
 DB 1441 CCGGCTGTGTCGAGGCTGTGTCGAGCTGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1500
 QY 1508 CACAGACCCCGGCTTCTCTGAGAGACCAAGAGATTATCTCTCTGCGGAGAGATGCGCAA 1567
 DB 1501 CACAGACCCCGGCTTCTCTGAGAGACCAAGAGATTATCTCTCTGCGGAGAGATGCGCAA 1560
 QY 1568 GCTCTGCTGAGAGCTGAGTGAAGATGAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1627
 DB 1561 GCTCTGCTGAGAGCTGAGTGAAGATGAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1620
 QY 1628 GAGCCGAGGCGGCTGTGCTGTGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1687
 DB 1621 GAGCCGAGGCGGCTGTGCTGTGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1680
 QY 1688 CAGTCTCTGACCTGAGTGAAGTGTGTCGTCGAGCTGTGTCGAGCTCTTCTTTTA 1747

Db 1021 CCCGCTGACGCGACGACCAAGACCTTCTACTCTCAGGCGACAGAGACAGCTGCG 1080
QY 1088 GCCCTCTTCTACTCAGCTCTCTGAGGCCAGCTGACTGAGCGCTGAGGAGCTGCGA 1147
Db 1081 GCCCTCTTCTACTCAGCTCTCTGAGGCCAGCTGACTGAGCGCTGAGGAGCTGCGA 1140
QY 1148 GACCATCTTCTGAGGCTTCCAGGCGCTGAGTCCAGGAGCTCCCGCAGGTTGCCGCT 1207
Db 1141 GACCATCTTCTGAGGCTTCCAGGCGCTGAGTCCAGGAGCTCCCGCAGGTTGCCGCT 1200
QY 1208 GCCCAGCGCTACTGAGCAATCGGCGCTGTTCTGAGCGCTGAGGAGCTCCAGGCGA 1267
Db 1201 GCCCAGCGCTACTGAGCAATCGGCGCTGTTCTGAGCGCTGAGGAGCTCCAGGCGA 1260
QY 1268 GTGCCCCCTAGCGGGGTCTCTCAGAGCGCACTGCCCGCTGAGCTGAGCTCACCCAGC 1327
Db 1261 GTGCCCCCTAGCGGGGTCTCTCAGAGCGCACTGCCCGCTGAGCTGAGCTCACCCAGC 1320
QY 1328 AGCCGCTGCTGCTGCGGGGAGAGCCCGCAGGCGCTGAGGCGCGCCCGCAGGAGGAG 1387
Db 1321 AGCCGCTGCTGCTGCGGGGAGAGCCCGCAGGCGCTGAGGCGCGCCCGCAGGAGGAG 1380
QY 1388 CACAGACCCCGCTGCTGCTGAGTGCAGCTGCTGCGCAGCAGACGCCCTGAGCTGTA 1447
Db 1381 CACAGACCCCGCTGCTGCTGAGTGCAGCTGCTGCGCAGCAGACGCCCTGAGCTGTA 1440
QY 1448 CGGCTTCTGAGGCGCTGCTGCTGCGCGCGCTGCTGCGCGCTTCTGAGGCTTCCAGGCA 1507
Db 1441 CGGCTTCTGAGGCGCTGCTGCTGCGCGCGCTGCTGCGCGCTTCTGAGGCTTCCAGGCA 1500
QY 1508 CACAGACCCCGCTTCTCAGAGAACACCAAGAGTTCTCTCCCTGAGGAGCATGCGCAA 1567
Db 1501 CACAGACCCCGCTTCTCAGAGAACACCAAGAGTTCTCTCCCTGAGGAGCATGCGCAA 1560
QY 1568 GCTCTCTGAGAGAGCTGAGCTGAGAGATGAGGCTGCGGAGCTGCGCTGAGCTGCGAG 1627
Db 1561 GCTCTCTGAGAGAGCTGAGCTGAGAGATGAGGCTGCGGAGCTGCGCTGAGCTGCGAG 1620
QY 1628 GAGCCAGAGGCTGCTGCTGCTGCGCGCAGAGACCGCTGCTGAGGAGATCTGAGC 1687
Db 1621 GAGCCAGAGGCTGCTGCTGCTGCGCGCAGAGACCGCTGCTGAGGAGATCTGAGC 1680
QY 1688 CAGTTCTGCACTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1747
Db 1681 CAGTTCTGCACTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1740
QY 1748 TGTCAAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTAACCGAAGAGTGTCTGAG 1807
Db 1741 TGTCAAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTAACCGAAGAGTGTCTGAG 1800
QY 1808 CAGTTGCAAGATTTGAGATCAAGCAGCAGCTTGAAGAGGCTGAGCTGCGGAGCTGTC 1867
Db 1801 CAGTTGCAAGATTTGAGATCAAGCAGCAGCTTGAAGAGGCTGAGCTGCGGAGCTGTC 1860
QY 1868 GAGAGCAGAGCTGAGGAGCAGATCGGAGAGACAGGCGCGCTGCTGAGCTGAGCTGAG 1927
Db 1861 GAGAGCAGAGCTGAGGAGCAGATCGGAGAGACAGGCGCGCTGCTGAGCTGAGCTGAG 1920
QY 1928 CTTCAATCCCAAGCTTGAAGGCTGCGGCTGCGGCTGCTGAGCAATGAGCACTGAGAGC 1987
Db 1921 CTTCAATCCCAAGCTTGAAGGCTGCGGCTGCGGCTGCTGAGCAATGAGCACTGAGAGC 1980
QY 1988 CAGAGCTTCCGAG 2047
Db 1981 CAGAGCTTCCGAG 2040
QY 2048 CAGAGCTCTCACTAG 2107
Db 2041 CAGAGCTCTCACTAG 2100
QY 2108 CTTGAGAGATCAAG 2167
Db 2101 CTTGAGAGATCAAG 2160

QY 2168 GCGGCTGAGCTGTA-----CATCCCCA 2191
Db 2161 GCGGCTGAGCTGTAATTTTGTCAAGGTGATGTGAAGGCGGCTGAGACACATCCCCA 2220
QY 2192 GAGCAGGCTCAGAGAGGTCATCGCAGCATCATCAAAACCCAGAAACAGCTACTGAGTGC 2251
Db 2221 GAGCAGGCTCAGAGAGGTCATCGCAGCATCATCAAAACCCAGAAACAGCTACTGAGTGC 2280
QY 2252 TCGGTATGCGGCTGCTCAAG 2307
Db 2281 TCGGTATGCGGCTGCTCAAG 2340
QY 2308 ----- 2307
Db 2341 CGTCTTACTTGAAGACCTCAGAGCGTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
QY 2308 ----- 2307
Db 2401 GACAGCCCGCTGAGAGGATGCGCTGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
QY 2308 ----- 2307
Db 2461 CAGTGCCTCTTGAAGCTTCTTCAAGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
QY 2310 CAGTGCCTCTTGAAGCTTCTTCAAGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2569
Db 2521 CAGTGCCTCTTGAAGCTTCTTCAAGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
QY 2370 CAGCTGCTGCTGAG 2429
Db 2581 CAGCTGCTGCTGAG 2640
QY 2430 GCTCTGCTGCTGAG 2489
Db 2441 GCTCTGCTGCTGAG 2700
QY 2490 CTTCTCAG 2549
Db 2701 CTTCTCAG 2760
QY 2550 GACAGTGTGAATCTTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2609
Db 2761 GACAGTGTGAATCTTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
QY 2610 GCGGCGCAG 2669
Db 2821 GCGGCGCAG 2880
QY 2670 GAG 2729
Db 2881 GAG 2940
QY 2730 GCGGCTTGAAG 2789
Db 2941 GCGGCTTGAAG 3000
QY 2790 TCAAGAGCTGTTCTGATTTGAG 2849
Db 3001 TCAAGAGCTGTTCTGATTTGAG 3060
QY 2890 CAGAGTCTCTGCTGAG 2909
Db 3061 CAGAGTCTCTGCTGAG 3120
QY 2910 TCAAGAGATTTGAAG 2969
Db 3121 TCAAGAGATTTGAAG 3180
QY 2970 CTTGCTACTCTCACTGAG 3029
Db 3181 CTTGCTACTCTCACTGAG 3240

QY 428 CTGCCCCAACGCGTGAACCGACTGCGGAGGAGCGGCGCTGCGGCTGCTGCTGCG 487
Db 421 CTGCCCCAACGCGTGAACCGACTGCGGAGGAGCGGCGCTGCGGCTGCTGCTGCG 480
QY 488 CCGCGTGGGCGGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
Db 481 CCGCGTGGGCGGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 548 GCGTCCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
Db 541 GCGTCCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 608 TCAGGCGCGGCG 667
Db 601 TCAGGCGCGGCG 660
QY 668 CTGGAACCAATAGCGTGAAGGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Db 661 CTGGAACCAATAGCGTGAAGGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGCGCGCGGCG 787
Db 721 GAGCGCGGCGGCG 780
QY 788 TGCCCTGAGCGCGGAGCG 847
Db 781 TGCCCTGAGCGCGGAGCG 840
QY 848 GCGTGAACCGAGTGAACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
Db 841 GCGTGAACCGAGTGAACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 908 CACTCTTTTGAAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
Db 901 CACTCTTTTGAAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 968 GCAACCAAGCGGCG 1027
Db 961 GCAACCAAGCGGCG 1020
QY 1028 CCGCGGTGAAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 1087
Db 1021 CCGCGGTGAAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 1080
QY 1088 GCGCTCTCTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 1147
Db 1081 GCGCTCTCTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 1140
QY 1148 GACCATCTTTCTGAGGCTTCCAGGCGCTGAGTGCAGAGGAGCTCCCGCAGGTTGCGCGCGCT 1207
Db 1141 GACCATCTTTCTGAGGCTTCCAGGCGCTGAGTGCAGAGGAGCTCCCGCAGGTTGCGCGCGCT 1200
QY 1208 GCGCCAGCGCTACTGCAATGCG 1267
Db 1201 GCGCCAGCGCTACTGCAATGCG 1260
QY 1268 GCGCGCGCTTACGCGGCTGCTTCAAGAGCACTGCGCGCGCTGCGAGTGCAGTGCAGTGCAGTGCAG 1327
Db 1261 GCGCGCGCTTACGCGGCTGCTTCAAGAGCACTGCGCGCGCTGCGAGTGCAGTGCAGTGCAGTGCAG 1320
QY 1328 AGCGCGGTCTGCTGCGCGGAGAGCG 1387
Db 1321 AGCGCGGTCTGCTGCGCGGAGAGCG 1380
QY 1388 CACACACCGCGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447
Db 1381 CACACACCGCGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1448 CCGCTTCTGCGGCGCTGCTGCG 1507
Db 1441 CCGCTTCTGCGGCGCTGCTGCG 1500
QY 1508 CACACACCGCGGTCTGCTGCGGAGAGCACTGCTGCTGCTGCGGAGAGCACTGCTGCTGCTGCTGCT 1567

Db 1501 CACAGAACCGCGCTTCTCTCAAGAACCAAGAACTTCTCTCTCTGCGGAGAGATGCCAA 1560
QY 1568 GCTTCTGCTGAGAGAGTGAAGTGAAGATGAGCGTGCAGGAGTGCAGTGCAGTGCAGTGCAG 1627
Db 1561 GCTTCTGCTGAGAGAGTGAAGTGAAGATGAGCGTGCAGGAGTGCAGTGCAGTGCAGTGCAG 1620
QY 1628 GAGCCAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1687
Db 1621 GAGCCAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1680
QY 1688 CAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1747
Db 1681 CAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 1748 TGTCACGAGAGCACGCTTCAAAAGAACGCGCTTCTTCTACCGAAGAGTGTGAGAG 1807
Db 1741 TGTCACGAGAGCACGCTTCAAAAGAACGCGCTTCTTCTACCGAAGAGTGTGAGAG 1800
QY 1808 CAACTTCAAAAGATGGAATGAGACAGCACTTGAAGAGGAGTGCAGTGCAGAGTGCAG 1867
Db 1801 CAACTTCAAAAGATGGAATGAGACAGCACTTGAAGAGGAGTGCAGTGCAGAGTGCAG 1860
QY 1868 GGAAGCAGAGGATGAGAGATGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1927
Db 1861 GGAAGCAGAGGATGAGAGATGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920
QY 1928 CTTATCTCCCAAGCTGAGCGGCGTGCAGCGGATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1987
Db 1921 CTTATCTCCCAAGCTGAGCGGCGTGCAGCGGATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1980
QY 1988 CAAAGCTTCCGAG 2047
Db 1981 CAAAGCTTCCGAG 2040
QY 2048 CAGCGTCTCAATGAGAGCGGCG 2107
Db 2041 CAGCGTCTCAATGAGAGCGGCG 2100
QY 2108 CTTGAGCATATTCAGAGAGGCTTGCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2167
Db 2101 CTTGAGCATATTCAGAGAGGCTTGCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
QY 2168 GCGCGCTGAGCTGTA-----CATCCCCA 2191
Db 2161 GCGCGCTGAGCTGTA-----CATCCCCA 2220
QY 2192 GAGCAGGCTCAGAGAGATGAGCAGCATATCAAAATCCCAAGAACAGTACTGCTGCTGCTGCTGCTGCTGCT 2251
Db 2221 GAGCAGGCTCAGAGAGATGAGCAGCATATCAAAATCCCAAGAACAGTACTGCTGCTGCTGCTGCTGCTGCT 2280
QY 2252 TCGGTATGCGGTGATTCAGAGAGGCG 2307
Db 2281 TCGGTATGCGGTGATTCAGAGAGGCG 2340
QY 2308 ----- 2307
Db 2341 CGTCTTACTTGAAGACCTTCAGCGCTGATGAGAGAGAGTTCGAGTGCAGTGCAGTGCAGTGCAG 2400
QY 2308 ----- 2307
Db 2401 GACACGCGCGCTGAGAGAGTCCGCTGCTATGAGCAGAGAGTCTCTCTGATGAGGCGAG 2460
QY 2308 -----G 2309
Db 2461 CAGTGCCTTTCAGAGCTTCTTCAAGCTTCAATGAGCAGCAGCGCGTGCAGATGAGGCGAG 2520
QY 2310 CAACTCTTACGCTCAGAGTGCAGAGGAGTCCCGCAGAGGCTCATCTCTTCCAGAGTGCAGTGCAG 2369
Db 2521 CAACTCTTACGCTCAGAGTGCAGAGGAGTCCCGCAGAGGCTCATCTCTTCCAGAGTGCAGTGCAG 2380
QY 2370 CAGCTTGTGCTAGCGCGCATGAGAGACAGAGTGTTCGCGGAGATTGCGCGGAGCGAGCT 2429

Db 2581 CAGCTGTGCTACGCGACATGAGAGAACAGCTGTTTGGGGGANTTGGCGGGAGCGGCT 2640
 Qy 2430 GCTCTCGCTTTGGTGGATGATTTCTTGTGGTGAACACTCACTCACTCAACCGGAAAC 2489
 Db 2641 GCTCTCGCTTTGGTGGATGATTTCTTGTGGTGAACACTCACTCACTCAACCGGAAAC 2700
 Qy 2490 CTTCCTCAGAGACCTCTGTCCGAGGTGTCCCTGAGTATGCTGCTGGTGAATTGGGAA 2549
 Db 2701 CTTCCTCAGAGACCTCTGTCCGAGGTGTCCCTGAGTATGCTGCTGGTGAATTGGGAA 2760
 Qy 2550 GACAGTGTGATGATCTCTGTGAGAGACGAGGCGCTGGTGGACGAGGCTTTTGTTCAGAT 2609
 Db 2761 GACAGTGTGATGATCTCTGTGAGAGACGAGGCGCTGGTGGACGAGGCTTTTGTTCAGAT 2820
 Qy 2610 GCCGAGCCCAAGGCTATTTCCCTGTGGGCTGTGCTGATTAACCCGAGCCCTGGAGGT 2669
 Db 2821 GCCGAGCCCAAGGCTATTTCCCTGTGGGCTGTGCTGATTAACCCGAGCCCTGGAGGT 2880
 Qy 2670 GCAGAGCGACTACTCCAGCTATGCGCGGACCTCCACAGAGGCACTTCACTTCAACCG 2729
 Db 2881 GCAGAGCGACTACTCCAGCTATGCGCGGACCTCCACAGAGGCACTTCACTTCAACCG 2940
 Qy 2730 CGGCTTCAAGGCTGGAGGAGACATGCTGCAAACTCTTTGGGCTTTGGGCTGAGTG 2789
 Db 2941 CGGCTTCAAGGCTGGAGGAGACATGCTGCAAACTCTTTGGGCTTTGGGCTGAGTG 3000
 Qy 2790 TCACAGCTGTTTCTGGATTTGAGGTGAACAGCTCCAGAGGCTGTGACCAATCTA 2849
 Db 3001 TCACAGCTGTTTCTGGATTTGAGGTGAACAGCTCCAGAGGCTGTGACCAATCTA 3060
 Qy 2850 CAAGATCTCTCTGCTGAGGCTGACAGGTTTCAAGCTATGCTGAGGCTCCCTTCA 2909
 Db 3061 CAAGATCTCTCTGCTGAGGCTGACAGGTTTCAAGCTATGCTGAGGCTCCCTTCA 3120
 Qy 2910 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTTGAACAGGCTCTCT 2969
 Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTTGAACAGGCTCTCT 3180
 Qy 2970 CTGCTACTCATCTCTGAAGACCAAGACGAGGATGCTGAGGCGGCGGCGGCGGCG 3029
 Db 3181 CTGCTACTCATCTCTGAAGACCAAGACGAGGATGCTGAGGCGGCGGCGGCGGCGGCG 3240
 Qy 3030 CGGCTCTGCTCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3089
 Db 3241 CGGCTCTGCTCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3300
 Qy 3090 GACTGAGACCGGCTGACCTAGTGCCTCTCTGGGCTGACCTGAGGCTGAGGCTGAGGCT 3149
 Db 3301 GACTGAGACCGGCTGACCTAGTGCCTCTCTGGGCTGACCTGAGGCTGAGGCTGAGGCT 3360
 Qy 3150 GCTGAGTGGAGGCTCCGCGGAGCAGCTGACTGCTGAGGCGGCGGCGGCGGCGGCG 3209
 Db 3361 GCTGAGTGGAGGCTCCGCGGAGCAGCTGACTGCTGAGGCGGCGGCGGCGGCGGCGGCG 3420
 Qy 3210 ACTGCTCTGAGCTTCAAGACCTCTGAGCTGATGCTGAGGCTGAGGCTGAGGCTGAGGCT 3269
 Db 3421 ACTGCTCTGAGCTTCAAGACCTCTGAGCTGATGCTGAGGCTGAGGCTGAGGCTGAGGCT 3480
 Qy 3270 GAGGAGACACGAGGCTGCTGACGCGGCTGAGCTGAGGCTGAGGCTGAGGCTGAGGCT 3329
 Db 3481 GAGGAGACACGAGGCTGCTGACGCGGCTGAGCTGAGGCTGAGGCTGAGGCTGAGGCT 3500
 Qy 3330 CACACCCAGGCGGCGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3389
 Db 3541 CACACCCAGGCGGCGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3600
 Qy 3390 CATGCTCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3449
 Db 3601 CATGCTCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
 Qy 3450 GAGTGTCCAGACACCTGCGGCTTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCT 3509
 Db 3661 GAGTGTCCAGACACCTGCGGCTTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCT 3720

Qy 3510 GGGCAGCTTTTCTTCTACAGAGAGCCCGGCTTCACTCCCAATAGGAATAGCATCC 3569
 Db 3721 GGGCAGCTTTTCTTCTACAGAGAGCCCGGCTTCACTCCCAATAGGAATAGCATCC 3780
 Qy 3570 CCGATTGCGCATTTGTTACCCCTTGGCCCTGCTGCTTGTGCTTCCACCCCAATCC 3629
 Db 3781 CCGATTGCGCATTTGTTACCCCTTGGCCCTGCTGCTTGTGCTTCCACCCCAATCC 3840
 Qy 3630 AGGTGAGACCTTGAAGAGAGCCCTGGAGCTTGGGAAATTTGAGTACCAAGGTG 3689
 Db 3841 AGGTGAGACCTTGAAGAGAGCCCTGGAGCTTGGGAAATTTGAGTACCAAGGTG 3900
 Qy 3690 CCTGTACAGAGCGAGGACCTTGAACCTTGGATGAGGCTTCCCTGAGTCAAAATGGGCG 3749
 Db 3901 CCTGTACAGAGCGAGGACCTTGAACCTTGGATGAGGCTTCCCTGAGTCAAAATGGGCG 3960
 Qy 3750 GAGTGTCTGTTGGAGTAAATTAATGATATATAGTTTTCAGTTTGAAGAAAA 3804
 Db 3961 GAGTGTCTGTTGGAGTAAATTAATGATATATAGTTTTCAGTTTGAAGAAAA 4015

RESULT 14
 AB22474
 ID AB22474 standard; CDNA; 4015 BP.
 AC AB22474;
 XX 25-MAR-2003 (first entry)
 DT 25-MAR-2003 (first entry)
 XX
 DE Human telomerase reverse transcriptase encoding cDNA SEQ ID NO:1.
 XX
 KM Human: telomerase reverse transcriptase; enzyme; hERT; chromosome 5;
 KM vulvectomy; antitumor; epithelial cell migration promoter; wound;
 KM epithelialization; skin wound; lesion; burn; surgical incision; ulcer;
 KM epithelial cell; keratinocyte; epidermal; mucosal; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 56..3454
 FT /*tag= a
 FT /product= "human telomerase reverse transcriptase"
 XX
 PN W0200291999-A2.
 XX
 PD 21-NOV-2002.
 PF 09-MAY-2002; 2002WC-US014867.
 XX
 PR 09-MAY-2001; 2001US-0289903P.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Jiang X, Chiu C, Harley CB;
 XX
 DR WPI; 2003-120591/11.
 DR P-PDB; ABP56676.
 XX
 PT Composition for treating wounds and enhancing epithelialization of a skin
 PT surface, comprises vector encoding telomerase reverse transcriptase or
 PT telomerized epithelial cells on a microparticle or a matrix.
 XX
 PS Disclosure; Page 31-32; 68pp; English.
 XX
 CC The present invention describes a pharmaceutical composition (I)
 CC comprising a vector encoding telomerase reverse transcriptase (hERT) in
 CC an excipient or device, or comprises telomerized epithelial cells on a
 CC microparticle or a matrix suitable for topical administration or
 CC administration to a wound site. (I) has vulvectomy and antitumor
 CC activities and can be used to promote epithelial cell migration. (I) is
 CC useful for treating a wound and enhancing epithelialization of a skin
 CC surface. The wound is especially skin wound including acute lesion such

Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Matches 3/9/; conservative 0; Mismatches 0; Indels 218; Gaps 2,

QY	768	TGCCCCATGAGCCGAGACGAGACGCCCGTTGGGACAGGGGTTCTGGGCTTCAACCCGAGACGAC	847
Db	761	TGCCCCATGAGCCGAGACGAGACGCCCGTTGGGACAGGGGTTCTGGGCTTCAACCCGAGAGAC	840
QY	848	GCGTGAACCGAGTGAACGCTGGTTTCTGTGTGTGTCACTTCGACAGACCCGCGAAGAAC	907
Db	841	GCGTGAACCGAGTGAACCGTGGTTTCTGTGTGTGTCACTTCGACAGACCCGCGAAGAAC	900
QY	908	CACCTCTTTGAGAGGGTGTGCTCTGTGGACGCGGCACCTCCACCATCCTGGTGGGCGGCA	967
Db	901	CACCTCTTTGAGAGGGTGTGCTCTGTGGACGCGGCACCTCCACCATCCTGGTGGGCGGCA	960
QY	968	GCACCAACGCGGAGCCCCCATCATCATCGGAGCAACAGTCCCTTGGGACACGCTTGTCC	1027
Db	961	GCACCAACGCGGAGCCCCCATCATCATCGGAGCAACAGTCCCTTGGGACACGCTTGTCC	1022
QY	1028	CCCGGTGACCCGAGACCAAGCACTTCTCTACTCCCTCAGGCGACAAAGAGACGTGCG	108
Db	1021	CCCGGTGACCCGAGACCAAGCACTTCTCTACTCCCTCAGGCGACAAAGAGACGTGCG	108
QY	1088	GCCTCTCTCTACTACTAGCTCTCTGAGGCCACGCTTGACTGCGCTCGAGAGTTCTGGA	1147
Db	1081	GCCTCTCTCTCTACTACTAGCTCTCTGAGGCCACGCTTGACTGCGCTCGAGAGTTCTGGA	1140
QY	1148	GACCATCTTTTGAGGTTTCAGGAGCCCTGATATCCAGAGGACTCCCGCAGGTGGCCCGCT	1207
Db	1141	GACCATCTTTTGAGGTTTCAGGAGCCCTGATATCCAGAGGACTCCCGCAGGTGGCCCGCT	1200
QY	1208	GCCCCAGGCTACTCTGCAAAATGCGGCCCCCTGTCTGTGAAGTCTTGGAAACACGCGCA	1267
Db	1201	GCCCCAGGCTACTCTGCAAAATGCGGCCCCCTGTCTGTGAAGTCTTGGAAACACGCGCA	1260
QY	1268	GTGCCCCCTACGGGAGTGTCTCTCAAGACGCACTGCGCCCTGAGACTGAGTCAACCCAGC	1327
Db	1261	GTGCCCCCTACGGGAGTGTCTCTCAAGACGCACTGCGCCCTGAGACTGAGTCAACCCAGC	1320
QY	1328	AGCCGGTGTCTGTGTCCCGGAGAAAGCCCCCAAGGCTCTGTGGCGGCCCCCGAGAGAGAGA	1387
Db	1321	AGCCGGTGTCTGTGTCCCGGAGAAAGCCCCCAAGGCTCTGTGGCGGCCCCCGAGAGAGAGA	1380
QY	1388	CACAGACCCCGTGTGTGTGTCAGCTGTCCGACACACAGCAGCCCTGTGGAGCTGTGA	1447
Db	1381	CACAGACCCCGTGTGTGTGTCAGCTGTCCGACACACAGCAGCCCTGTGGAGCTGTGA	1440
QY	1448	CGGTTTGTGTGGGCTGTGCTGTGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1507
Db	1441	CGGTTTGTGTGGGCTGTGCTGTGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1500
QY	1508	CAACGAAACGCGCGTCTCTCAGAGAACACCAAGATTATCTCCTGTGGAGAACATGACAA	1567
Db	1501	CAACGAAACGCGCGTCTCTCAGAGAACACCAAGATTATCTCCTGTGGAGAACATGACAA	1560
QY	1568	GCTGTGCTGTGACGAGGTGACGTGTGAAGAAAGAACGTGTGGGAGCTGTGCTGTGCGAG	1627
Db	1561	GCTGTGCTGTGACGAGGTGACGTGTGAAGAAAGAACGTGTGGGAGCTGTGCTGTGCGAG	1620
QY	1628	GAGCCCAAGGGGTTTGGCTGTGTTCGAGCGCAGACACCGTCTGTGAGAGATCTGTGC	1687
Db	1621	GAGCCCAAGGGGTTTGGCTGTGTTCGAGCGCAGACACCGTCTGTGAGAGATCTGTGC	1680
QY	1688	CAAGTTCTGTCACTGGGTGTATGAGTGTGTATCGATCGAGCTGTCAAGGTCTTCTTTTA	1747
Db	1681	CAAGTTCTGTCACTGGGTGTATGAGTGTGTATCGATCGAGCTGTCAAGGTCTTCTTTTA	1740
QY	1748	TGTTCACGAGAACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGATGTCTGAG	1807
Db	1741	TGTTCACGAGAACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGATGTCTGAG	1800
QY	1808	CAAGTTGCAAAAGATTGGAATCAGACAGACTTGAAGAGGTTCACTGTGGAGCTGTCTC	1867
Db	1801	CAAGTTGCAAAAGATTGGAATCAGACAGACTTGAAGAGGTTCACTGTGGAGCTGTCTC	1860

QY	1868	GAAGACAGAGGTCAAGGCGAGCATCCGGGAAGCCAGAGGCGCGCCCGTGCATGATCACAATCCG	1927
Dp	1861	GGAGACAGAGGTCAAGGCGAGCATCCGGGAAGCCAGAGGCGCGCCCGTGCATGATCACAATCCG	1920
QY	1928	CTTCATCCCAAGCCTGACGGGCTGCGGGCCGATTGTGAACATGACATGACATGATCGTGGAGC	1987
Dp	1921	CTTCATCCCAAGCCTGACGGGCTGCGGGCCGATTGTGAACATGACATGACATGATCGTGGAGC	1980
QY	1988	CAGAACGTTCCGACAGAGAAAGAAGGCGCGACGCTCTCACTCCGAGGCTGAAGAGCATGTT	2047
Dp	1981	CAGAACGTTCCGACAGAGAAAGAAGGCGCGACGCTCTCACTCCGAGGCTGAAGAGCATGTT	2040
QY	2048	CAGCGTGTCTCAACTACGACGCGGCGCGCGCGCCGACCTCTGTGGCGCCTCTGTGCTGAGG	2107
Dp	2041	CAGCGTGTCTCAACTACGACGCGGCGCGCGCGCCGACCTCTGTGGCGCCTCTGTGCTGAGG	2100
QY	2108	CCTGGACGATATTCACACAGGCGCTGGCGGACCTTGCTGCTGCTGTGCGGAGCCACAGACCC	2167
Dp	2101	CCTGGACGATATTCACACAGGCGCTGGCGGACCTTGCTGCTGCTGTGCGGAGCCACAGACCC	2160
QY	2168	GCCGCGCTGAGCGTGA-----CATCCCCA	2191
Dp	2161	GCCGCGCTGAGCGTGA-----CATCCCCA	2220
QY	2192	GAACAGGCTCAAGAGGTCATCGCCAGCATCATMAACCCAGAACACAGTACTGCTGCG	2251
Dp	2221	GAACAGGCTCAAGAGGTCATCGCCAGCATCATMAACCCAGAACACAGTACTGCTGCTGCG	2280
QY	2252	TCCGATATCCGCTGGTCCAGAGAGCGCCGACATGGGACATCCGCAAGGCTTCAAGA-----	2307
Dp	2281	TCCGATATCCGCTGGTCCAGAGAGCGCCGACATGGGACATCCGCAAGGCTTCAAGAGCCA	2340
QY	2308	-----	2307
Dp	2341	CGTCTCTACCTTGAACAGACCTCGACCGTACATGGACATGTTGCGGTCACTCGACAGA	2400
QY	2308	-----	2307
Dp	2401	GACCAAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGACCTCTCCGAAATGAGGCGCAG	2460
QY	2308	-----	2309
Dp	2461	CAGTGGCCTCTTCAGACGCTCTTCCATACGTTTCATGTGCGACACACGCCCGGCGCATCAAGGG	2520
QY	2310	CAAGTCTCACTCGATCGATGCCAGGGGATCCGCAAGGCTCATCTCTTCACGCTGCTTG	2369
Dp	2521	CAAGTCTCACTCGATCGATGCCAGGGGATCCGCAAGGCTCATCTCTTCACGCTGCTTG	2580
QY	2370	CAGCCTGTGCTACAGCGCGCATGAGAGAACCAACTGTGTTGCGGGAGTTGCGGCGGAGCGGGCT	2429
Dp	2581	CAGCCTGTGCTACAGCGCGCATGAGAGAACCAACTGTGTTGCGGGAGTTGCGGCGGAGCGGGCT	2640
QY	2430	GCTCCTGCGTTGTGTGATGATTTCTTGTTGTGTGACACTCAGCTCAACCCACGCGAAAC	2489
Dp	2641	GCTCCTGCGTTGTGTGATGATTTCTTGTTGTGTGACACTCAGCTCAACCCACGCGAAAC	2700
QY	2490	CTTCTCTACAGACCCCTGTGCCAGAGGTGCCCTGAAGATGCTGCGGTGTGTGTGAACTTGCGGAA	2549
Dp	2701	CTTCTCTACAGACCCCTGTGCCAGAGGTGCCCTGAAGATGCTGCGGTGTGTGTGAACTTGCGGAA	2760
QY	2550	GACAGTGTGTGAATCTCCCTGTGAGAAAGACAGAGCCTGTGTTGTGACACGCTTTGTTCAGAT	2609
Dp	2761	GACAGTGTGTGAATCTCCCTGTGAGAAAGACAGAGCCTGTGTTGTGACACGCTTTGTTCAGAT	2820
QY	2610	GCCGCGCCCAAGGCTTATTCCTCTGTGTGTGAGGCTGTGTGTGATATCCGGAACCTGTGAGGT	2669
Dp	2821	GCCGCGCCCAAGGCTTATTCCTCTGTGTGTGAGGCTGTGTGTGATATCCGGAACCTGTGAGGT	2880
QY	2670	GCAGAGCAGACTATTCAGACTATGCGCGGACCTCATCAGACAGCAAGTCTCACTTCAACCG	2729
Dp	2881	GCAGAGCAGACTATTCAGACTATGCGCGGACCTCATCAGACAGCAAGTCTCACTTCAACCG	2940
QY	2730	CGGCTTACAGGCTGGAGAGAACTATGCGTCCGAAACTCTTTGGGCTCTTGCGGCTGAAGTG	2789

Db	2941	CGGCTTCAAGGCTGGAGGAAATGCGTCCGAATCTTTGGGCTTTGGGGCTGAAGT	3000
QY	2790	TCACAGCCTGTTTCTGGATTTCAGGTGAACAGCTCCAGACGGTGGCAACCAATCTA	2849
Db	3001	TCACAGCCTGTTTCTGGATTTCAGGTGAACAGCTCCAGACGGTGGCAACCAATCTA	3060
QY	2850	CAAGATCTCTCGTGGAGGGGTACAGATTTCACGATATGATGGTGGAGGCTCCATTCA	2999
Db	3061	CAAGATCTCTCGTGGAGGGGTACAGATTTCACGATATGATGGTGGAGGCTCCATTCA	3120
QY	2910	TCAGCAAGTTTGAAGAAACCCACATTTTTCCTGCGGTATCTTGACAAGGCTTCCT	2969
Db	3121	TCAGCAAGTTTGAAGAAACCCACATTTTTCCTGCGGTATCTTGACAAGGCTTCCT	3180
QY	2970	CTGTATCTCCATCTTGAAAGCGAAGACGAGGGAATTCCTGGGGGCCAAGGGCGCGC	3029
Db	3181	CTGTATCTCCATCTTGAAAGCGAAGACGAGGGAATTCCTGGGGGCCAAGGGCGCGC	3240
QY	3030	CGGCGCTCTGCGCTCCAGAGCCGTGAGTGGATGTGCAACCAAGATTCCTGTCAAGCT	3089
Db	3241	CGGCGCTCTGCGCTCCAGAGCCGTGAGTGGATGTGCAACCAAGATTCCTGTCAAGCT	3300
QY	3090	GACTTCGACACCGTGTCACTTACGTGCCATCTCTGGGCTCACTCAGACAGCCAGACCA	3149
Db	3301	GACTTCGACACCGTGTCACTTACGTGCCATCTCTGGGCTCACTCAGACAGCCAGACCA	3360
QY	3150	GCTAGTACGGAAGTCCCGGGAGACGAGCTGACCTGGCCTGAGAGGCCAGACCCGCG	3209
Db	3361	GCTAGTACGGAAGTCCCGGGAGACGAGCTGACCTGGCCTGAGAGGCCAGACCCGCG	3420
QY	3210	ACTGCGCTCAGACTTCAAGACATCTCGGACTGATGGCCACCCGCCACACGCTCCGA	3269
Db	3421	ACTGCGCTCAGACTTCAAGACATCTCGGACTGATGGCCACCCGCCACACGCTCCGA	3480
QY	3270	GAGCAGACACAGCAGGCCCTGTCAACGCCGGGCTTTACGTCACAGAGGAGAGGGGCGGC	3329
Db	3481	GAGCAGACACAGCAGGCCCTGTCAACGCCGGGCTTTACGTCACAGAGGAGAGGGGCGGC	3540
QY	3330	CACACCCAGGCCCGCACCGCTGGAGGTCTAGAGCTGATGAGTGTGTCACAGGCTTG	3389
Db	3541	CACACCCAGGCCCGCACCGCTGGAGGTCTAGAGCTGATGAGTGTGTCACAGGCTTG	3600
QY	3390	CATATCCGGGCTGAAGGCTGAGTGCAGGCTGAGGCCAGCGAGTGCACAGCCAAAGGCT	3449
Db	3601	CATATCCGGGCTGAAGGCTGAGTGCAGGCTGAGGCCAGCGAGTGCACAGCCAAAGGCT	3660
QY	3450	GAGTGTCCAGACACCTGCGGTCTTCACTTCCCAACAGGCTGGCGCTCGGCTCCACCCA	3509
Db	3661	GAGTGTCCAGACACCTGCGGTCTTCACTTCCCAACAGGCTGGCGCTCGGCTCCACCCA	3720
QY	3510	GGGCGACATTTTCTCTCACAGAGACCCGGGCTTCCATCCCAATAGAAATPAGTCATCC	3569
Db	3721	GGGCGACATTTTCTCTCACAGAGACCCGGGCTTCCATCCCAATAGAAATPAGTCATCC	3780
QY	3570	CCAGATTCCGCAATTGTTCAACCCCTCGCCCTGCTCTTGTGCTTCCACCCCAACATCC	3629
Db	3781	CCAGATTCCGCAATTGTTCAACCCCTCGCCCTGCTCTTGTGCTTCCACCCCAACATCC	3840
QY	3630	AGGTGGAGACCCCTGAGAAAGAACCTTGGGACTCTGGGAATTTGAGAGTACCAAGGCTG	3689
Db	3841	AGGTGGAGACCCCTGAGAAAGAACCTTGGGACTCTGGGAATTTGAGAGTACCAAGGCTG	3900
QY	3690	CCCTGTACACAGCGGAGAGACCTTCGACCTGATGGGGGTCCCTGTGGGTCAAAATGGGGG	3749
Db	3901	CCCTGTACACAGCGGAGAGACCTTCGACCTGATGGGGGTCCCTGTGGGTCAAAATGGGGG	3960
QY	3750	GAGGTGCTGTGGAGTAAATTAATCTGAAATATATAGTTTTCAAGTTTGAAGAAAAA	3804
Db	3961	GAGGTGCTGTGGAGTAAATTAATCTGAAATATATAGTTTTCAAGTTTGAAGAAAAA	4015

RESULT 15

ID	ACC44482	standard; DNA; 4015 BP.
AC	ACC44482;	
DT	29-AUG-2003	(first entry)
DE	Human telomerase reverse transcriptase gene.	
KW	Gene; ds; human; telomerase reverse transcriptase; adipogenic capacity; primary preadipocyte cell; adipogenesis; obesity; adipocytokine; anorectic; adiponectin; insulin.	
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	CDS	56..3454
FT		/*tag= a
FT		/product= "telomerase reverse transcriptase"
XX	W02003031640-A2.	
XX	17-APR-2003.	
XX	07-OCT-2002; 2002MO-UB031635.	
XX	06-OCT-2001; 2001US-0327650P.	
XX	06-OCT-2001; 2001US-0327651P.	
XX	(BOST-) BOSTON MEDICAL CENT CORP.	
XX	Kirkland J, Tchuknia T;	
XX	WPI; 2003-421278/39.	
XX	P-PSDB; ABR58045.	
XX	New primary preadipocyte strain expressing telomerase reverse transcriptase, useful in research applications, screening assays, clinical applications, and in the administration of therapeutic agents, particularly for obesity.	
XX	Disclosure; Page 11-13; 53p; English.	
XX	The invention relates to the generation of primary preadipocyte cell strains that express telomerase reverse transcriptase (TERT- the catalytic subunit of telomerase), and maintain and/or enhance replicative potential and maintain adipogenic capacity of the cell. This sequence represents the gene encoding the TERT protein. The cell strain can be used in research to study all aspect of adipogenesis, especially in relation to researching treatments for e.g. obesity. The cell can also be used to identify adipogenesis modulators for use as therapeutic agents such as hormones, growth factors, cytokines, enzymes, cholesterol binding proteins, cholesterol removing proteins or their combinations. Alternatively, the therapeutic agent may be an adipocytokine, preferably adiponectin, or insulin	
XX	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;	
XX	Query Match	93.1%; Score 3559; DB 7; Length 4015;
XX	Best Local Similarity	94.6%; Pred. No. 0;
XX	Matches 3797; Conservative	0; Mismatches 0; Indels 218; Gaps 22
QY	8 GCAGGCGCTCGTTCGTCGCGACGTCGGGAAGCCCTGGCCCGCACCCCGCGATGCC	67
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QY	68 GCAGGCTCCCGCGTGCAGACCGGTGCGTCTGCTGTCGAGACCACTACCGCAGAGTGCT	127
Db	61 GCAGGCTCCCGCGTGCAGACCGGTGCGTCTGCTGTCGAGACCACTACCGCAGAGTGCT	120
QY	128 GCGGCTGGACAGTTCGTCGCGCGCGCTGGAGGCCCGCAGGCGTGGTGGAGCGCG	187
Db	121 GCGGCTGGACAGTTCGTCGCGCGCGCTGGAGGCCCGCAGGCGTGGTGGAGCGCG	180

QY	188	GGACCCGAGCGCTTTCCGCGCGCTGTGTAGGACCAAGTGCCTGGATGTGCGTGGACCTGGGACACG	247
Dp	181	GGACCCGAGCGCTTTCCCGCGCGCTGTGTAGGACCAAGTGCCTGGATGTGCGTGGACACG	240
QY	248	ACGCGCGCCCCCGCGCGCTTCCTTCGCGCAGAGTGTCTTGCTGAAGAGAGTGTGTGC	307
Dp	241	ACGCGCGCCCCCGCGCGCTTCCTTCGCGCAGAGTGTCTTGCTGAAGAGAGTGTGTGC	300
QY	308	CCGAGTGTGAGAGAGCTGTGTGCGACGCGCGCGCGAGAGACGTGTGCGCTTCGAGTTGTGC	367
Dp	301	CCGAGTGTGAGAGAGCTGTGTGCGACGCGCGCGCGAGAGACGTGTGCGCTTCGAGTTGTGC	360
QY	368	GCTGTGTGAGCGGGGCCCCGCGGGGCCCCCGAGGCTTTCACACACAGCTGTGCGAGCTTA	427
Dp	361	GCTGTGTGAGCGGGGCCCCGCGGGGCCCCCGAGGCTTTCACACACAGCTGTGCGAGCTTA	420
QY	428	CCTGCGCCAAACGAGTGAACGACGACTGTGCGGGAGCGAGGACGTGTGCGCTGTGCTGTGC	487
Dp	421	CCTGCGCCAAACGAGTGAACGACGACTGTGCGGGAGCGAGGACGTGTGCGCTGTGCTGTGC	480
QY	488	CCGCGTGTGGGCGACGACGTGTGTGTTCACCTGTGTGAGACGCTGTGCGCGCTCTTTGTGTGTGT	547
Dp	481	CCGCGTGTGGGCGACGACGTGTGTGTTCACCTGTGTGAGACGCTGTGCGCGCTCTTTGTGTGTGT	540
QY	548	GAGTTCGACGCTGCGCCTTACAGAGTGTGTGTGGGCGCGCGCTGTACAGAGCTCGGCGGTGCGAC	607
Dp	541	GAGTTCGACGCTGCGCCTTACAGAGTGTGTGTGGGCGCGCGCTGTACAGAGCTCGGCGGTGCGAC	600
QY	608	TCAGGCGCGGCGCCCCCGCCACACGCTTAGTGAACCCGAAAGCGCTTGTGGATGTCAAACGGGC	667
Dp	601	TCAGGCGCGGCGCCCCCGCCACACGCTTAGTGAACCCGAAAGCGCTTGTGGATGTCAAACGGGC	660
QY	668	CTGGAACCATTAGCCTCAGAGGAGGCGCGAGTCCCTCGAGCCTGTGCAGCGCCCGAGTGTGCGAG	727
Dp	661	CTGGAACCATTAGCCTCAGAGGAGGCGCGAGTCCCTCGAGCCTGTGTGCGAGCCTGTGTGCGAG	720
QY	728	GAGCGCGCGGGGAGAGTGTGTGACGCGCGAAGTCTGTGCGTGTGCCAAGAGCGCCAGGCTGTGC	787
Dp	721	GAGCGCGCGGGGAGAGTGTGTGACGCGCGAAGTGTGTGCGTGTGCCAAGAGCGCCAGGCTGTGC	780
QY	788	TGCCCTGTGAGCCGAGGCGGAGACGCGCTGTGTGGGACAGGGTCTCTGGGCGCCACCGCGGACGAC	847
Dp	781	TGCCCTGTGAGCCGAGGCGGAGACGCGCTGTGTGGGACAGGGTCTCTGGGCGCCACCGCGGACGAC	840
QY	848	GCGTGAACCGAGTGAACCTGTGTTCTGTGTGTGTGTCACTGTGCAGAACCCGCGCGAAGAAC	907
Dp	841	GCGTGAACCGAGTGAACCTGTGTGTTCTGTGTGTGTGTCACTGTGCAGAACCCGCGCGAAGAAC	900
QY	908	CACCTCTTTGAGAGGAGTGCCTCTGTGACGCGCACTGTCCACCCATTCGCTGTGGGCGCGACA	967
Dp	901	CACCTCTTTGAGAGGAGTGCCTCTGTGACGCGCACTGTCCACCCATTCGCTGTGGGCGCGACA	960
QY	968	GCAACCAAGCGGGGCCCCCAATCCACATGTGGGGCCACACAGTCCCTGTGGGACACGCTTGTGC	1027
Dp	961	GCAACCAAGCGGGGCCCCCAATCCACATGTGGGGCCACACAGTCCCTGTGGGACACGCTTGTGC	1020
QY	1028	CCCGGTGTACGCGGAGACAAAGACCTTCTCTACTCTCAGCGGACAAAGAGACGAGTGTGC	1087
Dp	1021	CCCGGTGTACGCGGAGACAAAGACCTTCTCTACTCTCAGCGGACAAAGAGACGAGTGTGC	1080
QY	1088	GCGCTCTTCTTACTCAAGTCTCTGAAGGCCCAAGCTGTGTGGGCTGTGAGGCTGTGTGA	1147
Dp	1081	GCGCTCTTCTTACTCAAGTCTCTGAAGGCCCAAGCTGTGTGGGCTGTGTGAAGGCTGTGTGA	1140
QY	1148	GACCATCTTTCGAGTTCACAGGCGCTGTGATGTCCAGAGGACCTCCCGCAGATTTGTGCGCGCT	1207
Dp	1141	GACCATCTTTCGAGTTCACAGGCGCTGTGATGTCCAGAGGACCTCCCGCAGATTTGTGCGCGCT	1200
QY	1208	GGCCCAAGCGGTATGTGGAATGTGGGCGCCGTTTCTGTGAGCTGTGTGGAAACAAGCGGCA	1267
Dp	1201	GGCCCAAGCGGTATGTGGAATGTGGGCGCCGTTTCTGTGAGCTGTGTGGAAACAAGCGGCA	1260

QY	1268	GTGCCCCCAAGGGGGTGTCTCTCAAGACGACCTGCCGCTCGAGGTGGGGTCAACCCAGC	1327
Db	1261	GTGGCCCTTAAGGGGGTGTCTCTCAAGACGACCTGCCGCTCGAGGTGGGGTCAACCCAGC	1320
QY	1328	AGCCGGTGTCTGTGCCCGGAGAACCCCAAGGCTCTGTGGCGGCCCCGAGAGAGAGA	1387
Db	1321	AACCCGGTGTCTGTGCCCGGAGAACCCCAAGGCTCTGTGGCGGCCCCGAGAGAGAGA	1380
QY	1388	CACAGACCCCCGTGGCTGGTGTACACTGTGTCCGACAGACAGACACCCCTGGCAGTGTGA	1447
Db	1381	CACAGACCCCCGTGGCTGGTGTACACTGTGTCCGACAGACAGACACCCCTGGCAGTGTGA	1440
QY	1448	CGGCTTTCGTGCCGGGCGCTGGCTTGGCGGCTGTGGTCCCAAGGCTCTGTGGCTCCAGGCA	1507
Db	1441	CGGCTTTCGTGGCGGCGCTGGCTTGGCGGCTGTGGTCCCAAGGCTCTGTGGCTCCAGGCA	1500
QY	1508	CAACGAAACGCCGCTTCTCTCAGGAAACCAACCAAGTTCACTCTCCCTGGGAAAGCATGCCAA	1567
Db	1501	CAACGAAACGCCGCTTCTCTCAGGAAACCAAGAAATTCACTCTCCCTGGGAAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAGAGCTGACCTGTGAAGATGAGCGTGGGGAATGCGCTTGTGGCTGGCGAG	1627
Db	1561	GCTCTCGCTGCAGAGCTGACCTGTGAAGATGAGCGTGGGGAATGCGCTTGTGGCTGGCGAG	1620
QY	1628	GAGCCCAAGGGGTGGCTGTGTTCCGGCCGACAGAGACCGTGTGCTGAGAGATCTTGGC	1687
Db	1621	GAGCCCAAGGGGTGGCTGTGTTCCGGCCGACAGAGACCGTGTGCTGAGAGATCTTGGC	1680
QY	1688	CAAGTTCCTGGAACCTGGCTGATGAGTGTATAGTGTGAGAGCTGTCTCAGGTCTTTCTTTTA	1747
Db	1681	CAAGTTCCTGGAACCTGGCTGATGAGTGTATAGTGTGAGAGCTGTCTCAGGTCTTTCTTTTA	1740
QY	1748	TGTCAACGAGAACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCCGAAAGAGTGTCTGGAG	1807
Db	1741	TGTCAACGAGAACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCCGAAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAAAGCATTTGGATTCAGACAGCACTTGAAGAGGGTGCAGCTGCCGAGCTGTCTC	1867
Db	1801	CAAGTTGCAAAAGCATTTGGATTCAGACAGCACTTGAAGAGGGTGCAGCTGCCGAGCTGTCTC	1860
QY	1868	GGAAGCAGAGGTCAAGGCGACATCGGGAAGCCAGAGGCCGCTGTGCTGACGTCACACCTCCG	1927
Db	1861	GGAAGCAGAGGTCAAGGCGACATCGGGAAGCCAGAGGCCGCTGTGCTGACGTCACACCTCCG	1920
QY	1928	CTTCAATCCCAAGCTGACGCGGCTTGGCGGCGAATTTGTAAACATGGACTTACGTCTGTGGAGC	1987
Db	1921	CTTCAATCCCAAGCTGACGCGGCTTGGCGGCGAATTTGTAAACATGGACTTACGTCTGTGGAGC	1980
QY	1988	CAGAAACGTTCCGCGAGAGAAAGAGAGGGCGGACGCTCTCACTCCGAGGGTGTGAAGGACCTGTT	2047
Db	1981	CAGAAACGTTCCGCGAGAGAAAGAGAGGGCGGACGCTCTCACTCCGAGGGTGTGAAGGACCTGTT	2040
QY	2048	CAGCGTGTCTCAACTACGAGCGGGGCGGCGGCCCGGCGCTCTCTGAGCGCTCTGTGTGTGGG	2107
Db	2041	CAGCGTGTCTCAACTACGAGCGGGGCGGCGGCCCGGCGCTCTCTGAGCGCTCTGTGTGTGGG	2100
QY	2108	CTGTGACGATTCACAGAGGGGCTTGGCGGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2167
Db	2101	CTGTGACGATTCACAGAGGGGCTTGGCGGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2160
QY	2168	GCCGCTTGAGCTGTGA-----CATCCGCCCA	2191
Db	2161	GCCGCTTGAGCTGTGA-----CATCCGCCCA	2220
QY	2192	GGAACAGGTCAACGAGGTCATTCGACAGATTCATTAACCCGAGAACAGCTATCTGCTGTGG	2251
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QY	2252	TGCGTATGCGGTGTTCAGAGAGCGGCGCCATGTGGGCAAGTCCGCAAGGCTTTCAAGAGCA	2307
Db	2281	TGCGTATGCGGTGTTCAGAGAGCGGCGCCATGTGGGCAAGTCCGCAAGGCTTTCAAGAGCA	2340
QY	2308	-----	2307

Db	2341	CGTCTACCTTGAACAGACCTCCAGCGGTACATGCAACAGTTGCTGGCTCACTTGACGA	240
QY	2308	-----	2307
Db	2401	GACCAGCCCGCTGAGGGATGCCGTGTCATGACAGAGCTCCTCTGAATGAGCCAG	2460
QY	2308	-----	2309
Db	2461	CAGTGCCTTTCGACGTCCTTCMAAGCTTATGTCGCAACAGCCGCTGGCATACAGGG	2520
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Db	2521	CAAGTCTCACTCCAGTGCACGAGGGATTCGCGAGGGCTCCATCCTCTTCACAGCTGCTTG	2580
QY	2370	CAGCCTGTGCTACGCGGACATGAGAAACAAGCTCTTTGCGGGGATTTGGGCGGGACGGACT	2429
Db	2581	CAGCCTGTGCTACGCGGACATGAGAAACAAGCTCTTTGCGGGGATTTGGGCGGGACGGACT	2640
QY	2430	GCTCCTCGCTTTGCTGATGATTTCTTTGTTGTGACACTTCACTCAACCGGAAAC	2489
Db	2641	GCTCCTCGCTTTGCTGATGATTTCTTTGTTGTGACACTTCACTCAACCGGAAAC	2700
QY	2490	CTTCTCTGAGACCTGTGCGAGGTGTCCTGATAGTATGCTGGGTGATGAACTTGCGGAA	2549
Db	2701	CTTCTCTGAGACCTGTGCGAGGTGTCCTGATAGTATGCTGGGTGATGAACTTGCGGAA	2760
QY	2550	GACAGTGTGAACTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCAACGCTTTTGTTCAGAT	2609
Db	2761	GACAGTGTGAACTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCAACGCTTTTGTTCAGAT	2820
QY	2610	GCGGCCCCACGGCCCTATTCCCTGTGTGGGCGCTGTGCTGATATCCCGACCTCTGAGGT	2669
Db	2821	GCGGCCCCACGGCCCTATTCCCTGTGTGGGCGCTGTGCTGATATCCCGACCTCTGAGGT	2880
QY	2670	GACAGAGCACTATCCACGATATGCCGGAACCTTCATCAGACCAAGTCTCACTTTCACACG	2729
Db	2881	GACAGAGCACTATCCACGATATGCCGGAACCTTCATCAGACCAAGTCTCACTTTCACACG	2940
QY	2730	CGGCTTCAAGCTGGAGGAAACATGCGTGGCAACTTTTGGGGTCTTGGCGCTGAAGTG	2789
Db	2941	CGGCTTCAAGCTGGAGGAAACATGCGTGGCAACTTTTGGGGTCTTGGCGCTGAAGTG	3000
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QY	2910	TCAAGCAATTTGAAAGAACCCCACTTTTTCGCGCGTATCTGACACGGCTTCCT	2969
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QY	2970	CTGCTACTCATCTTGAAGCCCAAGAACCGAGGATGTGTGCTGGGGGACCAAGGCGCGCG	3029
Db	3181	CTGCTACTCATCTTGAAGCCCAAGAACCGAGGATGTGTGCTGGGGGACCAAGGCGCGCG	3240
QY	3030	CGGCGCTCTGCTTCGAGAGCGGTGAGTGGCTGTGTCACCAAGCATTTCTGTCAAGCT	3089
Db	3241	CGGCGCTCTGCTTCGAGAGCGGTGAGTGGCTGTGTCACCAAGCATTTCTGTCAAGCT	3300
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Db	3301	GACTGCACACGTGTCACTTACGTGCACTCTGGGTCACTTCAGGACAGCCCAAGCGCA	3360
QY	3150	GCTGAGTCCGAAGCTCCCGGGGACAGCGTGACTGGCTGGAGGCGCGGCAACCCGGCG	3209
Db	3361	GCTGAGTCCGAAGCTCCCGGGGACAGCGTGACTGGCTGGAGGCGCGGCAACCCGGCG	3420
QY	3210	ACTGCGCTCAGACTTCAAGACCATCTTGACTGATGGCCACCGCGCCACAGCCAGGCGCA	3269

Db 3421 ACTGCCCTAGACTTCAGACATCTGAGTGTGAGCCACCCGCCACAGCCAGGCCGA 3480
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Search completed: February 29, 2004, 21:00:05
Job time : 966.534 secs

Db 3841 AAAAAAAAAA 3853

RESULT 2
LOCUS AR243330 3855 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 4 from patent US 645789.
ACCESSION AR243330
VERSION AR243330.1 GI:27290541
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 3855)
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Human telomerase catalytic subunit: diagnostic and therapeutic
methods
Patent: US 645789-A 4 05-NOV-2002;
Location/Qualifiers
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ORIGIN

Query Match 98.5%; Score 3767.8; DB 6; Length 3855;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

QY 8 GCAGCCCTCGTCTCTGCGCAGCGGAGAGCCCTGCGCCGCAACCCCGCGATGCC 67
Db 1 GCAGCCCTCGTCTCTGCGCAGCGGAGAGCCCTGCGCCGCAACCCCGCGATGCC 60

QY 68 GCGCGCTCCCGCTGCGCAGCGGAGAGCCCTGCGCCGCAACCCCGCGATGCC 127
Db 61 GCGCGCTCCCGCTGCGCAGCGGAGAGCCCTGCGCCGCAACCCCGCGATGCC 120

QY 128 GCGCGCTCCCGCTGCGCAGCGGAGAGCCCTGCGCCGCAACCCCGCGATGCC 187
Db 121 GCGCGCTCCCGCTGCGCAGCGGAGAGCCCTGCGCCGCAACCCCGCGATGCC 180

QY 188 GCGCGCTCCCGCTGCGCAGCGGAGAGCCCTGCGCCGCAACCCCGCGATGCC 247
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Db 241 GCGCGCTCCCGCTGCGCAGCGGAGAGCCCTGCGCCGCAACCCCGCGATGCC 300

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QY 368 GCGCGCTCCCGCTGCGCAGCGGAGAGCCCTGCGCCGCAACCCCGCGATGCC 427
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QY 1148 GACCATTTCTGAGTTCAGAGCCCTGAGATGCGAGAGGATCCCGGAGGTTGCGCGCT 1207
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QY 1448 CCGCTTGTGCGGCGCTGCGCTGCGCGAGTGTGTGCGGAGCTTGTGGAGTTCAGAGCA 1507
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DB 2161 GCGGCTGAGGCTGTA-----CATCCCCA 2220
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3752 GGTGTGTGAGAGTAAATATGATGATTTTCAAGTGTGAGAGTAAATATGATGATTTTCAAGTGTGAGAG 3811
3781 GGTGTGTGAGAGTAAATATGATGATTTTCAAGTGTGAGAGTAAATATGATGATTTTCAAGTGTGAGAG 3840
3812 AAAAAAAAAA 3824
3841 AAAAAAAAAA 3853

RESULT 4
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LOCUS AR393086 3855 bp mRNA linear PAT 18-DEC-2003
DEFINITION Sequence 4 from patent US 6617110.
ACCESSION AR393086
VERSION AR393086.1 GI:40118361
KEYWORDS
SOURCE Unknown.

Db 3841 AAAAAAAAAAAAAA 3853

RESULT 6

BD011046

Human telomerase catalytic subunit.

LOCUS

BD011046

BD011046.1 GI:18639419

JP 2001081042-A/3.

unidentified

unclassified

unclassified

DEFINITION

BD011046

BD011046.1 GI:18639419

JP 2001081042-A/3.

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KEYWORDS

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SOURCE

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ORGANISM

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REFERENCE

1. (bases 1 to 3855)

Sechi, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Mori, G.B.,

Harley, C.B. and Andrews, W.H.

Human telomerase catalytic subunit

Patent: JP 2001081042-A 3 27-MAR-2001.

GERON CORP. UNIVERSITY TECHNOLOGY CORP.

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Query Match

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Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

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Best Local Similarity 99.0%; Pred. No. 0;

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Q	1568	GCTCTGCTGAGAGAGCTGACGTGAAATAGAGCGTGGAGACTGGCTGTGGCTGGCAG	1627
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D	1981	CAGAACGTTCCGACAGAAAAAGAGGCGCAGCGTCTACCTCAGAGGTGAAAGCACTGTT	2040
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D	2101	CCTGAGCATATTCACAGGGCTTGGCGCACTTCTGTGCTGCTGTGGAGCCAGAGACCC	2160
Q	2168	GCCGCTGAGCTGTAA-----CATCCCCA	2191
D	2161	GCCGCTGAGCTGTAACTTTGTCAAGGTGATGTGACGGGCGGCTACGACCATCCCCA	2220
Q	2192	GGAAGGCTCAACGAGGTCACTCGCAGCATCATCAAAACCCAGAAACAGTATCTGGTGG	2251
D	2221	GGAAGGCTCAACGAGGTCACTCGCAGCATCATCAAAACCCAGAAACAGTATCTGGTGG	2280
Q	2252	TGGTATGCGGTGTTCAGAAAGGCGGCCCATGGGACGTCGCAAGGCTTTCAGAGGCA	2311
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D	2461	TTCCTGCGTTTGTGTGATGATTTCTGTGTGTGACACTTCACTTCAACGCGGAAACCT	2520
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Q	2552	CAGTGTGAACCTTCCCTGTAGAAAGAGAGGCGCTGGGTGGACAGGCTTTTGTTCAGATG	2611
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D	3121	CTTGACACCGGTCACTTACGTGCACTTCTGGGGTCACTAGAGACAGCCCAAGCAGC	3180
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ACCESSION	AX003121			
VERSION	AX003121.1	GI:9926983		
KEYWORDS				
SOURCE				
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1			
AUTHORS	Wick, M. and Hagen, G.			
TITLE	Regulatory dna sequences of the human catalytic telomerase sub-unit			
	gene, diagnostic and therapeutic use thereof			
	Patent: WO 933998-A 2 08-JUL-1999;			
JOURNAL	WICK MARESA (DE); BAYER AG (DE)			
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ORIGIN

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[illegible]


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LOCUS E36819
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36819

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VERSION E36819.1 GI:13022782
KEYWORDS JP 199253177-A/27.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4037)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
TITLE Calvin,B.H., and William,H.A.
JOURNAL Human telomerase catalytic subunit promoter
Patent: JP 199253177-A 27 21-SEP-1999;
JERON CORP. UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
PN JP 199253177-A/27
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
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09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
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R. SECHI, JOCHIMU RINGER, TORU NAKAMURA, KAREN B. CHAPMAN, PI GREG B
MORIN.
PI CALVIN B HAREI, WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
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DEFINITION	Sequence 343 from patent US 6617110.				
ACCESSION	AR393110				
VERSION	AR393110.1	GI:40118392			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 4037) Cech,T.R., Linsner,J., Nakamura,T., Chapman,K.B., Morin,G.B., Harley,C.B. and Andrews,W.H.				
TITLE	Cells immortalized with telomerase reverse transcriptase for use in drug screening				
JOURNAL	Patent: US 6617110-A 343 09-SEP-2003;				
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Matches 3810; Conservative	4; Mismatches 3; Indels 218; Gaps 2;				
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 VERSION AX810378.1 GI:38523892
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 AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
 HARLEY,C.B. and Andrews,W.H.
 TITLE Human telomerase catalytic subunit
 JOURNAL Patent: EP 133094-A 343 06-AUG-2003;
 Geron Corporation (US); University Technology Corporation (US)
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LOCUS AX391846
DEFINITION Sequence 1 from Patent WO0216555.
ACCESSION AX391846
VERSION AX391846.1 GI:19700428
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Jones, C.J., Kipling, D.G., Wilkinson, G., Mcsharry, B.D. and
AUTHORS Skinner, J.W.
TITLE Cell lines, their preparation and use
JOURNAL Patent: WO 021655-A 1 28-FEB-2002;
University of Wales College of Medicine (GB)
FEATURES
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ORIGIN
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Page 32

[illegible]

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Job time : 9652.49 secs

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US-10-044-539-4
 Sequence 4, Application US/10044539
 Publication No. US20030100093A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539
 FILING DATE: 11-Jan-2002

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3855 base pairs
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 MOLECULE TYPE: cdna

FEATURES:

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 FEATURE:
 NAME/KEY: CDS

LOCATION: 56..2479
 OTHER INFORMATION: /product= "delta-182 variant polypeptide"
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 US-10-044-539-4

Query Match 98.5%; Score 3767.8; DB 14; Length 3855;
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1 RESULT 3
2 US-09-733-294A-3
3 Sequence 3, Application US/09733294A
4 Patent No. US20020045586A1
5 GENERAL INFORMATION:
6 APPLICANT: Brett P. Monia
7 APPLICANT: William Gaarde
8 APPLICANT: Susan M. Freier
9 APPLICANT: Edward V. Marciewicz
10 TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
11 FILE REFERENCE: ISH-0527
12 CURRENT APPLICATION NUMBER: US/09/733,294A
13 CURRENT FILING DATE: 2000-12-07
14 PRIOR APPLICATION NUMBER: 09/517,423
15 PRIOR FILING DATE: 2000-05-16
16 NUMBER OF SEQ ID NOS: 108
17 SEQ ID NO 3
18 LENGTH: 4015
19 TYPE: DNA
20 ORGANISM: Homo sapiens
21 FEATURE:

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; NAME/KEY: CDS
; LOCATION: (56) ... (3454)
US-09-733-294A-3

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Query Match	93.1%	Score 3559;	DB 9;	Length 4015;
Best Local Similarity	94.6%;	Pred. No. 0;		
Matches 3797;	Conservative	0;	Mismatches	0;
			Indels	218;
			Gaps	2;

[illegible]

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QY	3090	GACTGGAACCGTGTCACTTAAGTCCACTCTGGGGGTCACTCAAGAAGCCCAAGCA	3148
Db	3301	GACTGGAACCGTGTCACTTAAGTCCACTCTGGGGGTCACTCAAGAAGCCCAAGCA	3360
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QY	3210	ACTGCGCTCAGACTTTCAAGACCATCTGGACTGATGGCACCCGCCCAAGCCAGCCGA	3265
Db	3421	ACTGCGCTCAGACTTTCAAGACCATCTGGACTGATGAGCACCCGCCCAAGCCAGCCGA	3480
QY	3270	GAGCAGAACCAAGGAGCGCCCTGTCAAGCCGGGGTCTAAGTCCCAAGGAGGAGGGCGGCG	3328
Db	3481	GAGCAGAACCAAGGAGCGCCCTGTCAAGCCGGGGTCTAAGTCCCAAGGAGGAGGGCGGCG	3540
QY	3330	CACACCCAGGCGCGGACCGCTGGAGGCTGAGAGCCTGAGTGAAGTGTGTCGCGAGAGCGTG	3389
Db	3541	CACACCCAGGCGCGGACCGCTGGAGGCTGAGAGCCTGAGTGAAGTGTGTCGCGAGAGCGTG	3600
QY	3380	CATGTCCGGCTGAAAGGCTGAAGTGTCCGGCTGAAGGCTAGGCGAAGTGTCAAGCCAAAGGCT	3448
Db	3601	CATGTCCGGCTGAAAGGCTGAAGTGTCCGGCTGAAGGCTAGGCGAAGTGTCAAGCCAAAGGCT	3663
QY	3450	GAGGTGTCCAGACACCTGCGCGCTTCACTTCCCAAGGCTGGGCGTGGCTCCACCCCA	3509
Db	3661	GAGGTGTCCAGACACCTGCGCGCTTCACTTCCCAAGGCTGGGCGTGGCTCCACCCCA	3720
QY	3510	GGGCGAGCTTTTCCACACAGAGAGCCCGGCTTCACTCCCAATAGAGAAATGTCTCATCC	3569
Db	3721	GGGCGAGCTTTTCCACACAGAGAGCCCGGCTTCACTCCCAATAGAGAAATGTCTCATCC	3780
QY	3570	CCAAGTTCCGCAATGTCTTCAACCCCTTGCCCTGTGCTCTTGTGCTTCCACCCCAACATCC	3629
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QY	3630	AGGTGGAAGACCTGAGAGAGACCTCGGAGGCTGCGGAAATTGAGAGTACCAAAAGGTGTG	3689
Db	3841	AGGTGGAAGACCTGAGAGAGACCTCGGAGGCTGCGGAAATTGAGAGTACCAAAAGGTGTG	3900
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RESULT 4
 US-09-990-080-1
 ; Sequence 1, Application US/09990080
 ; Patent No. US20020102686A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Geron Corporation
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
 ; FILE REFERENCE: 018/258c
 ; CURRENT APPLICATION NUMBER: US/09/990,080
 ; PRIORITY FILING DATE: 1998-08-03
 ; PRIOR APPLICATION NUMBER: US 09/052,864
 ; PRIOR FILING DATE: 1998-03-31
 ; NUMBER OF SEQ. ID NOS.: 21
 ; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-390-080-1

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Query Match	93.1%;	Score 3559;	DB 9;	Length 4015;
Best Local Similarity	94.6%;	Pred. No. 0;		
Matches 3797;	Conservative	0;	Mismatches	0;
			Indels	218;
			Gaps	2;

QY	8	GCACCGCTGCTCCTTGTGTCGCAAGTGGAGAACCTTGCCCCGCGCACCCCCGAGTATCC	67
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QY	68	GGCGGCTCCCCGCTGCGGAGGCGTGGGCTCCCTGCTGCGAGGCCATTCACCGCAGTGGCT	127
Db	61	GGCGGCTCCCCGCTGCGGAGGCGTGGGCTCCCTGCTGCGAGGCCATTCACCGCAGTGGCT	120
QY	128	GCCGCTGGCCACTTTCGTGTCGCGCGCTTGGGCCCCAGAGCTGAGCGGCTGTGACAGCGG	187
Db	121	GCCGCTGGCCACTTTCGTGTCGCGCGCTTGGGCCCCAGAGCTGAGCGGCTGTGACAGCGG	180
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Qy      2910  TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGACAGCGGCTCCCT
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Db      3241  CGGCGCTCTGCGCTCGAGGCGGCTGAGTGTGCTGACCAAGCATTCCTGCTCAAGCT
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RESULT 5

US-09-843-676-224

Sequence 224, Application US/09843676

Patent No. US20020164786A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

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?      Morin, Gregg B.
?      Harley, Calvin
?      Andrews, William H.
?      TITLE OF INVENTION: No. US20020164786A1 Telomerase
?      NUMBER OF SEQUENCES: 225
?      CORRESPONDENCE ADDRESS:
?      ADDRESS: Townsend and Townsend and Crew LLP
?      STREET: Two Embarcadero Center, 8th Floor
?      CITY: San Francisco
?      STATE: California
?      COUNTRY: United States of America
?      ZIP: 94111
?      COMPUTER READABLE FORM:
?      MEDIUM TYPE: Floppy disk
?      COMPUTER: IBM PC compatible
?      OPERATING SYSTEM: PC-DOS/MS-DOS
?      SOFTWARE: PatentIn Release #1.0, Version #1.30
?      CURRENT APPLICATION DATA:
?      APPLICATION NUMBER: US/09/843,676
?      FILING DATE: 26-Apr-2001
?      CLASSIFICATION: 536
?      PRIOR APPLICATION DATA:
?      APPLICATION NUMBER: US/08/854,050
?      FILING DATE: 09-MAY-1997
?      APPLICATION NUMBER: US 08/846,017
?      FILING DATE: 25-APR-1997
?      APPLICATION NUMBER: US 08/844,419
?      FILING DATE: 18-APR-1997
?      APPLICATION NUMBER: US 08/724,643
?      FILING DATE: 01-OCT-1996
?      ATTORNEY/AGENT INFORMATION:
?      NAME: Apple, Randolph T.
?      REGISTRATION NUMBER: 36,429
?      REFERENCE/DOCKET NUMBER: 015389-002930US
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (415) 576-0200
?      TELEFAX: (415) 576-0300
?      INFORMATION FOR SEQ ID NO: 224:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 4015 base pairs
?      TYPE: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE TYPE: cDNA
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 56..3454
?      OTHER INFORMATION: /product= "hTRT"
?      /note= "human telomerase reverse
?      transcriptase (hTRT) catalytic protein
?      component"
?      SEQUENCE DESCRIPTION: SEQ ID NO: 224:
?      US-09-843-676-224

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Query Match

Best Local Similarity 94.6%; Pred. No. 0; Mismatches 0; Indels 218; Gaps 2;

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Tue Mar 2 09:53:22 2004

us-09-424-686f-10.rnpb

Page 12

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Db	3241	CGGCGCTCTGCGCTCCGAGAGCGGTGCAGTGTGTGCAACAAGCATTTCTGTCTAAGCT	3301
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Db	3421	ACTGCGCTCAGACTTCAAGACCATCTTGACTGATGAGCAACCGGCCACAGCCAGGCGGCA	3481
Qy	3270	GAGCAGAACACGACGCGCTGTCAAGCTGGGCTTACGTCCAGAGGAGGAGGGGCGGCG	3321

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RESULT
US-09-95

; Sequence 1, Application US/09953052

Patent No. US20020173476A1

APPLICANT: Czech

Lingner, Joachim

! :
Nakamura, Toru
Chadman, Karen B

Morin, Gregg B.

Harley, Calvin B

Andrews, William

Inhibits

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and

STREET: Two Embarcadero

CITY: San Francisco

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DC

SOFTWARE: PatentIn Release
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APPLICATION NUMBER: US/

FILING DATE: 14-Sep-2000

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/

FILING DATE: <Unknown>

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FILING DATE: 18-APR-199

APPLICATION NUMBER: US

FILING DATE: 25-APR-199

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
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FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
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TYPE: nucleic acid
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Publication No. 70000004/00011

APPLICANT: Cech, Thomas R.

- ! Nakamura, Toru
- ! Chapman, Karen B
- ! Morin, Gregg B.
- ! Harley, Calvin

Andrews, William H
TITLE OF INVENTION: No. US200
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:

STREET: Two Embarcadero
CITY: San Francisco
STATE: California
COUNTRY: United States

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; SOFTWARE: PatentIn Release
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/1
; FILING DATE: 18-Jan-2003

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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8
FILING DATE: <Unknown>

FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 0
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 0

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T
REGISTRATION NUMBER: 36,

TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 576-020
TELEFAX: (415) 576-0300
INFORMATION FOR THE PUBLIC

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SEQUENCE CHARACTERISTICS:
      LENGTH: 4015 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single

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FEATURE:
NAME/KEY: CDS
LOCATION: EC 3AFA

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OTHER INFORMATION: /proc
/note= "human telomerase
transcriptase (hTERT) cat
component"
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US-10-054-295-224	Query Match	93.1%; Score
	Best Local Similarity	94.6%; Score

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2252 TCGGATAGCGGTGTCAGAGAGCGCCCATGAGCAAGTCCGAAAGGCTTTCAGAA 2307
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RESULT 10
US-10-054-611-224
Sequence 224, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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RESULT 13
US-10-044-539-1
Sequence 1, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Molin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product="hTRT"
/note="human telomerase reverse transcriptase (hTRT) catalytic protein component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-539-1

Db 2101 CTTGAGGATATTCACAGGAGCTGGGACCTTCGTGCTGTGCTGCGGAGCCCAAGAGCC 2160
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Db 2161 GCGGCTGAGCTGTAATTTGTCAAGGTGATGACGGGCGGTACGACCATCCCA 2220
Qy 2192 GACAGGCTGACGAGGATCATGCGCAGCATCATCAACCCAGAAACGTAATGCTGGG 2251
Db 2221 GACAGGCTGACGAGGATCATGCGCAGCATCATCAACCCAGAAACGTAATGCTGGG 2280
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Db 2281 TCGGTATGCGGTGCTGAGAGGCGCCCATGAGCACTTCGCAAGGCTTCAAGAAGCA 2340
Qy 2308 ----- 2307
Db 2341 GGTCTTACTTGAAGAGCTTCAGCCGTACATGCGACAGTTCGTGCTCACTGCAAGA 2400
Qy 2308 ----- 2307
Db 2401 GACAGCCCGCTAGAGGATGCGTGTATGAGCAGAGCTCTCTGTAATGAGGCCAG 2460
Qy 2308 -----G 2309
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Db 2521 CAGTGGCTCTTGAAGCTTCTTCAAGCTTATGACCAAGCCGCTGCGATGAGGG 2580
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Db 2581 CAGCTGTGCTTGAAGCTTCTTCAAGCTTATGACCAAGCCGCTGCGATGAGGG 2640
Qy 2430 GCTCTGCGTGTGATGATTTCTTGTGATGACCTCACTCACTCACTCACTCACTCACT 2489
Db 2641 GCTCTGCGTGTGATGATTTCTTGTGATGACCTCACTCACTCACTCACTCACTCACT 2700
Qy 2490 CTCTCTCAAGACCTTGTGATGATTTCTTGTGATGACCTCACTCACTCACTCACTCACT 2549
Db 2701 CTCTCTCAAGACCTTGTGATGATTTCTTGTGATGACCTCACTCACTCACTCACTCACT 2760
Qy 2550 GACAGTGTGATGATTTCTTGTGATGACCTCACTCACTCACTCACTCACTCACTCACT 2609
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Qy 2610 GCGGCGCCACGAGCTTATTCCTGTGATGATTTCTTGTGATGACCTCACTCACTCACT 2669
Db 2821 GCGGCGCCACGAGCTTATTCCTGTGATGATTTCTTGTGATGACCTCACTCACTCACT 2880
Qy 2670 GACAGGAGTACTTCAAGCTATGCGGAGCTTCACTCACTCACTCACTCACTCACTCACT 2729
Db 2881 GACAGGAGTACTTCAAGCTATGCGGAGCTTCACTCACTCACTCACTCACTCACTCACT 2940
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Db 3301 GACTGACACCTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3360
Qy 3150 GCTGAGTGGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3209
Db 3361 GCTGAGTGGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3420
Qy 3210 ACTGCTCTGAGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3269
Db 3421 ACTGCTCTGAGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3480
Qy 3270 GAGCAGACACGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCT 3329
Db 3481 GAGCAGACACGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCT 3540
Qy 3330 CACAGCAGGCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCT 3389
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Db 3601 CATGCTGCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3660
Qy 3450 GAGTGTGAGACACCTGCTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3509
Db 3661 GAGTGTGAGACACCTGCTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3720
Qy 3510 GAGGCTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCT 3569
Db 3721 GAGGCTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCT 3780
Qy 3570 CCAAGTGTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3629
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Qy 3630 AGGTGAGACCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCT 3689
Db 3841 AGGTGAGACCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCT 3900
Qy 3690 CCTGTACACAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3749
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Qy 3750 GAGTGTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 3804
Db 3961 GAGTGTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 4015

RESULT 14
US-10-385-882-1
Sequence 1, Application US/10385882
Publication No. US20030232409A1
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA
APPLICANT: FARRIS, James
APPLICANT: POSTER, Douglas
TITLE OF INVENTION: IMMORTAL PORCINE CELLS
FILE REFERENCE: 110 01700101
CURRENT FILING DATE: 2003-03-11
PRIORITY FILING DATE: 2002-03-11
PRIORITY FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1

LENGTH: 4027
TYPE: DNA
ORGANISM: ARTIFICIAL
FEATURE:
OTHER INFORMATION: Nucleotide sequence encoding telomerase reverse transcriptase
US-10-385-882-1

Query Match 93.0%; Score 3557; DB 15; Length 4027;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 3798; Conservative 0; Mismatches 5; Indels 218; Gaps 2;

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3847 GAGACCTCTGAG 3906
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3815 A 3815
4027 A 4027

RESULT 15
US-09-843-676-173
; Sequence 173, Application US/09843676
; Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
; Linsmeier, Joachim
; Nakamura, Toru

Chapman, Karen B.
Mortin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY:
LOCATION: 1..4029
OTHER INFORMATION: /note= "preliminary sequence for
human TRF cDNA insert of
plasmid pGRN121"
US-09-843-676-173
SEQUENCE DESCRIPTION: SEQ ID NO: 173:
Query Match 89.3%; Score 3414.8; DB 9; Length 4029;
Best Local Similarity 93.1%; Pred. No. 0;
Matches 3758; Conservative 0; Mismatches 51; Indels 227; Gaps 10;

248 ACGGCGCCCGCCCGCCCGCCCTCTTCCGCGAGGTGCTGCTGAAGAGTGTGAG 307
Db ANGGGCGCCCGCCCGCCCGCCCTCTTCCGCGAGGTGCTGCTGAAGAGTGTGAG 300
Qy CCGAGTGTCTGAGAGGTGTGTGCGAGCGCGCGGAGAAACGTGTGCTTGGCTTCCG 367
Db CCGAGTGTCTGAGAGGTGTGTGCGAGCGCGCGGAGAAACGTGTGCTTGGCTTCCG 360
Qy GCTGTGAGACGAGGCTA 427
Db GCTGTGAGACGAGGCTA 420
Qy CTTGCCCAACACGCTGACCGACGCTGCGGAGGAGACGCGGCGCTGTGCTGCG 487
Db CTTGCCCAACACGCTGACCGACGCTGCGGAGGAGACGCGGCGCTGTGCTGCG 480
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 19:45:38 ; Search time 7751.04 Seconds
(without alignments)

17359.163 Million cell updates/sec

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Perfect score: 3824

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Gapop 10.0, Gapext 1.0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; APPLICANT: Wick, Mareisa
; APPLICANT: Zubov, Dmitry
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; FILE REFERENCE: Bayer 10.203
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; PRIOR FILING DATE: 1998-06-09
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; SOFTWARE: Microsoft Word
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; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3860)
; OTHER INFORMATION: Nucleotides 2345 to 2526 of SEQ ID NO 1 were deleted to provide
; OTHER INFORMATION: this sequence.
US-09-424-686F-8

Query Match      98.8%; Score 3778; DB 20; Length 3860;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3824; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

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Db      61 CGATCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy      121 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db      121 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Qy      181 AGCGGAGGAGACCCGCGGCTTTCCGCGGCTGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db      181 AGCGGAGGAGACCCGCGGCTTTCCGCGGCTGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy      241 GGGACGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db      241 GGGACGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Qy      301 TGTGAGCCGAGTGTGAGAGGCTGTGAGAGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db      301 TGTGAGCCGAGTGTGAGAGGCTGTGAGAGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy      361 GCTTCGCGCTGTGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db      361 GCTTCGCGCTGTGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy      421 GCAAGTACCTTCCCAACAGGTGACCGAGCGACTGCGGAGGAGAGAGAGAGAGAGAGAGAGAG 480
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Qy      481 TGTGCGCGCGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db      481 TGTGCGCGCGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy      541 TGTGAGTGTGCTCCAGAGTGTGCTTACAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
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Qy      601 CTGCGCACTCAGAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
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Qy      661 AACGGGCTGTGAGACATAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db      661 AACGGGCTGTGAGACATAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy      721 GTGCGAGGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db      721 GTGCGAGGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy      781 GTGAGCGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db      781 GTGAGCGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy      841 GCAAGAGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db      841 GCAAGAGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy      901 AAGAAGCACTCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960

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Db	901	AAGAAGCACCCTTTTGAGAGGGGAGCTCTCTGGACAGCGCACCTCCACCCATCCGTGG	960
QY	961	GGCGGCAGACACACAGGGGGGCCCCCATTCACATAGCGGGGCACACAGTCCCTGGGACACGC	102
Db	961	GGCGGCAGACACACAGGGGGGCCCCCATTCACATAGCGGGGCACACAGTCCCTGGGACACGC	102
QY	1021	CTTGTCCCGCGGTGTAAGCGCGAGACCCAGACCTTCTTACTCTCTCAGGCGACAGGAGC	108
Db	1021	CTTGTCCCGCGGTGTAAGCGCGAGACCCAGACCTTCTTACTCTCTCAGGCGACAGGAGC	108
QY	1081	AGCTGGGGGCGCTCCCTTACTACTACAGTCTCTAGAGGCGCAGGCTGACCTGCGAGAGC	114
Db	1081	AGCTGGGGGCGCTCCCTTACTACTACAGTCTCTAGAGGCGCAGGCTGACCTGCGAGAGC	114
QY	1141	TCTGTAGAGACCATCTTTCTGAGGTTCCAGGCGCTTGANTCCAGGAGCTCCCGCAGGTTGC	120
Db	1141	TCTGTAGAGACCATCTTTCTGAGGTTCCAGGCGCTTGANTCCAGGAGCTCCCGCAGGTTGC	120
QY	1201	CCGCGCTGGCCCAAGCGCTACTGCGCAATAGCGGCGCCCTGTTCTGAGACCTGTTGGGAAC	126
Db	1201	CCGCGCTGGCCCAAGCGCTACTGCGCAATAGCGGCGCCCTGTTCTGAGAGTGTGTTGGGAAC	126
QY	1261	ACGCGCAGTGCCTCTACGCGGATGCTCTTCACAGCAGCATGCGCGCTCAGAGTCCAGTCA	132
Db	1261	ACGCGCAGTGCCTCTACGCGGATGCTCTTCACAGCAGCATGCGCGCTCAGAGTCCAGTCA	132
QY	1321	CCCCAGACGCGGGTGTCTGTGCGCCGGGAGAAACCCCAAGGCTGTGTGAGCGGCCCCGAGG	138
Db	1321	CCCCAGACGCGGGTGTGTGTGCGCCGGGAGAAACCCCAAGGCTGTGTGAGCGGCCCCGAGG	138
QY	1381	AGAGAGACACAGACCCCCCGTGGCTTGGTACAGTCTCTCCGACAGACAGACAGCCCTTCGC	144
Db	1381	AGAGAGACACAGACCCCCCGTGGCTTGGTACAGTCTCTCCGACAGACAGACAGCCCTTCGC	144
QY	1441	AGGTGTACGGGCTTGTGTGCGGGCGTGGCGCGCGGGCTGTGATGCCCAAGCGCTCTGAGGGCT	150
Db	1441	AGGTGTACGGGCTTGTGTGCGGGCGTGGCGCGCGGGCTGTGATGCCCAAGCGCTCTGAGGGCT	150
QY	1501	CCAGGACACAAAGAACGCGCTTCTTCAGAGAACCAAGAGATTCATCTCTCTGGGAGAGC	156
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QY	1561	ATGTGCAAGCTCTGTGCTGAGAGAGCTGATCGTGAATATAGAGGTGCGGACCTGCGCTTGGC	162
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Db	1621	TGCGCAGAGAGCCCAAGGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCTGAGAGAG	168
QY	1681	TCTCGGCGCAAGTTCCTGCACTGGGCTGATAGTGTGTATGCTGTGAGACCTGACAGCTT	174
Db	1681	TCTCGGCGCAAGTTCCTGCACTGGGCTGATAGTGTGTATGCTGTGAGACCTGACAGCTT	174
QY	1741	TCTTTTATGTACGAGAGACCAAGTTCAAAAAGACAGGCTCTTTTCTACCGGAAAGTG	180
Db	1741	TCTTTTATGTACGAGAGACCAAGTTCAAAAAGACAGGCTCTTTTCTACCGGAAAGTG	180
QY	1801	TCTGGACCAAGTTCGAAAGACATTGGATCAGACACATTGAAAGAGGTGAGCTGGCGG	186
Db	1801	TCTGGACCAAGTTCGAAAGACATTGGATCAGACACATTGAAAGAGGTGAGCTGGCGG	186
QY	1861	AGCTGTGAGAGCAGAGGTTCAGGACAGCATCGGAAAGCCAGGCGCGCTCTGTACATGCCA	192
Db	1861	AGCTGTGAGAGCAGAGGTTCAGGACAGCATCGGAAAGCCAGGCGCGCTCTGTACATGCCA	192
QY	1921	GACTCCGCTTCACTCCCAAGAGCTGAGCGGGCTCGGCGCATTTGTAAATGTAAGTAACTGCG	198
Db	1921	GACTCCGCTTCACTCCCAAGAGCTGAGCGGGCTCGGCGCATTTGTAAATGTAAGTAACTGCG	198
QY	1981	TGGGAGCCAGAGATGTTCCGAGAGAAAGAGGCGGAGCGTCTCACTCGAGGATGTAAG	204

Db	1981	TGGAGGCGCAGAACGTTCCGACAGAAAGAAAGAGGCGCGAGACGCTTCACCTCCGAGGGGTGAAGG	2040
OY	2041	CACGTTGAGGTGCTGTAACTAAGAGGGGGGGGGCGCGCCCGGGCTCTGGGGCGGCTCTGG	2100
Db	2041	CAGCTTTAGGGTGTCAACTTAAGAGGGGGGGGGCGCGCCCGGGCTCTGGGGCGCTCTGG	2100
OY	2101	TGCTGGGCGCTTGAGAGATATCCACAGGGCTTGGCGCACTTTGTCGTGCGTGGCGGGCC	2160
Db	2101	TGCTGGGCGCTTGAGAGATATCCACAGGGCGTGGCGCACTTGTGCTGCTGGTGTGGCGGGCC	2160
OY	2161	AGGACCCGGCGCGCTGAGCTGTA-----CA	2180
Db	2161	AGGACCCCGCGCGCTGAGCTGTAACCTTTGTCAAGTGTGATGTGACGGGCGCGTAACGACACCA	2220
OY	2185	TCCCCCAGAGACAGGCTCAACGAGGTGCAATCGCCAGCATCATGAAACCCCAAGAACGTAAT	2240
Db	2221	TCCCCCAGAGACAGGCTCAACGAGGTGCAATCGCCAGCATCATGAAACCCCAAGAACGTAAT	2280
OY	2245	GCGTGGCGTGGGTAATGCGGTGGTCCAGAGGGCGCGCCAGTGGGAGAGTCCGAGAGGCGCTTCA	2300
Db	2281	GCGTGGCGTGGGTAATGCGGTGGTCCAGAGGGCGCGCCAGTGGGAGAGTCCGAGAGGCGCTTCA	2340
OY	2305	AGAGGCAAGTCCCTAAGTCCAGTGGCACAGGGATCCCGACAGGCGCTTCATCTCTCCAGCGTG	2360
Db	2341	AGAGGCAAGTCCCTAAGTCCAGTGGCACAGGGATCCCGACAGGCGCTTCATCTCTCCAGCGTG	2400
OY	2365	CTGTGACACCTGTGCTAAGCGGACATAGAGAGAACAGCGTTTGGGGGATTCGGCGGGAGC	2420
Db	2401	CTGTGACACCTGTGCTAAGCGGACATAGAGAGAACAGCGTTTGGGGGATTCGGCGGGAGC	2460
OY	2425	GCGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACTTCAACCACGCG	2480
Db	2461	GCGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACTTCAACCACGCG	2520
OY	2485	AAAACTCTCTCAAGGACCCCTGGTCCGAGGGTCCCTGAGATATGGCTGGGTGGTAACCTG	2540
Db	2521	AAAACTCTCTCAAGGACCCCTGGTCCGAGGGTCCCTGAGATATGGCTGGGTGGTAACCTG	2580
OY	2545	CGGAAGACAGTGTGTAACCTTCCCTGTAGAGAACAGAGGCCCTGGGTGGCACGGCTTTTGT	2600
Db	2581	CGGAAGACAGTGTGTAACCTTCCCTGTAGAGAACAGAGGCCCTGGGTGGCACGGCTTTTGT	2640
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OY	2665	GAGGTGACAGCGCACTACTCCAGCTATGCCCCGACCTTCATCAGAGCCAGTCAACCTTC	2720
Db	2701	GAGGTGACAGCGCACTACTCCAGCTATGCCCCGACCTTCATCAGAGCCAGTCAACCTTC	2760
OY	2725	AACGGCGGCTTCAAGGCGTGGGAGGAAATGCGTGGGAAACCTTTGGGGTCTTGGCGGTG	2780
Db	2761	AACGGCGGCTTCAAGGCGTGGGAGGAAATGCGTGGGAAACCTTTGGGGTCTTGGCGGTG	2820
OY	2785	AAGTGTCAAGCTGTGTTTGTGATTTGCAAGGTGAACAGCCTCAAGACGGTGTGACCAAC	2840
Db	2821	AAGTGTCAAGCTGTGTTTGTGATTTGCAAGGTGAACAGCCTCAAGACGGTGTGACCAAC	2880
OY	2845	ATCTACAAAGATGCTCCTGCTGACAGGCGTAACAGTTTACAGCATGTGTGCTGCACTCCCA	2900
Db	2881	ATCTACAAAGATGCTCCTGCTGACAGGCGTAACAGTTTACAGCATGTGTGCTGCACTCCCA	2940
OY	2905	TTTCAATCAAGCAAGTTTGAAGAACCCCAATTTTTCGCGGTCATCTCTGACACGGCC	2960
Db	2941	TTTCAATCAAGCAAGTTTGAAGAACCCCAATTTTTCGCGGTCATCTCTGACACGGCC	3000
OY	2965	TCCCTCTCTACTCATCTCTGAAAGCCAAAGAACCAAGGATGTGCTGGGGGGCCAAAGGC	3020
Db	3001	TCCCTCTCTACTCATCTCTGAAAGCCAAAGAACCAAGGATGTGCTGGGGGGCCAAAGGC	3060
OY	3025	GCGCGCGGCGCTCTGCGCTTCAGAGGCCGTGACATGTGCTGTGACCAAGCATTTCTGCTC	3080
Db	3061	GCGCGCGGCGCTCTGCGCTTCAGAGGCCGTGACATGTGCTGTGACCAAGCATTTCTGCTC	3120

QY	3085	AAGTGA	CTG	GA	CAC	GGT	CT	CA	CTTA	AG	GG	CA	CTCC	GG	GG	GT	CA	CTCA	GA	GA	GA	GG	CC	GA	314					
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QY	3145	ACGCA	GTG	ATG	TCG	AA	GCT	CC	CG	GG	GA	CGA	CG	CT	GA	CTG	CC	CT	GA	GA	GG	CC	GA	CG	320					
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QY	3205	CCGCA	CTG	CC	CT	CA	CA	CTT	CA	AA	GA	CA	AT	CC	GA	CT	GA	CT	GA	AT	GG	CA	CC	CG	326					
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QY	3265	GCCGA	AG	CA	GA	CA	CA	CA	GA	AG	CT	CT	GA	CA	CG	CG	GG	CT	CTA	AG	CT	CC	GA	GG	332					
Db	3301	GCCGA	AG	CA	GA	CA	CA	CA	GA	AG	CT	CT	GA	CA	CG	CG	GG	CT	CTA	AG	CT	CC	GA	GG	336					
QY	3325	CGG	CC	CA	CA	CC	CA	GG	CC	CG	CA	CC	CG	CT	GA	AG	CC	CT	GA	AG	CT	GA	GT	TT	GG	CC	GA	338		
Db	3361	CGG	CC	CA	CA	CC	CA	GG	CC	CG	CA	CC	CG	CT	GA	AG	CC	CT	GA	AG	CT	GA	GT	TT	GG	CC	GA	342		
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QY	3445	GGG	CT	GA	GT	TC	CA	GA	CA	CT	CC	CG	CT	CT	CA	TT	CC	CC	CA	AG	CT	GG	CG	CT	GG	CT	CA	350		
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QY	3505	CCC	CA	GG	CC	CA	GG	CT	TT	CT	CT	CA	CA	GA	AG	CC	CG	CT	CA	CT	CC	CA	AT	AG	AA	AT	GC	356		
Db	3541	CCC	CA	GG	CC	CA	GG	CT	TT	CT	CT	CA	CA	GA	AG	CC	CG	CT	CA	CT	CC	CA	AT	AG	AA	AT	GC	360		
QY	3565	CAT	CC	CA	CA	AT	TC	GC	AT	TT	CA	CC	CT	GC	CT	GC	CT	CT	TT	GC	CT	TT	CA	CC	CC	CC	CA	362		
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QY	3685	G	T	G	T	C	C	T	G	T	A	C	A	C	A	G	G	A	G	A	C	C	T	G	A	C	T	G	A	374
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1 ZIP: 94111-3834
2 COMPUTER READABLE FORM:
3 MEDIUM TYPE: Floppy disk
4 COMPUTER: IBM PC compatible
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6 SOFTWARE: Patentin Release #1.0, Version #1.30
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8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/911,312
10 FILING DATE: 14-AUG-1997
11 CLASSIFICATION: 536
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 08/724,643
14 FILING DATE: 01-OCT-1996
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 08/844,419
17 FILING DATE: 18-APR-1997
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/846,017
20 FILING DATE: 25-APR-1997
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 08/851,843
23 FILING DATE: 06-MAY-1997
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/854,050
26 FILING DATE: 09-MAY-1997
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 08/912,951
29 FILING DATE: 14-AUG-1997
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 08/915,503
32 FILING DATE: 14-AUG-1997
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Bindorn, Gregory P.
35 REGISTRATION NUMBER: 38,440
36 REFERENCE/DOCKET NUMBER: 015389-002500US
37 TELECOMMUNICATION INFORMATION:
38 TELEPHONE: (415) 576-0200
39 TELEFAX: (415) 576-0300
40 INFORMATION FOR SEQ ID NO: 18:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 3855 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46 MOLECULE TYPE: cDNA
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49 LOCATION: 56..2476
50 OTHER INFORMATION: /product="hprt"
51 OTHER INFORMATION: /note="clone #712562"
52
53 US-08-911-312-18
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55 Query Match 98.5%; Score 3767.8; DB 13; Length 3855;
56 Best Local Similarity 99.0%; Pred. No. 0;
57 Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;
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60 1 GCACGCGTGCCTCTGCTGCGCACGTGGGAAGCCCTGAGCCCGCGGATGCC 60
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62 68 GCGGCGTCCCCCGCGCGCGAGCGCGTCCCTCGTGTGCGAGCGACATACGCGAGGTCT 127
63 GCGGCGTCCCCCGCGCGCGAGCGCGTCCCTCGTGTGCGAGCGACATACGCGAGGTCT 120
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65 128 GCGCGTGCACGTTGCTGTGCGGCGCTGTGGAGCCCGAAGGCTGTGTGACGCGG 187
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73
74 248 ACGGCGCGCGCGCGCGCGCGCTTCTTCCGCGCAGGTGTCTGTGGAAGAGCTGTGCG 307

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Db	241	ACGGCCCCCCCCCGCGCCCCCTCTCTTCCGCGAGGTGTCTGTCCGTAAGAGAGCTGTGTGGC	300
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Db	301	CCGAGTGTGTGAAGGTGTGTGTGCGAGAGCGCGCGTAAGAACTGTGTGTGGCTTCGGCTTCGC	360
QY	368	GCTGTGTGAACGGGGCCCCCGCGGGGGCCCCCGAGGCTTTCACACACAGCTGTGCACACTA	427
Db	361	GCTGTGTGAACGGGGCCCCCGCGGGGGCCCCCGAGGCTTTCACACACAGCTGTGCACACTA	420
QY	428	CTTGTCCCAACACAGGTGACCGAGCACTGTGGGGGGAGCGGGGTGTGGGGGTGTGTGTGTGGC	487
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QY	488	CCGCGTGTGTGACGACGTGTGTGTACCTGTGTGTGACAGCTGTGCGGCTCTTGTGTGTGT	547
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QY	548	GCGTCCGACGTGTGCGCTACCAAGGTGTGTGGGGGGCGCGCGGTGTGTACAGACTGTGCGGTGTGCAC	607
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QY	668	CTTGAACCATTAGCGTCAAGGAGGCGGGGTCCCCCTGGGCGCTGTGCACGCCCCGGGTGTGGAG	727
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QY	728	GAGGCGCGGGGGCAGTGTCCAGCCGAAATGTTCGCTGTTCCTCAAGAGGCCCAAGCGGTGTGGC	787
Db	721	GAGGCGCGGGGGCAAGTGTCCAGCGAAATGTTCGCTGTTCCTCAAGAGGCCCAAGCGGTGTGGC	780
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Db	841	GCGTGTGAACCGAGTGAACCGT	900
QY	908	CACCTCTTTGAGAGGTGTGCGCTCTGTGTGACGCGGCACTCCCAACCATTCGTTGGGCGCGCA	967
Db	901	CACCTCTTTGAGAGGTGTGCGCTCTGTGTGACGCGGCACTCCCAACCATTCGTTGGGCGCGCA	960
QY	968	GCACACAGCGGGCCCCCCCATTCACATCGGGCGACCAACGTCTCTGGGACACGCTTGTGTCC	1027
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Db	1201	GCCCCAGCGCTACTGGCAAAATGGCGCCCTGTTCCTGTAGAGTGTGTGTGTGTGTGTGTGTGTGT	1260
QY	1268	GTCGCCCTTACGAGGTGTCTCTTCAACACGCACTGTCCGCGCTGTGAGTGTGTGTGTGTGTGTGT	1327
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QY	1328	AGCGCGGTGTCTGTGTGCCCGGAGAAAGCCCCCAGAGGTCTGTGTGTGTGTGTGTGTGTGTGTGT	1387

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QY	1388	CACAAACCCCCGTCCGCTCTGTGTCAAGTGTCTCCGCGACACACAGACCCCTGTGCAAGTGA	144
Db	1381	CACAAACCCCCGTCCGCTCTGTGTCAAGTGTCTCCGCGACACAGACACCCCTGTGCAAGTGA	144
QY	1448	CGGCTTCTGTGCGGAGCTGCTGCGCGGCTGGTGGCCCCAGGCTCTGTGGGCTTCAAGCA	150
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Db	1501	CACGAAAGCGCGCTTCCACAGAAACCAAGAACTCATCTCCCTGGGGAAGCATGCCCCA	156
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Db	1561	GCTCTCGCTGCAGAGCTGACGCTGGAAATGACGCTGCGGACATGCGCTTGTGCTGCGAG	162
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RESULT 4
 US-08-911-312A-18
 Sequence 18. Application: US/08911312A
 GENERAL INFORMATION:
 APPLICANT: Ceeh, Thomas R.
 APPLICANT: Lininger, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Hartley, Calvin B.
 APPLICANT: Andrews, William
 TITLE OF INVENTION: Telomerase Reverse Transcriptase
 NUMBER OF SEQUENCES: 171
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/911.312A
 FILING DATE: 14-AUG-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:

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1 APPLICATION NUMBER: US 08/915,503
2 FILING DATE: 14-AUG-1997
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Einhorn, Gregory P.
5 REGISTRATION NUMBER: 38,440
6 REFERENCE/DOCKET NUMBER: 01589-002500US
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (415) 576-0200
9 TELEFAX: (415) 576-0300
10 INFORMATION FOR SEQ ID NO: 18:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 3855 base pairs
13 TYPE: nucleic acid
14 STRANDEDNESS: single
15 TOPOLOGY: linear
16 MOLECULE TYPE: cDNA
17 FEATURE:
18 NAME/KEY: CDS
19 LOCATION: 56..2476
20 OTHER INFORMATION: /product= "hprt"
21 OTHER INFORMATION: /note= "clone #12562"
22 US-08-911-312A-18
23
24 Query Match 98.5%; Score 3767.8; DB 13; Length 3855;
25 Best Local Similarity 99.0%; Pident. No. 0;
26 Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1
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Db 2641 CGGCCAGAGCTTATCCCTGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
QY 2672 AGAGAGAGATCCGAGAGAGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2731
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Db 2941 AGAGAGATCCGAGAGAGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
QY 2972 GCTACTCACTCAGAGAGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3031
Db 3001 GCTACTCACTCAGAGAGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060
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QY	1088	GCCCTTCCTTCTACTCACTCACTCTCTGTAAGGCCCAAGCTGACATGAGCGCTCGAGAGCTGTGGA	1147
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QY	1148	GACCAATCTTTCGAGGTTCACAGGCCCTGATATGACAGGACTCCCGCAGATTGCCCGGCT	1207
Db	1141	GACCAATCTTTCGAGGTTCACAGGCCCTGATATGACAGGACTCCCGCAGATTGCCCGGCT	1200
QY	1208	GCCCCAGCGCTACTGAGCAATGCGAGCCCTCTTTCTTGAGAGCTGCTTGGAAACACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGAGCAATGCGAGCCCTCTTTCTTGAGAGCTGCTTGGAAACACAGCGCA	1260
QY	1268	GTGCCCCCTAACGGGGGTGCTCTTAACAGCAGCTGCCCGTTCGAGAGCTGGCGGTACCCCAAGC	1327
Db	1261	GTGCCCCCTAACGGGGGTGCTCTTAACAGCAGCTGCCCGTTCGAGAGCTGGCGGTACCCCAAGC	1320
QY	1328	AGCCGATGTCTGTGCGCCGGGAGAACCCACAGGACTCTGTATGCGCGCCCCCGAGAGAGAGGA	1387
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QY	1388	CACAAACCCCGCTGCGCTGTGTGTACAGTGTCTCCGCAGACACAGACGCCCTTGACAGTGTGA	1447
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QY	1568	GCTTCGCTGACGAGACTGACCTGTGAAGATGACCTGTGGGACTGTGCGCTTGTGACGCGAG	1627
Db	1561	GCTTCGCTGACGAGACTGACCTGTGAAGATGACCTGTGGGACTGTGCGCTTGTGACGCGAG	1620
QY	1628	GAGCCCAAGGGGTTGGCTGTGTTCCGAGCCGACAGACACCGTCTGCGTGAAGAGATCTGGC	1687
Db	1621	GAGCCCAAGGGGTTGGCTGTGTTCCGAGCCGACAGACACCGTCTGCGTGAAGAGATCTGGC	1680
QY	1688	CAAGTTCCTGCACTGAGCTGATGAGTGTATAGTGTGAGCGTGCACAGTCTCTTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGAGCTGATGAGTGTATAGTGTGAGCGTGCACAGTCTCTTTCTTTTA	1740
QY	1748	TGTCAAGAGAACCAACGTTTCAAAAGAACAGGCTCTTTTCTAACGGGAAGATGTCTGAG	1807
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QY	1808	CAAGTGTGAAGACATTTGGAATCAGACACACTTGAAGAGGGTGAAGACGTGCGGGAGCTGTC	1867
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QY	1868	GGAAAGCAGAGGTCAAGGACAGCATCGGAAAGCCAGAGCCGACCTGTCTGAAGTCCAGACTTCG	1927
Db	1861	GGAAAGCAGAGGTCAAGGACAGCATCGGAAAGCCAGAGCCGACCTGTCTGAAGTCCAGACTTCG	1920
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QY	1988	CAGAACGTTCCGACAGAGAAAAGAGAGGCCAGACGTTCTCACTCAAGAGTGAAGACACTGTT	2047
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QY	2972	GCTACTGCATCTCTAAAGCCAAAGACGAGGAGTGTGCTGGGGGCCAAGGGCGCCGCG	3031
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QY	3032	GCCCTCTGCCCTCCGAGGCGGTGACAGGCTGTGTCACCAAGCAATTCTGTCTCAAGCTGA	3091
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QY	3092	CTTCGACACCGTGTCACTTACGTGCATCTCTGGGGTCACTTCAGGACAGCCACGACGAC	3151
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QY	3152	TGAATTCGAAAGCTCCGCGGACGACGCTGACTCCTCTGAGGCGCGACGCCAACCCGCGAC	3211

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QY 3212 TGCCCTCAGACTTCAAGACCATCTGAGACTGATGAGCACCAGCCAGCCAGCCAGG 3271
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RESULT 9
US-09-721-477-4
Sequence 4, Application US/09721477
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,477
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1..3855
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FEATURE:
NAME/KEY: CDS
LOCATION: 56..2479
OTHER INFORMATION: /product="delta-182 variant
polypeptide"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-721-477-4
Query Match 98.5%; Score 3767.8; DB 31; Length 3855;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;
QY 8 GCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 67
Db 1 GCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 68 GCGCGCTCCCGGCTGCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
Db 61 GCGCGCTCCCGGCTGCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 128 GCGCGTGGCAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Db 121 GCGCGTGGCAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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Db 181 GAGCCCGGCGGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

[illegible]

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Db	2761	GCTTCAAGGCTGGGAGGAAACAATGCTGTGGCAAACCTCTTTGGGGGCTTGGCGGTGAAGTCT	2820
QY	2792	ACAGCCTGTATTTCTGAATTTGTGAGGTGAACAAGCCTTCCAGACGGGTGTGACCAACAATCTTACA	2851
Db	2821	ACAGCCTGTATTTCTGAATTTGTGAGGTGAACAAGCCTTCCAGACGGGTGTGACCAACAATCTTACA	2880
QY	2852	AGATCCCTCCCTGTCCAGACGGCTGACAGGTTTACACGATGTGTGCTGTCCAGTCTCCCATTTATCT	2911
Db	2881	AGATCCCTCCCTGTCCAGACGGCTGACAGGTTTACACGATGTGTGCTGTCCAGTCTCCCATTTATCT	2940
QY	2912	AGCAAGTTTGGAGAACCCCAACATTTTTCCTGGCGCTCATCTCTGACACGGCTCCCTCT	2971
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QY	2972	GCTATCTCATCTTAAAGCCAAAGAACGAGGAATGTGTGCTGGGGGCTCAAGGGCGCGCGG	3031
Db	3001	GCTATCTCATCTTAAAGCCAAAGAACGAGGAATGTGTGCTGGGGGCTCAAGGGCGCGCGG	3060
QY	3032	GCCTCTGTCCCTCCGAGCGCGTGTGCATGTGTGTGCACAAAGCATTCCTGTCAAGCTGA	3091
Db	3061	GCCTCTGTCCCTCCGAGCGCGTGTGCATGTGTGTGCACAAAGCATTCCTGTCAAGCTGA	3120
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QY	3332	CACCCAGGCGCGCACGCTGTGGAGTGTGAGGGCTGTGATGTGTGTGGCGAGGCTCAGCA	3391
Db	3361	CACCCAGGCGCGCACGCTGTGGAGTGTGAGGGCTGTGATGTGTGTGGCGAGGCTCAGCA	3420
QY	3392	TGTCCGGCTGAAGGCTGTAGTGTCCGGCTGAGAGGCTTGAAGCGATGTCCAAGCCAAAGGCTGA	3451
Db	3421	TGTCCGGCTGAAGGCTGTAGTGTCCGGCTGAGAGGCTTGAAGCGATGTCCAAGCCAAAGGCTGA	3480
QY	3452	GTGTCCAGACACCTGTGCGTCTTTCACCTTCCCAAGGCTGTGGCGTCCGCTCCACCCAGG	3511
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QY	3512	GCCAGCTTTTCTTCCACAGAGAGCCCGGCTTCCACTCCCCACATNAGAAATGTGTCAATCCCC	3571
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Db	3601	AGATTGCGCAATTTGTCAACCCCTGTGCGCTGTGCTCTCTTTGGCTTCCACCCCCACCATTCAG	3660
QY	3632	GTGAGACACCTGTGAGAAAGAACCTGTGGAGCTGTGTGGAAATTTGGAGTGTACAAAGGTGTGCC	3691
Db	3661	GTGAGACACCTGTGAGAAAGAACCTGTGGAGCTGTGTGGAAATTTGGAGTGTACAAAGGTGTGCC	3720
QY	3692	CTGTACACAGGCGAGGACCTGTGACCTGTGATGTGGGCTCCCTGTGTGGTCAAAATTTGGGGGGA	3751
Db	3721	CTGTACACAGGCGAGGACCTGTGACCTGTGATGTGGGCTCCCTGTGTGGTCAAAATTTGGGGGGA	3780
QY	3752	GGTGTCTGTGGAGGTAAATACTGAATATATAGATTTTTCAGTTTGTGAAAAAATTTAAAAA	3811
Db	3781	GGTGTCTGTGGAGGTAAATACTGAATATATAGATTTTTCAGTTTGTGAAAAAATTTAAAAA	3840
QY	3812	AAAAAAAAAAAAA 3824	

QY	1028	CCCGGTGTAACGGCCAGAACCAACAACATTCCTCTTAATCTCTCAGCCGACAGAGACCACTGCG	108
Db	1021	CCCGGTGTAACGGCCAGAACCAACAACATTCCTCTTAATCTCTCAGCCGACAGAGACCACTGCG	1080
QY	1088	GCCCTCTCTTCCACTCACTCACTCTCTAGCTCTCTAGAGCCACCTGACTGCGCTGCGAGGCTCTGAG	1147
Db	1081	GCCCTCTCTTCCACTCACTCACTCTCTAGAGCCACCTGACTGCGCTGCGAGGCTCTGAG	11467
QY	1148	GACCAATCTTCTGGGTTCCAGGCGCCGTGGATGTCACAGGACCTCCCGCAGATTGCCCGGCT	1207
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QY	1448	CGGCTTCTGTGCGGAGCTGCTGCTGCGCGCTGTGTCGCCCAAGCTCTTGAGCTCCAGCA	15077
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QY	1508	CAACCAAGCGCGCTTCCCTCAGGAAACACCAAGAAATTCACTCCCTGGGAAAGCATGCGCA	1567
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QY	1568	GCTCTCGCTGACAGAGACTGACGTGGAAATGATGACGTGCGGACCTGCGCTTGTGCTGCGCAG	1627
Db	1561	GCTCTCGCTGACAGAGACTGACGTGGAAATGATGACGTGCGGACCTGCGCTTGTGCTGCGCAG	1620
QY	1628	GAGCCACAGGCGTGTGACTGTCTCCGCGCGCAGAGACCGCTGTGCTGAGAGATGCTGCGC	1687
Db	1621	GAGCCACAGGCGTGTGACTGTCTCCGCGCGCAGAGACCGCTGTGCTGAGAGATGCTGCGC	1680
QY	1688	CAAGTTCCTGCACTGCTGATGATGATGTGTAGCTGCTGAGCTGCTCAAGTCTTCTTTTA	1747
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QY	1748	TGTCACGAGACCAAGTTCCTTCAAAAGAACAGGCTCTTTTCTAACCGGAAAGATGCTGAG	1807
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QY	1808	CAAGTTCGAAAGCATTTGGAAATCAACACACTTGAAGAGGTGACGCTGCGGAGCTGTCTC	1867
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QY	1868	GGAAACAGAGTCAAGCAGCATTCGAGAAACAGAGGCCCTCTGTGCTGACGTCCAAACTCCG	1927
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RESULT 12
 US-10-044-692-4
 Sequence 4, Application US/10044692
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Linger, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/044,692
 FILING DATE: 11-Jan-2002
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/912,951
 FILING DATE: <unknown>
 APPLICATION NUMBER: US 08/954,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3855 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..3855
 OTHER INFORMATION: /note="nucleic acid sequence with an open reading frame encoding a delta-182 variant polypeptide"
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-044-692-4
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 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;
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 Db 121 GCGGCTGAGCACTTGTGTCGCGGCTGAGGAGCCGAGGCTGAGGCTGTCGCAAGTGAAG 180
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 Qy 248 ACAGCGCGCGCGCGCGCGCGCTTCCGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307
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Db 1801 CAAGTTCCAAAGCATTTGGATTCAGACAGCACTTGAAGAGGTCAGCTGGGGAGCTGTTC 1860
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/ 1861 GGAAGCAGAGGTCAGGAGCATGCGGAAGCAGGCGCGCTGCTGACGTCCAGACTCCG 1920
Qy 1928 CTTATATCCCAAGCTTCAAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1987
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Db 3841 ACCATCCAGGTGGAGACCTGAGAGGACCTGGAGCTCTGGAAATTGAGTGACCA 3900
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Db 4021 AAAAAAAAAAAAAAAAAA 4042
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Search completed: March 1, 2004, 22:57:45
Job time : 7781.54 secs

RESULT 10
US-10-767-701-9739
; Sequence 9739, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 9739
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAV03-CLUS33367_1
US-10-767-701-9739

Query Match 1.4%; Score 53.4; DB 6; Length 1092;
Best Local Similarity 45.0%; Pred. No. 0.0063;
Matches 201; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

QY 39 GCCCTGCCCCCGCCACCCCGGATGCGCGCTCCCGCTGCGAGCCGTGCGCTCC 98
DB 177 GGGCTTGGCGCGCGCGCGCTCCACCCCTCCCGCGCGCGCTCCCGCTCCCGCGCG 236
QY 99 CTGCTGGCGAGCACTACCGGAGAGTGTGCGCTGCGCACTTCGTGCGCGCGCGCGCG 158
DB 237 CGCCCG 236
QY 159 CCGGAGCG 218
DB 297 CCG 356
QY 219 CAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 278
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RESULT 11
US-10-767-701-30024
; Sequence 30024, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 30024
; LENGTH: 522

TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: 9848339
US-10-767-701-30024

Query Match 1.4%; Score 53.2; DB 6; Length 522;
Best Local Similarity 49.4%; Pred. No. 0.0053;
Matches 167; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

QY 122 GGTGCTCCCGCTGCGCACTTGTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCG 181
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RESULT 12
US-10-767-701-8805
; Sequence 8805, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
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; SEQ ID NO 8805
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; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAV03-CLUS6975_1
US-10-767-701-8805

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Matches 199; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

QY 126 CTGCG 185
DB 23 CTCTCTGTGTATGCG 82
QY 186 GGGAGCG 245
DB 83 CACGACCG 142
QY 246 GCG 305
DB 143 GCGTGGCG 202
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Db 5608 GCGCCGCTCTCTCCGCGCAGCTG---CCGCTGCCGCTTGACCTTCCGCCAGGGCAC 5552
QY 608 TCAGGC--CCGGCCCCCGCCACAGCTAGTGGACCCGGAAGGCTCTGGAGATGGAAAGG 665
Db 5551 GCGAGCGGGCGGCTCTCTCCGCGCAGCTCGCGAAAGCGCGGCTCGGCTCCAGCTCT 5492
QY 666 GCGTGAACATAGCAGTACAGGAGAGCGGGGCTCCCGCTGAGGCTGCG 712
Db 5491 GCTTGAATTTCTCGTGTGTGAGGCGGACCTCTCTCAGGCTTGGCC 5445

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US-10-767-471-603/c
; Sequence 603, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 603
; LENGTH: 11409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-603

Query Match 1.4%; Score 52; DB 6; Length 11409;
Best Local Similarity 44.2%; Pred. No. 0.031;
Matches 184; Conservative 6; Mismatches 226; Indels 0; Gaps 0;

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Db 1943 CCTCTCAGCAGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1884
QY 77 CCGCTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 136
Db 1883 ACTCTGTGCTCGCGCGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1824
QY 137 CACGTTGCTGCGCGCTGAGGCGCCAGAGGCTGAGCTGAGCGCGGAGCGCGGCG 196
Db 1823 CCACTCTGTTTACGACGAGCTCCGCTRCGGAAGGCTGCTGCTGCTGCTGCTGCTGCT 1764
QY 197 GCGTTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256
Db 1763 GCGCGGCTCGCGCTCGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1704
QY 257 CCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
Db 1703 TCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1644
QY 317 GCAGAGGCTGCTGCGAGCGCGCGCGAGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 376
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Db 1583 GTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1528

Search completed: March 1, 2004, 23:56:46
Job time : 58.1579 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 17:50:03 ; Search time 6059.79 Seconds
(without alignments)
18844.394 Million cell updates/sec

Title: US-09-424-686F-10
Perfect score: 3824
Sequence: 1 gtttcagcagcagcgcgcgc.....aaaaaaaaaaaaaaaaaa 3824

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: em_estro:*
8: em_hic:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	980	25.6	1584	29	AY407350 Pan trogl
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4	465.4	12.2	468	10	AM270031 X57603.X

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12	340.4	8.9	599	14	CF531069
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14	317.8	8.3	364	13	BO258274
15	316.4	8.3	360	9	AA811084
16	290.8	7.6	614	10	BB651920
17	284.4	7.4	315	9	AA748707
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23	243	6.4	610	10	BE514188
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37	132	3.5	641	28	AZ972318
38	128.8	3.4	875	13	BU122597
39	123.8	3.2	813	12	BG198331
40	114.8	3.0	654	13	BM862610
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ALIGNMENTS

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LOCUS
DEFINITION Homo sapiens TERT gene, VIRAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION
AY407349
VERSION
AY407349.1 GI:39763320
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1826)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1826)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission

DEFINITION Pan troglodytes TERT gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY407350
VERSION AY407350.1 GI:39763321
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
1 (bases 1 to 1584)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalraj, A.,
Todd, M.A., Tenenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trices
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1584)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalraj, A.,
Todd, M.A., Tenenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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QY 1816 AAAGCATTTGATCAGACAGCACTTGAAGAGAGTGTGAGCTGCGGAGCTGTGCGAAGAG 1875
DB 181 AAAGCATTTGATCAGACAGCACTTGAAGAGAGTGTGAGCTGCGGAGCTGTGCGAAGAG 240
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DB 241 AGGTCAAGGAGCATTCGGAAGACAGAGCGCGCTGCTGATGCTGACATTCGCTTATCC 300
QY 1936 CCAAGCTGACGGGCTGCGGCGCATTTGTGAACATGTGACTACGTCGCGGAGCGAGAGGT 1995
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QY 2248 TCGCTCGTATGCGCTGCTC----- 2267
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 ACCESSION AY407351
 VERSION AY407351.1 GI:39763322
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanendbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE
 AUTHORS Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanendbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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 Best Local Similarity 61.5%; Pred. No. 6,9e-68; Indels 227; Gaps 4;
 Matches 1128; Conservative 0; Mismatches 480;

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QY 1696 TGCACCTGGCTGATGAGTGTGACGTCGTCGAGCTGCTGCTTTCTTTATGTCAGG 1755
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QY 1936 CCAAGCTTGAAGGAGCTGCGGCGAGTGTGAGCAATGAGCTACGTCGTGAGAGCGCAAGCT 1995
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QY 1996 TCCGAG-AGAAAAGAGGCGAGCGCTCACTCGAGGAGTGAAGCACTGTCAGCGG 2054
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 Bonaldi, M. F., Lennon, G. and Soares, M. B. (1996) Genome
 Research 6(19): 791-806. RNA was prepared from harvested
 cells of SNU-16 culture. SNU-16 cell was obtained from
 Korean Cell Line Bank (KCLB). SNU-16 was established from
 ascitic fluids of Korean patients by Park J.G. et al.
 (1990), Cancer Res 50: 2773-2780."

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Korean Cell Line Bank (
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Bonardo, M.F., Lennon, G. and Soares, M.B. (1996), genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNV-16 culture. SNV-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNV-16 cell was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

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Bonardo, M.F., Lennon, G. and Soares, M.B. (1996), genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNV-16 culture. SNV-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNV-16 cell was established from
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(1990), Cancer Res 50: 2773-2780."

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Bonardo, M.F., Lennon, G. and Soares, M.B. (1996), genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNV-16 culture. SNV-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNV-16 cell was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

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ORIGIN

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				Gaps 0;

QY	255	GTGAACTTCCCTGTGAGAAACAGAGCCCTGGGTGGCAACGGCTTTTGTTCAGATGCCGGCC	261
Db	1	GTGAATTTCCCTGTGAAAGACAGAGCCCTGGGTGGCAACGGCTTTTGTTCAGATGCCGGCC	60
QY	2617	CACGCGCTATTTCCCTCTGTGGCGGCTGCTGTGTGATACCCGGAACCTTGAGGTGCAAGAC	2676
Db	61	CACGCGCTATTTCCCTCTGTGGCGGCTGCTGTGTGATACCCGGAACCTTGAGGTGCAAGAC	120
QY	2677	GACTACTCCAGCTATGACCCTGGACCTCCATACAGAACCACTCAACCTTCAACCGCGGCTTC	2733
Db	121	GACTACTCCAGCTATGACCCTGGACCTCCATACAGAACCACTCAACCTTCAACCGCGGCTTC	180
QY	2737	AAGCGTGGAGGAAACATGCTGCAAACTCTTTGGGGCTCTTGCGGGCTGAAGTGCACAGC	2796
Db	181	AAGCGTGGAGGAAACATGCTGCAAACTCTTTGGGGCTCTTGCGGGCTGAAGTGCACAGC	240
QY	2797	CTGTCTCTGATTTTGACAGGTGAACAGCGCTCCAGACGGTGTGCACAAACATCTACAAAGATC	2855
Db	241	CTGTCTCTGATTTTGACAGGTGAACAGCGCTCCAGACGGTGTGCACAAACATCTACAAAGATC	300
QY	2857	CTCCTCTCAGGCGGTACAGGTTTACGACATGTGTGTGAGAGGCTCCCATTTACATAGCA	2916
Db	301	CTCCTCTCAGGCGGTACAGGTTTACGACATGTGTGTGAGAGGCTCCCATTTACATAGCA	360
QY	2917	GTTTGGAAAGACCCCAATTTTCTGTGGGTCAATCTGTACACAGGCTTCCCTGTGCTAC	2976
Db	361	GTTTGGAAAGACCCCAATTTTCTGTGGGTCAATCTGTACACAGGCTTCCCTGTGCTAC	420
QY	2977	TCCATCTGAAAGCCCAAGACGAG 3001	
Db	421	TCCATCTGAAAGCCCAAGACGAG 445	

RESULT 6	BM453198	925 bp	mRNA	linear	EST 05-FEB-2002				
LOCUS	BM453198								
DEFINITION	AGENEOUT 6387556 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5529840								
ACCESSION	BM453198								
VERSION	BM453198.1	GI:18502238							
KEYWORDS	EST.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
REFERENCE	1 (bases 1 to 925)								
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .								
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)								
JOURNAL	Unpublished (1995)								
COMMENT	Contact: Robert Strausberg, Ph.D.								

found through the I.M.A.G.E. Consortium/LLNL at
http://image.llnl.gov
Plate: LLNL2208 row: p column: 01
High quality sequence stop: 646.
location/Qualifiers
1. .925

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found through the I.M.A.G.E. Consortium/LLNL at
http://image.llnl.gov
Plate: LLAM2208 row: p column: 01
High quality sequence stop: 646.
location/Qualifiers
1. .925

```

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found through the I.M.A.G.E. Consortium/LLNL at
http://image.llnl.gov
Plate: LLAM2208 row: p column: 01
High quality sequence stop: 646.
location/Qualifiers
1. .925

```

found through the I.M.A.G.E. Consortium/LLNL at
http://image.llnl.gov
Plate: LLNL2208 row: p column: 01
High quality sequence stop: 646.
location/Qualifiers
1. .925

```

found through the I.M.A.G.E. Consortium/LLNL at
http://image.llnl.gov
Plate: LLAM2208 row: p column: 01
High quality sequence stop: 646.
location/Qualifiers
1. .925

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found through the I.M.A.G.E. Consortium/LLNL at
http://image.llnl.gov
Plate: LLAM2208 row: p column: 01
High quality sequence stop: 646.
location/Qualifiers
1. .925

```

found through the I.M.A.G.E. Consortium/LLNL at
http://image.llnl.gov
Plate: LLNL2208 row: p column: 01
High quality sequence stop: 646.
location/Qualifiers
1. .925

```

found through the I.M.A.G.E. Consortium/LLNL at
http://image.llnl.gov
Plate: LLAM2208 row: p column: 01
High quality sequence stop: 646.
location/Qualifiers
1. .925

```

ORIGIN

Query Match	11.5%	Score 441.6;	DB 12;	Length 925;
Best Local Similarity	95.7%	Pred. No. 6.5e-45;		
Matches 465;	Conservative 0;	Mismatches 19;	Indels 2;	Gaps 1;

QY	2280	CATGGGCAACGTCCGCAAGGCTTCAAGAGCAATGCTCAATGCAATGGCAAGGGATCCC	233
Db	344	CATGTCACCAACGCGCGGCATACAGGGCAATGCTTACGTCAATGCAAGGATCCC	403
QY	2340	GAGAGGCTTCATCCTCTCCACAGCTGCTCTGCAAGCTGTGCTACGCGCATGAGACAA	2399
Db	404	GAGAGGCTTCATCCTCTCTCAAGCTGCTCTGCAAGCTGTGCTACGCGCATGAGACAA	463
QY	2400	GCCTGTTTGCGGGGATTTGGCGGGACGAGGCTGCTCGCTGTTGGTGGATGATTTCTGTT	2455
Db	464	GCTGTTTTCGGGGATTTGGCGGGACGAGGCTGCTCTGCTGTTGGTGGATGATTTCTGTT	523
QY	2460	GGTGACACCTCACTTCACCCACGCGAAACCTTCTCAGGACCTGTGTCAGAGTGTCCC	2519
Db	524	GGTGACACCTCACTTCACCCACGCGAAACCTTCTCAGGACCTGTGTCAGAGTGTCCC	583
QY	2520	TGAGTATGAGCTGCGGTGGAACTTGGGGAGACAGAGTGGAATCTCCGTGTAAGACGA	2579
Db	584	TGAGTATGAGCTGCGGTGGAACTTGGGGAGACAGAGTGGAATCTCCGTGTAAGACGA	643
QY	2580	GGCCCTGGGTGGCAACGGCTTTTGTTCAGATGCGGCGCCACGCGCTATTCCCTGTGTCCG	2633
Db	644	GGCCCTGGGTGGCAACGGCTTTTGTTCAGATGCGGCGCCACGCGCTATTCCCTGTGTCCG	703
QY	2640	CCCTGCTGTGATACCCGGACCTCTGAGGTGCGACGACTACTCCAGTTAGCCCGAC	2699
Db	704	CCCTGCTGTGATACCCGGACCTCTGAGGTGCGACGACTACTCCAGTTAGCCCGAC	763
QY	2700	CTTCATCAGAGCGAGTCTCACTTTCAACCGGCTTCAA--GACTGGAGGAACATGCT	2757
Db	764	CTTCATCAGAGCGAGTCTCACTTTCAACCGGCTTCAAAGGCTGGAGGAACATGCT	823
QY	2758	CGCAAA 2763	
Db	824	CGCAAA 829	

RESULT	7
BG917907	
LOCUS	
DEFINITION	BG917907 851 bp mRNA linear EST_05-JUN-2001 6028205301 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4945887 5' , -
ACCESSION	BG917907
VERSION	BG917907
KEYWORDS	Mus musculus (house mouse)
SOURCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (baes 1 to 851) NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS	

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNL0903 row: k column: 08
High quality sequence stop: 753.
Location/Qualifiers

FEATURES
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1. 851
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:494987"
/sex="female, virgin"
/issue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-Sport6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 11.0%; Score 419; DB 12; Length 851;
Best Local Similarity 71.9%; Pred. No. 4e-42;
Matches 579; Conservative 0; Mismatches 215; Indels 11; Gaps 2;

2440 TTGGTGGATGATTTCTTGTGTGACACCTCACCAGCGGAAACCTTCCTCAGG 2499
38 TTGTGTGATGACTTCTGTGAGGAGCCTCCTCAGACCAAGCAAACTTCCTCAGC 97
2500 ACCCTGATCGAGGTCTCCCTGAGTATGCTGCTGCTGCTGCTGCTGCTGCTG 2559
98 ACCCTGATCGAGGTCTCCCTGAGTATGCTGCTGCTGCTGCTGCTGCTGCTG 157
2560 AACTTCCTGATGAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2619
158 AACTTCCTGATGAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 217
2620 GGCCTATTCCTGATGAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTG 2679
218 TGCTGTTCCTGATGAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTG 277
2680 TACTCAGCTATGAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2739
278 TACTCAGCTATGAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 337
2740 GCTGAGGAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2799
338 GCTGAGGAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 397
2800 TTTCTGATTTGAGGTGAACGCTTCAGAGCTGTGCTGCTGCTGCTGCTGCTGCTG 2859
398 TTTCTGATTTGAGGTGAACGCTTCAGAGCTGTGCTGCTGCTGCTGCTGCTGCTG 457
2860 CTGCTGAGGAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2919
458 CTGCTGAGGAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 517
2920 TGGAGAACCCCACTTTTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2979
518 AGGAGAACCCCACTTTTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 577
2980 ATCTGAAGCGAAGAACGAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3039

Db 578 ATCTGAAGGTCAAGATTCAGAGGAGCTAAAGGCTGTGGCTC-----CTT 627
Qy 3040 CCTCCAGAGCCCGTGCAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3098
Db 628 TCTCTGAGAGCCCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 687
Qy 3099 CCGTGTACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3158
Db 688 TCTGTATCTGACAAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 747
Qy 3159 GAAGCTCCCGGAGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3218
Db 748 GAAGCTCCCGGAGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807
Qy 3219 AGACTTCAGAGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3243
Db 808 AGACTTCAGAGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 832

RESULT 8
AM276315/c 416 bp mRNA linear EST 03-JAN-2000
LOCUS x110b12.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2759711 3'
DEFINITION mRNA sequence.
ACCESSION AM276315
VERSION AM276315.1 GI:6663345
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 416)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Chris Koskialuk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/dbtrp/image/image.html
Seq primer: -40UP from Gabc
High quality sequence stop: 413.
Location/Qualifiers

FEATURES

source
1. 416
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2759711"
/issue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu28"
/note="Organ: lung; Vector: pCMV-Sport6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."

ORIGIN

Query Match 10.9%; Score 416; DB 10; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.1e-41;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3383 AGGCTGATGTCGGCTGAGGCTGAGTGTGCTGAGGCTGAGGCTGAGGCTGAGGCTG 3442
Db 416 AGGCTGATGTCGGCTGAGGCTGAGTGTGCTGAGGCTGAGGCTGAGGCTGAGGCTG 357
Qy 3443 AAGGCTGATGTCGGCTGAGGCTGAGTGTGCTGAGGCTGAGGCTGAGGCTGAGGCTG 3502
Db 356 AAGGCTGATGTCGGCTGAGGCTGAGTGTGCTGAGGCTGAGGCTGAGGCTGAGGCTG 297

gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCAGCAGC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 9.8%; Score 379.6; DB 13; Length 851;
Best Local Similarity 77.6%; Pred. No. 2,7e-37;
Matches 457; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

2306 GAGGCAAGTCTTACAGTCCAGGAGATCCCGAGGCTTCATCTCTCCAGCCTGC 2365
262 GTGACAGTCTTACAGTCCAGGAGATCCCGAGGCTTCATCTCTCCAGCCTGC 321
2366 TCTCAGCCTGTGTACAGGAGATGAGAAAGAGCTTTGGGGATTCCGGGGAGC 2425
322 TCTCAGTCTGT 381
2426 GAGTCTCTCTGT 2485
382 GGT 441
2486 AAGCTCTCTCAGAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2545
442 AAGCTCTCTCAGAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 501
2546 GGAAGCAGT 2605
502 AGAAGCAGT 561
2606 AGATGCGGCGCCAGCGGCTTATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2665
562 AGCTGCTGT 621
2666 AGGTGAGAGAGCAGTCTCAGTATGCGGAGCTCCATTCAGAGCAGTCCACCTTCA 2725
622 AGGTGTTCTGT 681
2726 ACCGCGCTTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2785
682 AGAGTGTCTTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 741
2786 AGGTGAGAGCAGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2845
742 AGGTGAGAGCAGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 801
2846 TCTTCAAGATCTCTGT 2894
802 TATTAAGAGATCTCTGT 850

RESULT 11

LOCUS CFS31121 688 bp mRNA linear EST 12-SEP-2003
DEFINITION UI-M-FYO-csp-m-21-0-UI.r1 NIH BMAP_FYO Mus musculus cDNA clone
IMAGE:30355988 5', mRNA sequence.
ACCESSION CFS31121
VERSION CFS31121.1 GI:34583085
KEYWORDS EST,
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES

Location/Qualifiers
source

Seq primer: pX-5.

1..688
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355988"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="MD10B (T1 phage resistant)"
/clone_lib="NIH BMAP FYO"
/note="Organ: Brain; Vector: pX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGAGCAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 9.1%; Score 346.2; DB 14; Length 688;
Best Local Similarity 73.9%; Pred. No. 3.6e-33;
Matches 438; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

47 CCGGCGACCCCGAGTCCGCGGCTCCCGCTGCGAGCCGCTGCTCTGCTGCG 106
63 CCGGCGCTTGTGAGCAGATGACCGCGGCTCTCGTGTGCGCGGCTGCTGCTGCG 122
107 CAGCCACTTACCGAGAGTGTGCGCTGTGCGACGTTGTGCGGCGCTGCGGCGCCGAGG 166
123 CAGCCAGTACCGAGAGTGTGCGCGCTGCGCAACTTGTGCGGCGCTGCGGCGCGAGG 182
167 CTGCGGCTGTGTGAGCGCGGAGACCGCGGCGCTTCCGCGGCTGTGCGGCGCGAGTGCCT 226
183 CAGCGGCTTGTGAGAACCGGAGGACCGAGAGATCTACCGGACTTGTGTTCCCAAGGCT 242
227 GGTGTGCTGCTGT 286
243 AGTGTGATCAGCTGT 302
287 CTGCGTAAAGAGT 346
303 ATCCCTAAAGAGT 362
347 GTGTGTGCTTGT 406
363 GTGTGTGCTTGT 422
407 CACACAGAGGT 466
423 CACTAGAGCTGT 482
467 GCGGTGGGCGCTGT 526

Db 483 TCGATGATGCTACTGTTAGCGCGAGTGGCGACGACCTGCTGCTACTGCTGGACCA 542
 QY 527 CTGCGGCTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586
 Db 543 CTGTGCTCTTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
 QY 587 GTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
 Db 603 GTCTAACCCCTCATCTCTACTGACGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655

RESULT 12
 CFS31069 649 bp mRNA linear EST 12-SEP-2003
 LOCUS UI-M-FY0-csp-c-19-0-UI-r1 NIH BMAP_FY0 Mus musculus cDNA clone

DEFINITION IMAGE:30355746 5', mRNA sequence.
 CFS31069
 ACCESSION CFS31069.1 GI:34583033

KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 649)
 NIH-MGC <http://mgi.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed By: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: PYX-5.

FEATURES
 Location/Qualifiers

1..649
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 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30355746"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (TI phage resistant)"
 /clone_id="NIH BMAP FY0"
 /note="Organ: Brain; Vector: PYX-Asc; Site: 1: Ecor I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to RNA size fraction. Ligated with Ecor I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 8.9%; Score 340.4; DB 14; Length 649;
 Best Local Similarity 77.3%; Pred. No. 1.9e-32;
 Matches 413; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 47 CCGGCGCACCCCGGATGCGCGCGCTCCCGCTGCGGAGCCGCTGCGCTCCTGCTGCG 106

Db 26 CCGGCGCTTGAGACATGACCCCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 85
 QY 107 CAGCCACTACCGGAGATGCT 166
 Db 86 CAGCCACTACCGGAGATGCT 145
 QY 167 CTGCGGCT 226
 Db 146 CAGCGGCT 205
 QY 227 GGTGCT 286
 Db 206 AGTGTGCT 265
 QY 287 CTGCGGCT 346
 Db 266 ATCCCTGAAAGAGCT 325
 QY 347 CGTGTGCT 406
 Db 326 CGTGTGCT 385
 QY 407 CAGCCACTACCGGAGATGCT 466
 Db 386 CACTGCT 445
 QY 467 GCGGTGCT 526
 Db 446 TCGATGATGCTACTGCT 505
 QY 527 CTGCGGCTCTTTGCT 580
 Db 506 CTGTGCTCTTTTACTTCTGCT 559

RESULT 13

LOCUS BB618671

DEFINITION BB618671 RIKEN full-length enriched, 8 days embryo Mus musculus

ACCESSION BB618671
 CDNA clone 5730412M20 5', mRNA sequence.

VERSION BB618671.1 GI:16458173

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 599)

AUTHORS Arikawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Komuro, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takekida, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arikawa, T., et al. 2001)
 Unpublished (2001)

TITLE Yoshinide Hayashizaki

COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,
URL:ftp://genome.gsc.riken.go.jp/,
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komuro, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Itawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,


```

Db      69  GACATCGAGCACTTCTGACAGACACACCTCTATGCTGATCTGAGATGGCGCC 128
QY      1235  CTTGTTCTGAGCTGCTTGGGAGACCAACGCGCAGTGCCTTACGGGGTGTCTCTCAAGAC 1294
Db      129  CTTGTTCTCAACAGCTGTGTGTAACCATGACAGATGCAATATGTCAAGCTCTCAAGTCC 188
QY      1295  GCACTGCGCCCTGCGAGCTGCGGTCAACCCAGACAGCCGCTGTGTGCGCCGGAGAGACC 1354
Db      189  ACATGTGAGGTTTGAACAGCAACCAACGAGTGAACAGATGCTT----- 232
QY      1355  CCAAGGCTCTGTGGCGGCCCCCGAGAGAGACACAGACCCCGTGCCTGATGAGCT 1414
Db      233  -----TGACACAGCCACCCGACCTCATGATTT 263
QY      1415  GCTCCGCGACAGACAGACCCCTGCGAGGTGACGCTTGTGCGGCTGCTCTGCGCG 1474
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Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
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cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
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FEATURES

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was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - Oligo (dT) primer
[5'-TGTTACCAATCTGAGTGGAGAGCGCGCTCATTTTCTTTTCTTTT-3',
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 8.3%; Score 316.4; DB 9; Length 340;
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 Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B.,
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 Cells immortalized with telomerase reverse transcriptase for use in
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 Human telomerase catalytic subunit
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RESULT 8
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 KEYWORDS JP 2001081042-A/27.
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 (Bases 1 to 4037)
 AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
 Harley,C.B. and Andrews,W.H.
 TITLE Human telomerase catalytic subunit
 JOURNAL Patent: JP 2001081042-A 27 27-MAR-2001;
 GERON CORP. UNIVERSITY TECHNOLOGY CORP
 COMMENT OS Unidentified
 PN JP 2001081042-A/27
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 PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
 25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
 09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
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 R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN,PI
 MORIN,
 PI CALVIN B HARLEY,WILLIAM H ANDREWS
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LOCUS AR104587 4015 bp DNA linear PAT 14-FEB-2001
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ACCESSION AR104587
VERSION AR104587.1 GI:12817295
KEYWORDS
SOURCE Unknown:
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech, T.R. and Lingner, J.
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Best Local Similarity 89.9%; Pred. No. 0;
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AR175848
LOCUS AR175848 4015 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 224 from patent US 6309867.
ACCESSION AR175848
VERSION AR175848.1 GI:17917147
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 224 30-OCT-2001;
FEATURES
source 1..4015
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ORIGIN
Query Match 82.4%; Score 3306.6; DB 6; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

Qy 8 GCAGCGCTGCTGCTCTGCTGCGACGTGAGGAGCCCTGCGCCGCGCCGCGATGCC 67
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Qy 128 GCGCGCTGCG 187
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Qy 188 GGAACCG 247
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Qy 788 TGCCTCCCTGAGCG 847
Db 781 TGCCTCCCTGAGCG 840

Qy 848 GCGTGAACCGAGTGAACGCTGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
Db 841 GCGTGAACCGAGTGAACGCTGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900

Qy 908 CACCTCTTTGAGAGGCTGTGCTCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 967
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Qy 1568 GCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1627
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Qy 1628 GAGCCAGAGGAGT 1687
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RESULT 12
E36793 4015 bp DNA linear PAT 18-JUN-2001
LOCUS Human telomerase catalytic subunit promoter.
DEFINITION E36793.1 GI:13022756
VERSION E36793.1
KEYWORDS JP 199253177-A/1.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 4015)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 199253177-A 1 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
PN JP 199253177-A/1
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503, PT
R SECHI, JOCHIMU RINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
MORIN, CALVIN B HAREI, WILLIAM H ANDREWS
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PC C12N15/09, A61K31/70, A61K38/55, A61K39/395, A61K48/00,
PC C12Q1/02,
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Query Match 82.4%; Score 3306.6; DB 6; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

Qy 8 GGAGGCTCTGCTCTGCTGCGACGATGGGAAGCCCTGGGCCCCGGGACACCCCGGAGATGCC 67
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QY	1748	TGTCAACGGAGCACGCTTCAAAAAGACGCTCTTTTCAACGGAGACATGTCTGGAG	1807
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 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS Morin, G.B.
 TITLE Human telomerase catalytic subunit variants
 JOURNAL Patent: US 6337200-A 1 08-JAN-2002;
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Query Match 82.4%; Score 3306.6; DB 6; Length 4015;
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 Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 8 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 67
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 QY 188 GAGCCCGGCGCTTTCGCGCGCTGTGTGAGCCCAAGTGTGCTGTGCTGCTGCTGCTG 247
 Db 181 GAGCCCGGCGCTTTCGCGCGCTGTGTGAGCCCAAGTGTGCTGTGCTGCTGCTGCTG 240
 QY 248 ACG 307
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QY	1508	CACGAAACGCGCGCTTCTCTCAGGAAACACCAAGATTCATCTGCTCGGGGAACATGCCAA	1567
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Dp	1561	GCTTCTGCTGTGACGAGCTGACCTGGAAGATGAGCGTGCGGGACCTGCGCTTGTGCTGCGAG	1620
QY	1628	GAGCCACAGGGGTGTGAGCTGTGTTCCGGCGCAGAGACAGCTCTGCGTGAAGAGATCTGAG	1687
Dp	1621	GAGCCACAGGGGTGTGAGCTGTGTTCCGGCGCAGAGACAGCTCTGCGTGAAGAGATCTGAG	1680
QY	1688	CAAGTTCTGTGCACTGGCGTGAATGATGTGTACGTGCTGAGCTGCTCAAGTCTTTTCTTTTA	1747
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QY	1748	TGTCAACGAGACCAAGTTTCAAAAACAGAGCTCTTTTCTTCAACCGAAGAGTGTGAGAG	1807
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Query Match	82.4%	Score 3306.6;	DB 6;	Length 4015;
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Matches 3618;	Conservative	0;	Mismatches 359;	Indels 46;
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[illegible]

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Qy 1208 GCCCAGGCTGAGTTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1267
Db 1201 GCCCAGGCTGAGTTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1260
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Db 1321 AGCCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1380
Qy 1388 CACAGACCCCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1447
Db 1381 CACAGACCCCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1440
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Db 1501 CAAAGAACCCCTTCTCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1560
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 Hatley,C.B. and Andrews,W.H.
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 reverse transcriptase
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 Best Local Similarity 89.9%; Pred. No. 0;
 Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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 DB 1 GGAAGGCTGAGCTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 QY 68 GCGGCTCCCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 127
 DB 61 GCGGCTCCCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 QY 128 GCGGCTGCTGAG 187
 DB 121 GCGGCTGCTGAG 180
 QY 188 GGAACCGGAGGCTTCCGCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247
 DB 181 GGAACCGGAGGCTTCCGCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 QY 248 ACGGCGGCTCCCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307
 DB 241 ACGGCGGCTCCCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 308 CCGAGTGTGAG 367
 DB 301 CCGAGTGTGAG 360
 QY 368 GCTGCTGAG 427
 DB 361 GCTGCTGAG 420
 QY 428 CTTGCTGAG 487
 DB 421 CTTGCTGAG 480
 QY 488 CCGGCTGAG 547
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 QY 548 GCGTCCGAG 607
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 QY 608 TCAGGCGGCGGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
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 QY 668 CTGGAACCATAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
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 QY 788 TGCCCTTGAAGCGAG 847
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 QY 848 GCGTGAACCATAGCTGAG 907
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Qy      3455 GGGAGAGCTGGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3514
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Qy      3515 GCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3574
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Qy      3575 CTGTGTGCAACCCAGGCGCAAG-----GGCTTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3629
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Qy      3690 CCAAGTACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3749
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RESULT 3

AAV60320 standard; cDNA; 4023 BP.

AAV60320;

04-DEC-1998 (first entry)

Human telomerase gene referred to as hEST2.

Catalytic subunit; human; telomerase; telomere maintenance; diagnosis;

treatment; cancer; ss.

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OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      CDS      59..3458
XX              /*tag= a
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XX      MO9837181-A2.
XX
XX      PD      27-AUG-1998.
XX
XX      PF      20-FEB-1998; 98MO-US003404.
XX
XX      PR      20-FEB-1997; 97US-0038750P.
XX      PR      20-MAY-1997; 97US-0047151P.
XX      PR      01-AUG-1997; 97US-0054549P.
XX      PR      14-AUG-1997; 97US-0055762P.
XX      PR      30-OCT-1997; 97US-0064322P.
XX
XX      PA      (WEHD ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX      PI      Counter CM, Meyerson M, Weinberg RA;
XX
XX      DR      WPI; 1998-495367/42.
XX      DR      P-PSDB; AAW71376.
XX
XX      PT      New isolated human telomerase catalytic sub-unit gene - used to develop
XX      PT      products for increasing or reducing the life span of cells such as cancer
XX      PT      cells or transformed cells.
XX
XX      PS      Claim 5; Fig 5A-B; 96dp; English.
XX
XX      CC      The present sequence encodes the catalytic subunit of a human telomerase
XX      CC      holoenzyme. Disruption of the telomerase gene alters telomere
XX      CC      maintenance. The DNA is essential for telomerase activity, and the
XX      CC      protein is physically associated with telomerase and a constituent of
XX      CC      active telomerase complex. The products can be used for increasing or
XX      CC      reducing the lifespan of cells such as cancer cells or transformed cells.
XX      CC      They can also be used in the diagnosis and treatment of malignancies. In
XX      CC      addition, cells with a longer lifespan can be transplanted into or
XX      CC      grafted onto an individual (e.g. as skin grafts, as systems for delivery
XX      CC      of therapeutic proteins, such as hormones and enzymes), to whom they
XX      CC      provide therapeutic benefit
XX
XX      SQ      Sequence 4023 BP; 668 A; 1363 C; 1277 G; 715 T; 0 U; 0 Other;
XX
XX      Query Match      82.5%; Score 3311.4; DB 2; Length 4023;
XX      Best Local Similarity 89.9%; Pred. No. 0;
XX      Matches 3624; Conservative 0; Mismatches 361; Indels 46; Gaps 5;

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QY 425 CTACCTGCTGAGCGGGGCCCCCGGGGGGCGCTTCCAGACCAACGCTGCGCAG 484
Db 421 CTACCTGCTGAGCGGGGCCCCCGGGGGGCGCTTCCAGACCAACGCTGCGCAG 480
QY 485 GCGCGCTGAGCGGGGCCCCCGGGGGGCGCTTCCAGACCAACGCTGCGCAG 544
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Db 661 GCGCTGAGACCTAGCTGAGGAGGCGGGGCCCCCGGGGGGCGCTTCCAGACCAACGCTGCGCAG 720
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Db 1081 GCGGCGCTTCTTCTGAGCTCTGAGGAGCGCGCACTCCAGACCAACGCTGCGCAG 1140
QY 1145 GAGGAGCACTTCTTCTGAGCTCTGAGGAGCGCGCACTCCAGACCAACGCTGCGCAG 1204
Db 1141 GAGGAGCACTTCTTCTGAGCTCTGAGGAGCGCGCACTCCAGACCAACGCTGCGCAG 1200
QY 1205 CCGCGCGGTGAGCGCGGAGCAAGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1264
Db 1201 CCGCGCGGTGAGCGCGGAGCAAGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1260
QY 1265 GCGGCGCTTCTTCTGAGCTCTGAGGAGCGCGCACTCCAGACCAACGCTGCGCAG 1324
Db 1261 GCGGCGCTTCTTCTGAGCTCTGAGGAGCGCGCACTCCAGACCAACGCTGCGCAG 1320
QY 1325 AGGAGCGGTGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1384
Db 1321 AGGAGCGGTGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1380
QY 1385 GAGGAGCACTTCTTCTGAGCTCTGAGGAGCGCGCACTCCAGACCAACGCTGCGCAG 1444
Db 1381 GAGGAGCACTTCTTCTGAGCTCTGAGGAGCGCGCACTCCAGACCAACGCTGCGCAG 1440
QY 1445 GTACGCTTCTGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1504

Db 1441 GTACGCTTCTGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1500
QY 1505 GAGGAGCACTTCTTCTGAGCTCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1564
Db 1501 GAGGAGCACTTCTTCTGAGCTCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1560
QY 1565 CAGGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1624
Db 1561 CAGGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1620
QY 1625 CAGGAGCGCGGGGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1684
Db 1621 CAGGAGCGCGGGGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1680
QY 1685 GCGGAGCTTCTGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1744
Db 1681 GCGGAGCTTCTGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1740
QY 1745 TTAGCTCAGGAGCACTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1804
Db 1741 TTAGCTCAGGAGCACTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1800
QY 1805 GAGGAGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1864
Db 1801 GAGGAGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1860
QY 1865 GTGAGGAGCACTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1924
Db 1861 GTGAGGAGCACTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1920
QY 1925 CCGGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1984
Db 1921 CCGGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 1980
QY 1985 AGGAGGAGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2044
Db 1981 AGGAGGAGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2040
QY 2045 GTTCAAGGAGCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2104
Db 2041 GTTCAAGGAGCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2100
QY 2105 GCGGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2164
Db 2101 GCGGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2160
QY 2165 CCGGCGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2224
Db 2161 CCGGCGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2220
QY 2225 CAGGAGGAGCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2284
Db 2221 CAGGAGGAGCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2280
QY 2285 GCGTGGAGCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2344
Db 2281 GCGTGGAGCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2340
QY 2345 CAGGAGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2404
Db 2341 CAGGAGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2400
QY 2405 GAGGAGCACTTCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2464
Db 2401 GAGGAGCACTTCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2460
QY 2465 CAGGAGGAGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2524
Db 2461 CAGGAGGAGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2520
QY 2525 GCGGAGCTTCTGAGGAGCTGAGGAGCGCGCACTTCTTCTGAGCGCGCACTCCAGACCAACGCTGCGCAG 2584

Db 2521 GGGAGAGTCTTCACTGTCAGTCCAGGAGATCCGCAAGGCTCCATCCTTCCACGCTGCT 2580
 QY 2585 CTGAGAGCTGTGCTACGAGGACATGAGAAACAAGCTTTTGGGGGATTTGGGGGACG 2644
 Db 2581 CTGAGAGCTGTGCTACGAGGACATGAGAAACAAGCTTTTGGGGGATTTGGGGGACG 2640
 QY 2645 GCTGCTCTGAGTGTGAGTGAATTTCTTGTGTGAGACCTTCACTCACTCACTCACTCA 2704
 Db 2641 GCTGCTCTGAGTGTGAGTGAATTTCTTGTGTGAGACCTTCACTCACTCACTCACTCA 2700
 QY 2705 AACCTTCTGAGAGCTCTGAGTCCGAGGATGCTGAGTATGAGTGTGAGTGAATTTGAG 2764
 Db 2701 AACCTTCTGAGAGCTCTGAGTCCGAGGATGCTGAGTATGAGTGTGAGTGAATTTGAG 2760
 QY 2765 GAGAGAGTGTGAGTGAATTTCTTGTGTGAGACCTTCACTCACTCACTCACTCACTCA 2824
 Db 2761 GAGAGAGTGTGAGTGAATTTCTTGTGTGAGACCTTCACTCACTCACTCACTCACTCA 2820
 QY 2825 GATGCGGAGGACGAGGCTTATTCCTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2884
 Db 2821 GATGCGGAGGACGAGGCTTATTCCTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2880
 QY 2885 GGTGAGAGAGGAGTACTTCACTGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2944
 Db 2881 GGTGAGAGAGGAGTACTTCACTGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2940
 QY 2945 CCGGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3004
 Db 2941 CCGGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3000
 QY 3005 GTGTCAAGGCTGTCTTCTGATTTGAGAGTGAACAGCTTCAAGGAGGAGGAGGAGGAG 3064
 Db 3001 GTGTCAAGGCTGTCTTCTGATTTGAGAGTGAACAGCTTCAAGGAGGAGGAGGAGGAG 3060
 QY 3065 CTGAGAGTCTCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3124
 Db 3061 CTGAGAGTCTCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3120
 QY 3125 TCATCAGAGTGTGAGAGAACCCACATTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 3184
 Db 3121 TCATCAGAGTGTGAGAGAACCCACATTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 3180
 QY 3185 CCTGTGTACTCATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3234
 Db 3181 CCTGTGTACTCATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240
 QY 3235 TGAGCTCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3294
 Db 3241 TGAGCTCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3300
 QY 3295 CTGAGGCTTGAAGAGTCTTAACTTCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 3354
 Db 3301 GCTGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3360
 QY 3355 CAGGCTCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3414
 Db 3361 CAGGCTCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3420
 QY 3415 CTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3451
 Db 3421 GGGAGCTGCTTGAAGAGTCTTAACTTCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
 QY 3452 CTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3511
 Db 3481 CAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3540
 QY 3512 CTGAGCTTCTGTGTTTGGCTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAG 3571
 Db 3541 GCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3600
 QY 3572 GGCCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3626
 Db 3601 CTGAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3660

QY 3627 CACCCCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3686
 Db 3621 GCTGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3719
 QY 3687 TTCCAGTCAACGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3746
 Db 3720 CCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3779
 QY 3747 GCTGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3806
 Db 3780 ATCCCAAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3832
 QY 3807 TTCTTCTGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3866
 Db 3833 CCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3892
 QY 3867 CCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3926
 Db 3893 CCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3952
 QY 3927 CAAATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3986
 Db 3953 CAAATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4012
 QY 3987 AAAAAAAAAA 3997
 Db 4013 AAAAAAAAAA 4023

RESULT 4
 ABL53711
 ID ABL53711 standard; cDNA; 4070 BP.
 AC ABL53711;
 XX 17-JUN-2002 (first entry)
 DT 17-JUN-2002 (first entry)
 XX Human telomerase catalytic subunit hTERT cDNA.
 DE Human telomerase catalytic subunit hTERT cDNA.
 XX hTERT; telomerase; reverse transcriptase; immortalisation; human;
 KM vaccine; enzyme; gene; ss.
 OS Homo sapiens.
 OS Homo sapiens.
 PN W0200216555-A2.
 XX 28-FEB-2002.
 PD 17-AUG-2001; 2001WO-GB003726.
 PF 17-AUG-2000; 2000GB-00020246.
 PR 17-AUG-2000; 2000US-0225734P.
 XX (UWMA-) UNIV MALES COLLEGE OF MEDICINE.
 PA Jones CJ, Kipling DG, Wilkinson G, Mcsharry B, Skinner JW;
 FI WPI; 2002-315462/35.
 DR Novel hTERT-immortalized cell line (human telomerase reverse
 PT transcriptase) useful for human vaccine production and preparation of
 PT antigen, such as a virus or virus-derived agent.
 XX Example 1; Fig 1; 64p; English.
 XX The present sequence is that of hTERT cDNA in plasmid pGRN121. hTERT is
 CC the catalytic subunit of human telomerase. Claimed immortalized cell
 CC lines for use in vaccine production are adapted to express hTERT.
 CC Suitable cell lines comprise human diploid fibroblasts, e.g. MRC-5 or
 CC M18 cells, transfected with hTERT cDNA or infected by a retrovirus
 CC carrying hTERT cDNA, and are capable of supporting antigen production. A
 CC method for preparing such cell lines using recombinant techniques is

QY 1508 CAAGAAAGCCGCTTCTCTAGAGAACACCAAGATTATCTCCTGGGAGAGATGCCAA 1567
DB 1501 CAAGAAAGCCGCTTCTCTAGAGAACACCAAGATTATCTCCTGGGAGAGATGCCAA 1560
QY 1568 GCTCTGCTGAGAGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAG 1627
DB 1561 GCTCTGCTGAGAGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAG 1620
QY 1628 GAGCCAGAGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1687
DB 1621 GAGCCAGAGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1680
QY 1688 CAAGTCTGCTGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1747
DB 1681 CAAGTCTGCTGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1740
QY 1748 TGTCAAGAGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1807
DB 1741 TGTCAAGAGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1800
QY 1808 CAAGTCTGCTGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1867
DB 1801 CAAGTCTGCTGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1860
QY 1868 GAGAGAGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1927
DB 1861 GAGAGAGAGTGAAGTGAAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1920
QY 1928 CTATATCCCAAGCTGAAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1987
DB 1921 CTATATCCCAAGCTGAAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1980
QY 1988 CAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2047
DB 1981 CAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2040
QY 2048 CAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2107
DB 2041 CAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2100
QY 2108 CTTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2167
DB 2101 CTTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2160
QY 2168 GCGGCTGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2227
DB 2161 GCGGCTGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2220
QY 2228 GAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2287
DB 2221 GAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2280
QY 2288 TCGATAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2347
DB 2281 TCGATAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2340
QY 2348 CGTCTGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2407
DB 2341 CGTCTGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2400
QY 2408 GAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2467
DB 2401 GAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2460
QY 2468 CAGTGAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2527
DB 2461 CAGTGAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2520
QY 2528 CAGTGAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2587
DB 2521 CAGTGAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2580

QY 2588 CAGCTGTGCTACGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2647
DB 2581 CAGCTGTGCTACGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2640
QY 2648 GCTCTGCTGAGTGAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2707
DB 2641 GCTCTGCTGAGTGAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2700
QY 2708 CTTCTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2767
DB 2701 CTTCTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2760
QY 2768 GAGAGTGAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2827
DB 2761 GAGAGTGAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2820
QY 2828 GCGGCTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2887
DB 2821 GCGGCTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2880
QY 2888 GAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2947
DB 2881 GAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 2940
QY 2948 CAGCTGTGCTACGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3007
DB 2941 CAGCTGTGCTACGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3000
QY 3008 TCAAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3067
DB 3001 TCAAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3060
QY 3068 CAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3127
DB 3061 CAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3120
QY 3128 TCAAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3187
DB 3121 TCAAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3180
QY 3188 CAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3237
DB 3181 CAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3240
QY 3238 CTTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3297
DB 3241 CTTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3300
QY 3298 GAGTGAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3357
DB 3301 GAGTGAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3360
QY 3358 GCTGTGCTGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3417
DB 3361 GCTGTGCTGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3420
QY 3418 TCGATAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3454
DB 3421 TCGATAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3480
QY 3455 GAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3514
DB 3481 GAGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3540
QY 3515 GCGGCTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3574
DB 3541 GCGGCTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3600
QY 3575 CTTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3629
DB 3601 CTTGAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3660
QY 3630 CCGTCTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 3689

Db 3661 GAGGTCCAGACACCTCCCTCT-TACCTTCCCAAGGCTGCGCTCCACCCC 3719
 QY 3690 CCACTCAACCTCTCTCCCTCCCTGACACTTGTCCAGCATCAGGAGTTTCTGATCCG 3749
 Db 3720 AGGCGCAGCTTCTCTCAGCAGGAGCCGCTTCCACTCCCATAGAAATGTCATC 3779
 QY 3750 CTGAATTCAGACCATGTCAGCTGAGGCTGAGCTTAAGCTTCACTTCTGTTTC 3809
 Db 3780 CCCGATTCGCATTTTTCACCTT-----CGCCCTGCTTCTTCTTCCACCCC 3832
 QY 3810 TTTCTGTGTGTGAGACCTTGAAGAGACCTTGAAGCTCTGGAATTTGAGTACCA 3869
 Db 3833 CACCATCAGGTGAGACCTTGAAGAGACCTTGAAGCTCTGGAATTTGAGTACCA 3892
 QY 3870 AAGGTGCGCTCTGACAGGCGGAGACCTTGAAGCTTGAAGGCTCTGAGTCA 3929
 Db 3893 AAGGTGCGCTCTGACAGGCGGAGACCTTGAAGCTTGAAGGCTCTGAGTCA 3952
 QY 3930 ATTGGGGGAGAGTGTCTGAGAGTAAATATCTGAATATGATTTTCACTTTGAAA 3989
 Db 3953 ATTGGGGGAGAGTGTCTGAGAGTAAATATCTGAATATGATTTTCACTTTGAAA 4012
 QY 3990 AAA 3992
 Db 4013 AAA 4015

RESULT 6

AAZ20279 standard; cDNA; 4015 BP.

AAZ20279;

17-JAN-2000 (first entry)

Human telomerase reverse transcriptase (hTERT) cDNA.

Telomerase reverse transcriptase; human; hTERT; cell proliferation;

cancer; ss.

Homo sapiens.

Key

Location/Qualifiers
56..3454
/*tag= a

MO9950386-A2.

07-OCT-1999.

31-MAR-1999; 99MO-US007097.

31-MAR-1998; 98US-00052864.

03-AUG-1998; 98US-00128354.

(GERO-) GERON CORP.

Morin GB;

WPI; 1999-610842/52.

P-PSDB; AAY32090.

New catalytic polypeptide and polynucleotide, useful for increasing
catalytic activity in a cell.

Disclosure, Fig 2, 24pp, English.

This is the nucleotide sequence of cDNA encoding human telomerase reverse
 transcriptase (hTERT, see AAY32090). Human telomerase is a target for
 diagnosing and treating diseases relating to cell proliferation and
 senescence, such as cancer, or for increasing the proliferative capacity
 of a cell. A claimed method for increasing the proliferative capacity of

CC a vertebrate cell, especially a human or other mammalian cell, involves
 CC introducing into the cell a recombinant hTERT polynucleotide encoding an
 CC hTERT variant in which residues 192-323, 200-271, 200-271, 222-
 CC 240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A
 CC claimed method for reducing telomerase activity in a cell involves
 CC introducing a recombinant polynucleotide encoding an hTERT variant having
 CC a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or
 CC 1055-1071. The polynucleotides are obtained by mutagenesis of the hTERT
 CC coding sequence
 XX

SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 82.4%; Score 3306.6; DB 2; Length 4015;

Best Local Similarity 89.9%; Pred. No. 0; Mismatches 359; Indels 46; Gaps 5;

Db 8 GCGAGCTGCGTCTGCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 67
 QY 1 GCGAGCTGCGTCTGCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 60
 Db 68 GCGAGCTGCGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 127
 QY 61 GCGAGCTGCGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 120
 Db 128 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 187
 QY 121 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 180
 Db 188 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 247
 QY 181 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 240
 Db 248 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 307
 QY 241 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 300
 Db 308 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 367
 QY 301 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 360
 Db 368 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 427
 QY 361 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 420
 Db 428 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 487
 QY 421 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 480
 Db 488 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 547
 QY 481 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 540
 Db 548 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 607
 QY 541 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 600
 Db 608 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 667
 QY 601 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 660
 Db 668 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 727
 QY 661 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 720
 Db 728 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 787
 QY 721 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 780
 Db 788 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 847
 QY 781 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 840
 Db 848 GCGAGCTGCGCAGTCTGCGCAGTGGAAAGCCCTGCGCCCGGACACCCCGGATGCC 907

Db 841 GCGTGAACGAGTACCGTGGTTTCTGTGTCTCACTCCAGACCCGCCAGAGAGC 900
Qy 908 CACCTCTTGAAGGGTGTGCTCTCTGGACAGCGCACTCCCACTCCGCGGCGCA 967
Db 901 CACCTCTTGAAGGGTGTGCTCTCTGGACAGCGCACTCCCACTCCGCGGCGCA 960
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Db 1021 CCCGCTGACGCCGAGACCAAGCACTTCTCTCACTCTCAAGCGACCAAGAGCACTGCG 1080
Qy 1088 GCGCTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1147
Db 1081 GCGCTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1140
Qy 1148 GACCATCTTCTGAGGTTCCAGGCTCTGAGTCCAGGAGCTCCCGAGTTGCGCGCT 1207
Db 1141 GACCATCTTCTGAGGTTCCAGGCTCTGAGTCCAGGAGCTCCCGAGTTGCGCGCT 1200
Qy 1208 GCGCCAGGCTACTGAGAAATGCGGCTGTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1267
Db 1201 GCGCCAGGCTACTGAGAAATGCGGCTGTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1260
Qy 1268 GTGCGCTCTGAGGTTGCTCTCAAGAGCACTGCGCGCTGAGTCTGAGTCTGAGTCTGAG 1327
Db 1261 GTGCGCTCTGAGGTTGCTCTCAAGAGCACTGCGCGCTGAGTCTGAGTCTGAGTCTGAG 1320
Qy 1328 AGCGGTTGTCTGAGGTTGCTCTCAAGAGCACTGCGCGCTGAGTCTGAGTCTGAGTCTGAG 1387
Db 1321 AGCGGTTGTCTGAGGTTGCTCTCAAGAGCACTGCGCGCTGAGTCTGAGTCTGAGTCTGAG 1380
Qy 1388 CACAGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1447
Db 1381 CACAGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Qy 1448 CGGCTTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1507
Db 1441 CGGCTTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Qy 1508 CAAAGAAAGCGCTCTCTCAAGAGCACTGCGCGCTGAGTCTGCTGAGTCTGAGTCTGAG 1567
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Qy 1568 GCTCTGCTGAGAGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1627
Db 1561 GCTCTGCTGAGAGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1620
Qy 1628 GAGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1687
Db 1621 GAGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Qy 1688 CAACTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1747
Db 1681 CAACTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Qy 1748 TGTACAGGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1807
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Qy 1808 CAACTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1867
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Qy 1868 GGAAGAGAGGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 1927
Db 1861 GGAAGAGAGGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 1920
Qy 1928 CTTATCTCCCAAGCTGAGCGGCTGCGCGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1987
Db 1921 CTTATCTCCCAAGCTGAGCGGCTGCGCGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1980
Qy 1988 CAGAAAGTTCGAG 2047
Db 1981 CAGAAAGTTCGAG 2040
Qy 2048 CAGCGTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 2107
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Db 2101 CTTGAGAGATTCACAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 2160
Qy 2168 GCGGCTGAGGCTGCTTGTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2227
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Db 2221 GGAAGGCTCAAGAGGCTGATGCTGAGAGTCAATCAAGAGGCTGAGAGGCTGAGAGGCTGAGAG 2280
Qy 2288 TCGGTATGCGGTGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 2347
Db 2281 TCGGTATGCGGTGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 2340
Qy 2348 GGTCTCTACCTTGAAGAGCTTCAAGCGGTACATGAGAGTCTGAGTCTGAGTCTGAGTCTGAG 2407
Db 2341 GGTCTCTACCTTGAAGAGCTTCAAGCGGTACATGAGAGTCTGAGTCTGAGTCTGAGTCTGAG 2400
Qy 2408 GACCAAGCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 2467
Db 2401 GACCAAGCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 2460
Qy 2468 CAGTGGCTCTTTCAGAGCTTCTTCTACAGCTTATGAGTCAAGAGGCTGAGAGGCTGAGAGGCTGAG 2527
Db 2461 CAGTGGCTCTTTCAGAGCTTCTTCTACAGCTTATGAGTCAAGAGGCTGAGAGGCTGAGAGGCTGAG 2520
Qy 2528 CAACTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2587
Db 2521 CAACTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2580
Qy 2588 CAGCTGTGCTACAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2647
Db 2581 CAGCTGTGCTACAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2640
Qy 2648 GCTCTGCTGCTTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2707
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Db 2701 CTTCTCTGAGAGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2760
Qy 2768 GACAGTGTGAATCTTCTCTGAGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 2827
Db 2761 GACAGTGTGAATCTTCTCTGAGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 2820
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Db 2941 GCGGCTTCAAGGCTGAGAGAGAGTCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3000
Qy 3008 TCAAGAGCTGTTCTGAGATTTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 3067
Db 3001 TCAAGAGCTGTTCTGAGATTTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 3060

QY 3068 CAAGATCCTCTGTCGAGGCGTACAGTTTCAAGCATGTGTCTGAGCTCCATTTC 3127
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 QY 3128 TCAGCAAGTTTGAAGAAGCCCAATTTTCTCGCGGTATCTTGAACAGGCTCTCC 3187
 Db 3121 TCAGCAAGTTTGAAGAAGCCCAATTTTCTCGCGGTATCTTGAACAGGCTCTCC 3180
 QY 3188 CTGTACTCATCTCTGAAGCAAGCAAGAGGATGCTGCGGCGCCAGAGGCGCCG 3237
 Db 3181 CTGTACTCATCTCTGAAGCAAGCAAGAGGATGCTGCGGCGCCAGAGGCGCCG 3240
 QY 3238 CCTAGTGGAGAGAGTGTCTGCTGCTGTGTGTATGTGTGAGAGATCTGAATCTG 3297
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 QY 3298 GGCTTAGAAGATTCTTACCCCTTTTGGCATCAGAAAGTGTAAACCAACATCTGAC 3357
 Db 3301 GACTCGACACCGGTGTCACTAAGTGTGCGGTCTCTGAGTCACTGAGACAGCCAGAGCA 3360
 QY 3358 GCTGTCTGCGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3417
 Db 3361 GCTGT 3420
 QY 3418 TTGTGGAGT 3454
 Db 3421 ACTGCGCTCAAGACTTCAAGACATCTGTGATGTATGCGCAACCGCCAGAGCCGCA 3480
 QY 3455 GGGAGAGCTGT 3514
 Db 3481 GAGAGAGACACAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3540
 QY 3515 GCTCTCTCTGT 3574
 Db 3541 CACACCGAGCGCGACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3600
 QY 3575 CTGTGTGAAGCCAGGCGCAAG-----GGCTTAGAAGAGAGCGCCAGGCTAACCC 3629
 Db 3601 CATGTCTGTGTGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3660
 QY 3630 CCTCTGT 3689
 Db 3661 GAGT 3719
 QY 3690 CCAATCAAGCTCTGT 3749
 Db 3720 AGGCGCAGCTTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3779
 QY 3750 CTGAATTTCAAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3809
 Db 3780 CCGAGATTCGCGCATTTTCAACCCCT-----CGCCCTGCGCTCTGTGTGTGTGT 3832
 QY 3810 TTCTGT 3869
 Db 3833 CACATTCAGGT 3892
 QY 3870 AAGGT 3929
 Db 3893 AAGGT 3952
 QY 3930 ATTGGGGGGAGGT 3989
 Db 3953 ATTGGGGGGAGGT 4012
 QY 3990 AAA 3992
 Db 4013 AAA 4015

RESULT 7
 AA230154
 ID AA230154 standard; cDNA; 4015 BP.

XX AA230154;
 AC 26-JAN-2000 (first entry)
 DT
 XX
 DE cDNA encoding a human telomerase reverse transcriptase (TRT).
 KW Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
 KW dendritic cell; telomerase activity; cancer cell; proliferating cell;
 KW immunological destruction; telomerase; cancer; proliferation disease; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 56..3454
 FT /tag= a
 FT /product= "telomerase reverse transcriptase"
 PN W09950392-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 30-MAR-1999; 99WO-US006898.
 XX
 PR 31-MAR-1998; 98US-0112006P.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Gaeta FCA;
 DR WPI: 1999-610845/52.
 XX
 DR P-PSDB: AA43621.
 XX
 PT Eliciting an in vivo immune response for prevention and treatment of
 PT cancers.
 XX
 PS Disclosure; Fig 2; 26p; English.
 CC
 CC The present sequence encodes a human telomerase reverse transcriptase
 CC (TRT) polypeptide. The protein is used in the method of the invention.
 CC The specification describes a method for activating a T lymphocyte,
 CC comprising contacting the T lymphocyte with a dendritic cell that
 CC expresses a TRT peptide in the context of a MHC class I or MHC class II
 CC molecule. The protein causes induction of an in vivo immunological
 CC response to telomerase activity. Cancer cells are characterized by
 CC expression of endogenous TRT gene and the presence of detectable
 CC telomerase activity. Therefore, by eliciting a specific immune response
 CC to TRT or to TRT-expressing cells, it is possible to selectively target
 CC proliferating cells for immunological destruction. The method is used for
 CC eliciting an in vivo immune response to telomerase by activating a T
 CC lymphocyte, and is useful for prevention and treatment of cancers and
 CC other proliferation diseases/conditions
 XX
 SO Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
 Query Match 82.4%; Score 3306.6; DB 2; Length 4015;
 Best Local Similarity 89.9%; Pred. No. 0;
 Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;
 QY 8 GCAGCGGT 67
 Db 1 GCAGCGGT 60
 QY 68 GCGCGTCTCCCGCTGT 127
 Db 61 GCGCGTCTCCCGCTGT 120
 QY 128 GCGCGT 187
 Db 121 GCGCGT 180
 QY 188 GACCGCGCGCTTTCCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 247

QY 2408 GACCAAGCCCGCTGAGGATGCCCTGCTCATCGACAGAGCTCCTCCCTGAAATAGGCGCAG 2467
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 Db 3181 CTGCTATCTCATCTCTGAAAGCAGAAACGCAAGTATG-----GAGGTGCTTGG 3240
 QY 3238 CCTCAGTGGAGCAGTGTCTGCTGTGCTGTGTTAGTGTGACAGAGACTGAGTAAATCTG 3297
 Db 3241 CGGCGCTCTGCGCTCCAGAGCGCTGACGTGTGTGACAGAGACTGAGTAAATCTG 3300
 QY 3298 GCGCTTGAAGATCTTACCCCTTTTGCATCAGAAAGTGTAAACCAACCACTGTGAG 3357
 Db 3301 GACTCGACACCGTGTCACTTACGTGCCACTCTGCGGTCACTCAGAGACGCCAGAGCA 3360
 QY 3358 GCTGTGTGCGCGCTCTCTGTGGGTGAGACAGACCTGATGAGAAAGGACAGAGCTG 3417
 Db 3361 GCTGTGTGCGCGCTCTCTGTGGGTGAGACAGACCTGATGAGAAAGGACAGAGCTG 3420
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 QY 3750 CTGAATTCAGAGCATGTGCAACCTGCGGCTCTGAGCTTAACAGTCTTCTGTCTC 3809
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 Db 3833 CACCATTCAGAGTGTGAGACCTCTGAGAGGACCTTGAGAGCTCTGAGAAATTTGAGTACCA 3892
 QY 3870 AAGGTGCGCTGTGACAGAGGAGGACCTTGACCTGAGATGAGGAGTCCGTGGGTCAA 3929
 Db 3893 AAGGTGCGCTGTGACAGAGGAGGACCTTGACCTGAGATGAGGAGTCCGTGGGTCAA 3952
 QY 3930 ATTGGGGGAGGTGTGTGAGGTAATAATCTGAATATGAGTTTTCAGTTTGAATA 3989
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 QY 3990 AAA 3992
 Db 4013 AAA 4015

RESULT 8
 ID AAH45901
 XX AAH45901 standard; DNA; 4015 BP.
 AC
 XX
 DT 06-SEP-2001 (first entry)
 XX
 DE Human hTERT gene.
 XX
 KM Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;
 XX detection; beta-region; diagnosis; cancer; ds.
 OS Homo sapiens.
 FH
 FT Key
 FT Location/Qualifiers
 FT 1..274
 FT /tag= a
 FT /number= 1
 FT 275..1628
 FT /tag= b
 FT /number= 2
 FT 1629..1824
 FT /tag= c
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 FT 1825..2005
 FT /tag= d
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 FT 2186..2341
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QY 848 GCGTGAACGAGTACCGTGGTTCCTGTGTGTGTCTGACCTTGCCAGAACCCGCGAAGAGC 907
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QY 908 CACCTCTTTGAGAGGTGTGCTCTGTGGACGCGGCACTCCCACTCCGTTGGGCGGCCA 967
Db 901 CACCTCTTTGAGAGGTGTGCTCTGTGGACGCGGCACTCCCACTCCGTTGGGCGGCCA 960
QY 968 GCACACGCGGAGCCGCCCATCATCGGCGCACACGTCCTGAGGACAGCCTTGTCC 1027
Db 961 GCACACGCGGAGCCGCCCATCATCGGCGCACACGTCCTGAGGACAGCCTTGTCC 1020
QY 1028 CCGGTGTACGCGAGACCAAGACCTTCTTACTCTTCAAGGAGCAAGAGACAGTGTCC 1087
Db 1021 CCGGTGTACGCGAGACCAAGACCTTCTTACTCTTCAAGGAGCAAGAGACAGTGTCC 1080
QY 1088 GCCCTCTTCTTACTCTGAGTCTCTGAGGCGCAGCTGAGTGTGAGGCTGTGGA 1147
Db 1081 GCCCTCTTCTTACTCTGAGTCTCTGAGGCGCAGCTGAGTGTGAGGCTGTGGA 1140
QY 1148 GACCATCTTCTGTGGTTCAGAGCCCTGTGATGCCAGGACCTCCGCGAGGTTGCCGCT 1207
Db 1141 GACCATCTTCTGTGGTTCAGAGCCCTGTGATGCCAGGACCTCCGCGAGGTTGCCGCT 1200
QY 1208 GCCCAGCGCTACTGAGAAATGCGGCCCTGTTCTGAGAGTGTGAGGAGCAAGCGCA 1267
Db 1201 GCCCAGCGCGTACTGAGAAATGCGGCCCTGTTCTGAGAGTGTGAGGAGCAAGCGCA 1260
QY 1268 GTGCCCTTACGAGGAGTCTCTCAAGACGACCTGCGGCTGAGAGTGTGAGGAGTGTG 1327
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Db 1321 AGCCGATGTCTGTGCGCGAGAGAGCCGAGGCTGTGAGGAGGCGCCGAGAGAGAG 1380
QY 1388 CACAGACCCCGTGTGCTGTGAGAGTGTCTCCGCGAGACAGACGCGCTGTGAGAGTGTG 1447
Db 1381 CACAGACCCCGTGTGCTGTGAGAGTGTCTCCGCGAGACAGACGCGCTGTGAGAGTGTG 1440
QY 1448 CGGCTTGTGTGAGGAGTGTGCGGCGGCGGCTGTGAGGAGGCGCCGAGAGAGAG 1507
Db 1441 CGGCTTGTGTGAGGAGTGTGCGGCGGCGGCTGTGAGGAGGCGCCGAGAGAGAG 1500
QY 1508 CAACGAAAGCGGCTTCTCAAGAAACCAAGAAATTCATCTCCCTGAGAGAGTGTG 1567
Db 1501 CAACGAAAGCGGCTTCTCAAGAAACCAAGAAATTCATCTCCCTGAGAGAGTGTG 1560
QY 1568 GCTTCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1627
Db 1561 GCTTCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1620
QY 1628 GAGCCAGAGGAGTGTGCTGTGCTGCGGCGGAGAGACAGCTGTGAGAGAGTGTGAG 1687
Db 1621 GAGCCAGAGGAGTGTGCTGTGCTGCGGCGGAGAGACAGCTGTGAGAGAGTGTGAG 1680
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QY 1748 TGTCAAGAGAGACAGTGTGAGAGAGAGCTTTTCTTCAAGAGAGTGTGAGAG 1807
Db 1741 TGTCAAGAGAGACAGTGTGAGAGAGAGCTTTTCTTCAAGAGAGTGTGAGAG 1800
QY 1808 CAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1867
Db 1801 CAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1860
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Db 1861 GGAAGAGAGAGTGTGAGAGTGTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1920
QY 1928 CTTCAATCCCAAGCTGTGAGAGGCTGTGAGAGGAGTGTGAGAGTGTGAGAGTGTGAG 1987

Db 1921 CTTCAATCCCAAGCTGTGAGAGGCTGTGAGAGGAGTGTGAGAGTGTGAGAGTGTGAGAG 1980
QY 1988 CAGAAAGTTCGAGAGAGAGAGAGGCGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2047
Db 1981 CAGAAAGTTCGAGAGAGAGAGAGGCGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2040
QY 2048 CAGAGTGTCACTACAGAGAGGCGAGGCGGCGGCTTCTGAGGAGTGTGAGAGTGTG 2107
Db 2041 CAGAGTGTCACTACAGAGAGGCGAGGCGGCGGCTTCTGAGGAGTGTGAGAGTGTG 2100
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Db 2101 CTTGAGAGTGTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2160
QY 2168 GCCGCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2227
Db 2161 GCCGCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2220
QY 2228 GGAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2287
Db 2221 GGAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2280
QY 2288 TCGATATGCGGTGTGAGAGAGGCGGCGGAGTGTGAGAGTGTGAGAGTGTGAGAG 2347
Db 2281 TCGATATGCGGTGTGAGAGAGGCGGCGGAGTGTGAGAGTGTGAGAGTGTGAGAG 2340
QY 2348 GGTCTTCACTTGAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2407
Db 2341 GGTCTTCACTTGAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2400
QY 2408 GACAGAGGCGGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2467
Db 2401 GACAGAGGCGGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2460
QY 2468 CAGTGGCTTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2527
Db 2461 CAGTGGCTTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2520
QY 2528 CAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2587
Db 2521 CAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2580
QY 2588 CAGCTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2647
Db 2581 CAGCTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2640
QY 2648 GCTCTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2707
Db 2641 GCTCTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2700
QY 2708 CTTCTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2767
Db 2701 CTTCTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2760
QY 2768 GACAGTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 2827
Db 2761 GACAGTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 2820
QY 2828 GCCGAGCAGAGGCTTATCCCTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2887
Db 2821 GCCGAGCAGAGGCTTATCCCTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2880
QY 2888 GCAAGAGTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2947
Db 2881 GCAAGAGTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2940
QY 2948 CGGCTTCAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 3007
Db 2941 CGGCTTCAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 3000
QY 3008 TCAAGAGTGTGTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 3067

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Db 3001 TCACAGCTGTTTGTGATTTGAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTA 3060
QY 3068 CAAGATCCTCTGTGAGGAGGCGTACAGATTTCAGCATGTTGTGTGAGTCCCATTTCA 3127
Db 3061 CAAGATCCTCTGTGAGGAGGCGTACAGATTTCAGCATGTTGTGTGAGTCCCATTTCA 3120
QY 3128 TCAGCAGTTTGAAGAAACCCACATTTTCTGCGCGTATCTTGACAGCGGCTCCCT 3187
Db 3121 TCAGCAGTTTGAAGAAACCCACATTTTCTGCGCGTATCTTGACAGCGGCTCCCT 3180
QY 3188 CTGCTACTCCATCCGTGAAGCCCAAGACGAGATGT-----GGAGGTGCTCG 3237
Db 3181 CTGCTACTCCATCCGTGAAGCCCAAGACGAGATGT-----GGAGGTGCTCG 3240
QY 3238 CTTGAGTGGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3297
Db 3241 CGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
QY 3298 GGGCTTAGGAAGTTTGAACCCCTTTTGGCATCAGAAATGTTTAAACCAACACTGTGAG 3357
Db 3301 GACTGACACCGGTGTACCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
QY 3358 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3417
Db 3361 GCTGAGTGGAAAGTCCCGGGGAGAGAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 3420
QY 3418 TCTGGAGAGTCCATCTTCCCACTTGTCT-----GCTG 3454
Db 3421 ACTGCTCTGACACTTCAAGACATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
QY 3455 GGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3514
Db 3481 GAGCAGACACAGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
QY 3515 GCTCTCTCTGTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3574
Db 3541 CACACCCAGAGCCCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
QY 3575 CTTGTGCAAAACCCAGGCGCAAG-----GGCTTAGAGAGAGGCGCAGGCGCTAACCCCA 3629
Db 3601 CATGTCGGCTGGAAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
QY 3630 CCTCTGAGAGAGAGAGGCGCTGATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3689
Db 3661 GAGGTGCGAGACACTGCGCTCT-TCATTTCCCAAGGCTGCGCTGCGCTGCGCTGCGCTGCG 3719
QY 3690 CCAATCAACCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3749
Db 3720 AGGCGCAGCTTTTCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3779
QY 3750 CTGAATTCAGAGCATGTGAACCTGCGGTCTGAGCTTAAAGCTTCACTTCTGTTTC 3809
Db 3780 CCCAGATTGCGCATTTTCAACCCCT-----CGCCCTGCTGCTTGTGCTTCCACCC 3832
QY 3810 TTTTGTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3869
Db 3833 CACCATCAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3892
QY 3870 AAGGTGTGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3929
Db 3893 AAGGTGTGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3952
QY 3930 ATTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3989
Db 3953 ATTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4012
QY 3990 AAA 3992
Db 4013 AAA 4015

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RESULT 9
AAD46821

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ID AAD46821 strand; cDNA; 4015 BP.
AC AAD46821;
XX 27-JAN-2003 (first entry)
DT
DE Human telomerase reverse transcriptase (TERT) cDNA.
XX Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
XX transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
XX telomerase reverse transcriptase; gene; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "Human telomerase reverse transcriptase"
XX
XX WO2002/4948-A2.
XX
XX 26-SEP-2002.
XX
XX 21-MAR-2002; 2002MO-CA000378.
XX
XX 21-MAR-2001; 2001US-0277811P.
XX
XX (GERO-) GERON CORP.
XX
XX Denning C, Clark AJ, Schiff JM;
XX
XX MPI: 2002-759895/82.
XX
XX P-PSDB; AAE29226.
XX
XX Mammalian cells, useful for producing animal tissues with carbohydrate
XX antigens that are compatible for transplantation into human patients.
XX
XX Disclosure; Page 33-34; 71pp; English.
XX
XX The invention relates to animal tissues with carbohydrate antigens that
XX are compatible for transplantation into human patients. The mammalian
XX cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
XX transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
XX fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
XX with carbohydrate antigens that are compatible for transplantation into
XX human patients. The present sequence is human telomerase reverse
XX transcriptase (TERT) cDNA used in the invention.
XX
XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
SQ
Query Match 82.4%; Score 3306.6; DB 6; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3518; Conservative 0; Mismatches 359; Indels 46; Gaps 5;
QY 8 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 67
Db 1 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 68 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
Db 61 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 128 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Db 121 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 188 GAGCCGCGGCTTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
Db 181 GAGCCGCGGCTTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 248 AGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 307
Db 241 AGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300

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QY 308 CCGAGTGTGAGAGGCTGTCCGAGCGCGGCGGAAACGTGTGTGCTTGGCTTGGCTTGG 367
DB 301 CCGAGTGTGAGAGGCTGTCCGAGCGCGGCGGAAACGTGTGTGCTTGGCTTGGCTTGG 360
QY 368 GCTGTGAGACGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 427
DB 361 GCTGTGAGACGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 428 CTTGCTCCACACGCGTGTACGACGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
DB 421 CTTGCTCCACACGCGTGTACGACGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
QY 488 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 547
DB 481 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
QY 548 GAGCTTCCAGGCTGTGCTTACGAGGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607
DB 541 GAGCTTCCAGGCTGTGCTTACGAGGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
QY 608 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 667
DB 601 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 668 CTGAGACCATAGCGTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 727
DB 661 CTGAGACCATAGCGTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
QY 728 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 787
DB 721 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 788 TGCCCTTGAGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 847
DB 781 TGCCCTTGAGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
QY 848 GCGTGTGACCGAGTGTGCTGT 907
DB 841 GCGTGTGACCGAGTGTGCTGT 900
QY 908 CACCTCTTGTGAGGAGGT 967
DB 901 CACCTCTTGTGAGGAGGT 960
QY 968 GCACCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1027
DB 961 GCACCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
QY 1028 CCGGCTGTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 1087
DB 1021 CCGGCTGTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 1080
QY 1088 GCGCTCTTCTTACTGT 1147
DB 1081 GCGCTCTTCTTACTGT 1140
QY 1148 GACCATCTTGT 1207
DB 1141 GACCATCTTGT 1200
QY 1208 GCGCCAGCGGCTGTGAGAAATGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1267
DB 1201 GCGCCAGCGGCTGTGAGAAATGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1260
QY 1268 GTGCGCTTGTGAGGAGGT 1327
DB 1261 GTGCGCTTGTGAGGAGGT 1320
QY 1328 AGCGGCTGT 1387
DB 1321 AGCGGCTGT 1380

QY 1388 CACAGACCCCGCTGCGCTGT 1447
DB 1381 CACAGACCCCGCTGCGCTGT 1440
QY 1448 CCGCTTGT 1507
DB 1441 CCGCTTGT 1500
QY 1508 CACAGAGCGGCGGCTTCTTCAAGAGACCAAGAGTTTCACTTCTTGTGTGTGTGTGTGTGT 1567
DB 1501 CACAGAGCGGCGGCTTCTTCAAGAGACCAAGAGTTTCACTTCTTGTGTGTGTGTGTGTGT 1560
QY 1568 GCTTGT 1627
DB 1561 GCTTGT 1620
QY 1628 GAGCCAGGCGGCTGT 1687
DB 1621 GAGCCAGGCGGCTGT 1680
QY 1688 CAGGTTCTGTGACGT 1747
DB 1681 CAGGTTCTGTGACGT 1740
QY 1748 TGTCAAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCAACCGAAGAGTGTGTGTGTGT 1807
DB 1741 TGTCAAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCAACCGAAGAGTGTGTGTGTGT 1800
QY 1808 CAAATTGTGAAAGCATTTGAAATTCAGACACTTGAAGAGGTGTGTGTGTGTGTGTGTGTGT 1867
DB 1801 CAAATTGTGAAAGCATTTGAAATTCAGACACTTGAAGAGGTGTGTGTGTGTGTGTGTGTGT 1860
QY 1868 GGAAGCAGAGGT 1927
DB 1861 GGAAGCAGAGGT 1920
QY 1928 CTTTCAATCCCAAGCTGT 1987
DB 1921 CTTTCAATCCCAAGCTGT 1980
QY 1988 CAGAAAGTTCCGACAGAAAGAGAGGCGGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2047
DB 1981 CAGAAAGTTCCGACAGAAAGAGAGGCGGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
QY 2048 CAGCGTGTCTTCAATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2107
DB 2041 CAGCGTGTCTTCAATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2100
QY 2108 CCGTGTGAGATATTCACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2167
DB 2101 CCGTGTGAGATATTCACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2160
QY 2168 GCGGCTGTGAGTGTACTTGT 2227
DB 2161 GCGGCTGTGAGTGTACTTGT 2220
QY 2228 GAGCAGGCTTCAACGAGAGT 2287
DB 2221 GAGCAGGCTTCAACGAGAGT 2280
QY 2288 TCGGTATGCGGT 2347
DB 2281 TCGGTATGCGGT 2340
QY 2348 GGTCTTCACTTGT 2407
DB 2341 GGTCTTCACTTGT 2400
QY 2408 GACCAAGCGGCTGTGAGAGT 2467
DB 2401 GACCAAGCGGCTGTGAGAGT 2460
QY 2468 CAGTGTGCTCTTTCAGAGCTTCTTACGCTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2527

Db	2461	CAGTGGCCTCTCGACGCTTCTCTACGCTTATGTCGCCACACGCGCTGGCATTCAGGGG	2520
Qy	258	CAAGTCTCAAGTCCAGATGCCAGGGGATCCCGAAGGGCTCAATCCTCTTCAACGCTGCTGG	2587
Db	2521	CAAGTCTCAAGTCCAGATGCCAGGGGATCCCGAAGGGCTCAATCCTCTTCAACGCTGCTGG	2580
Qy	2588	CAGCCTGTGCTACGGCGCATGAGAAACAAGTGTTCGGGGGATTCGGCGGACGGGCT	2647
Db	2581	CAGCCTGTGCTACGGCGCATGAGAAACAAGTGTTCGGGGGATTCGGCGGACGGGCT	2640
Qy	2648	GCTCTCGCTTTGGTGATGATTTCTTGTTGATGACCTCACTCACTCAACCCAGCGAAAC	2707
Db	2641	GCTCTCGCTTTGGTGATGATTTCTTGTTGATGACCTCACTCACTCAACCCAGCGAAAC	2700
Qy	2708	CTTCTCTCAGAACCTCGGTCCAGAGGTGCTCCAGATATGCGTCGGTGAACCTTGGCGAA	2767
Db	2701	CTTCTCTCAGAACCTCGGTCCAGAGGTGCTCCAGATATGCGTCGGTGAACCTTGGCGAA	2760
Qy	2768	GACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCAACGCTTTTGTTCAGT	2827
Db	2761	GACAGTGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCAACGCTTTTGTTCAGT	2820
Qy	2828	GCGGGCCCAACGGCCATATCCCTGGTGGCGCTGTGTGTGATATCCGCGAACCTCGAGAGT	2887
Db	2821	GCGGGCCCAACGGCCATATCCCTGGTGGCGCTGTGTGTGATATCCGCGAACCTCGAGAGT	2880
Qy	2888	GCAGAGCAGTACTTCACAGCTATGCCCCGAGCTCCATCAGAGCCAGTGTCAACCTTCAACCG	2947
Db	2881	GCAGAGCAGTACTTCACAGCTATGCCCCGAGCTCCATCAGAGCCAGTGTCAACCTTCAACCG	2940
Qy	2948	CGGCTTCAAGGCTGGGAGGAAATACGCTCGCAACTCTTTGGGGCTTGGCGGCTGAAAGTG	3007
Db	2941	CGGCTTCAAGGCTGGGAGGAAATACGCTCGCAACTCTTTGGGGCTTGGCGGCTGAAAGTG	3000
Qy	3008	TCACAGCCTGTTTCTGATTTGCAAGTTTGCAAGTGACAGCTCCAGACGGTGGCAACCAATCTA	3067
Db	3001	TCACAGCCTGTTTCTGATTTGCAAGTTTGCAAGTGACAGCTCCAGACGGTGGTCAACCAATCTA	3060
Qy	3068	CAAGATCCTCCTGCTGCGAGGGGTACAGGTTTCAACGATGTGTCTGCGACCTCCCATTTTCA	3127
Db	3061	CAAGATCCTCCTGCTGCGAGGGGTACAGGTTTCAACGATGTGTCTGCGACCTCCCATTTTCA	3120
Qy	3128	TCAGCAAGTTTGGAAAGAACCCCAATTTTCTCGGCTCATCTCTGACACGAGCTCCCT	3187
Db	3121	TCAGCAAGTTTGGAAAGAACCCCAATTTTCTCGGCTCATCTCTGACACGAGCTCCCT	3180
Qy	3188	CTGCTACTCTCATCTCTGAAAGCCAGAGACGCAAGTATGT-----GCAGGTGCTCGG	3237
Db	3181	CTGCTACTCTCATCTCTGAAAGCCAGAGACGCAAGTATGTCTGCTGGGGGCAAGGGCGCGCG	3240
Qy	3238	CCTCAGTGGCAGAGTGCCTGCTGCTGCTGTATGATGTGTGAGAGACATGATGATATCTG	3297
Db	3241	CGGCCCTCTGCGCTCCGAGGCGGTGTCAGATGTGTCGCCACAGAGATCTGTCTCAAGCT	3300
Qy	3298	GGCTTTAGGAAGTTCTTACCCCTTTTTCGATCAGGAAGTGTTTAACCCACCACTGTACG	3357
Db	3301	GACTCGACACCGTGTCACTACGTACGCACTCCTGGGGTCACTCAGGACAGCCAGACGCA	3360
Qy	3358	GCTGCTGCACCGCCCTCTGCTGGGGGTAGACAGACCTGATGAAAGGACAGAGAGCTG	3417
Db	3361	GCTGAGTGGAAAGCTCCCGGGGAGAGAGCTGATGCTCCTTGGAGGCGGACGACCAACCGGCG	3420
Qy	3418	TCTGGGAGCTGCATCTTCCCACTTGTCTCT-----GCTTG	3454
Db	3421	ACTGCGCTCAACATTCAGAGCCATCTGATGATGAGCCACCCGCGCAACGCAAGGCCGA	3480
Qy	3455	GGAGAGCCTGGGGGCGCTGTCTCTCTGTTTCCCATGATGGGATTTGGGGGCGCTG	3514
Db	3481	GAGCAGACACACAGCAGCCCTGTGCAAGCGGGCTTCAAGTCCAGGGAGAGAGGGGCGGCG	3540
Qy	3515	GCGCTCTCTGTTTGGCCCTGTGTGGAGATTTGGGCTGTCTCCCGTCCATGACCTTAAGGCC	3574

Db	3541	CACACCACAGGCGCCGACACCGCTGGGAGTCTAGAGGCTGAGTGAAGTCTTTGGCCAGGCGCTG	3600
QY	3575	CTTGTCGAAACCCACGGCCAAAG-----GGCTTAGAGAGAGCCAGGCCAGGCTTACCCAC	3629
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGAGGCTGAGCCGAGTGTCAAGCCAAAGGACT	3650
QY	3630	CCCTCTCAGAGGACGAGAGGCGCGGTATATACCAGCAGAGCCCGCGCGCCGTCCTGCTTC	3689
Db	3661	GAGTGTCCAGAGACACCTGCCGTCT-TACTTTCGCCACAGGCTGGCGGTCCGAGCTCAACCC	3719
QY	3690	CCAGTCAACCGTCTCTGCGCCCTGAGCACTTTGTCAGACATGAGGAGGTTTCTGATCCGT	3749
Db	3720	AGGGCCGAGCTTTTCTCACCAGAGGCGCCGGCTTCCACTCCCACTAGAAATATGATCATC	3779
QY	3750	CTGAATTTCAAGCATGTGCGAACCCTGGGTCCTGAGCTTAAACAGCTCTAATTTCTGTTC	3809
Db	3780	CCCGAATTTGGCAGATGTTTCAACCT-----CGCCTGCCCTCTCTTGCTTCCACCC	3832
QY	3810	TTTCTGTGTTGTGAGACCTCTGAGAGAGACCTTGAGGCTCTGTGGAAATTTGAGTGACCA	3869
Db	3833	CACCATCCAGGTGAGACCTCTGAGAGAGACCTTGAGGAGCTCTGTGGAAATTTGAGTGACCA	3892
QY	3870	AAGGTGTGCCCTGTACACAGGCGAGACCCCTGCACCTGAAATGGGGGCGCCCTGTGGGTCAA	3929
Db	3893	AAGGTGTGCCCTGTACACAGGCGAGACCCCTGCACCTGAAATGGGGGCGCCCTGTGGGTCAA	3952
QY	3930	ATTGGGGGAGAGTGTCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGGAAAA	3989
Db	3953	ATTGGGGGAGAGTGTCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGGAAAA	4012
QY	3990	AAA 3992	
Db	4013	AAA 4015	

RESULT 10
 ID ABA97534 standard; DNA; 4015 BP.
 XX ABA97534;
 AC
 DT 05-APR-2002 (first entry)
 XX
 DE Cancer cell discrimination method related human DNA.
 XX
 KW Human; telomerase; enzyme; cancer cell discrimination; gene;
 KW reverse transcriptase; ds.
 XX
 OS Homo sapiens.
 XX
 PN JP2001305791-A.
 XX
 PD 06-NOV-2001.
 XX
 PF 02-MAY-2000; 2000JP-00138250.
 XX
 PR 02-MAY-2000; 2000JP-00138250.
 XX
 PA (KANE/) KANEUCHI H.
 PA (KAMI/) KAMIMORI M.
 XX
 DR WPI; 2002-134853/18.
 XX
 PT Discrimination of a cancer cell in a sample tissue, comprises determining
 PT the expression level of a reverse transcriptase component of telomerase
 PT using a hybridization assay.
 XX
 PS Claim 2; Page 9-10; 16pp; Japanese.
 XX
 CC The present invention relates to a method for the discrimination of a
 CC cancer cell in a sample tissue, which involves determining the expression
 CC level of a reverse transcriptase component of telomerase in a cell
 CC constituting the sample tissue by an in situ hybridization of the mRNA of

QY 2048 CAGCGTCTCAACTACGAGCGGCGCGCGCCCGGCTCTGAGCGGCTGCTGCTG 2107
Db 2041 CAGCGTCTCAACTACGAGCGGCGCGCGCCCGGCTCTGAGCGGCTGCTGCTG 2100
QY 2108 CCGTGAAGATTCACAGAGGCTGCGGCGCTTCTGCTGCTGCTGCTGCTGCTG 2167
Db 2101 CCGTGAAGATTCACAGAGGCTGCGGCGCTTCTGCTGCTGCTGCTGCTGCTG 2160
QY 2168 GCGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2227
Db 2161 GCGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
QY 2228 GAGAGAGCTCAAGAGAGATGATGCGGCGCTGCTGCTGCTGCTGCTGCTG 2287
Db 2221 GAGAGAGCTCAAGAGAGATGATGCGGCGCTGCTGCTGCTGCTGCTGCTG 2280
QY 2288 TCGGTATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2347
Db 2281 TCGGTATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
QY 2348 CCGTCTACCTTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2407
Db 2341 CCGTCTACCTTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
QY 2408 GACGAGCGCTGAGGAGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2467
Db 2401 GACGAGCGCTGAGGAGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
QY 2468 CAGTGGCTCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2527
Db 2461 CAGTGGCTCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
QY 2528 CAGGTCTACGCTGAGTGGCAGAGGATCCCGAGGAGCTGCTGCTGCTGCTG 2587
Db 2521 CAGGTCTACGCTGAGTGGCAGAGGATCCCGAGGAGCTGCTGCTGCTGCTG 2580
QY 2588 CAGCTGTGCTACGAGGATGAGGAGAAAGCTGCTGCTGCTGCTGCTGCTG 2647
Db 2581 CAGCTGTGCTACGAGGATGAGGAGAAAGCTGCTGCTGCTGCTGCTGCTG 2640
QY 2648 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2707
Db 2641 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
QY 2708 CTTCTCTAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2767
Db 2701 CTTCTCTAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
QY 2768 GACAGTGTGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2827
Db 2761 GACAGTGTGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
QY 2828 GCGCGCGCAGCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2887
Db 2821 GCGCGCGCAGCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
QY 2888 GAGAGAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2947
Db 2881 GAGAGAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
QY 2948 CCGCTTCAAGAGCTGAGGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3007
Db 2941 CCGCTTCAAGAGCTGAGGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
QY 3008 TCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3067
Db 3001 TCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060
QY 3068 CAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3127
Db 3061 CAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3120

QY 3128 TCAGCAAGTTGGAGAGACCCCAATTTTCTGCGCTGATCTGAGACGCGCTCCCT 3187
Db 3121 TCAGCAAGTTGGAGAGACCCCAATTTTCTGCGCTGATCTGAGACGCGCTCCCT 3180
QY 3188 CTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3237
Db 3181 CTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
QY 3238 CCGTCAAGTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3297
Db 3241 CCGTCAAGTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
QY 3298 GCGTCTGAGAGTCTTACCTCTTTTTCGATCAGAGAGTGTGTTAACCAACCTGCTG 3357
Db 3301 GAGTTCAGACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
QY 3358 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3417
Db 3361 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420
QY 3418 TCTGGAGCTGCCATCTTCCACTTGTCTT-----GCTG 3454
Db 3421 ACTGCCCTGAGCTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3480
QY 3455 GAGAGAGCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3514
Db 3481 GAGAGAGCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3540
QY 3515 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3574
Db 3541 CACACCCAGGCGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3600
QY 3575 CTTGTGCAAAACCGAGGCAAG-----GCTTGAAGAGAGGCGAGGCGTACCCGAC 3629
Db 3601 CATGTCCGCTGAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
QY 3630 CCGTCTCAGAGAGAGAGGCGGCTATCAGACAGAGAGAGGCGGCGCTGCTGCTGCTG 3689
Db 3661 GAGTGTGAGAGAGAGAGGCGGCTATCAGACAGAGAGAGGCGGCGCTGCTGCTGCTG 3719
QY 3690 CAGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3749
Db 3720 AGGCGCAGCTTTTCTCAGAGAGAGGCGGCTTCCATCCCAATAGAGATGCTGCTGCTG 3779
QY 3750 CTGAAATTCAGAGCAATGCTGAACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3809
Db 3780 CCGAGATTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3832
QY 3810 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3869
Db 3833 CACCATTCAGAGTGGAGAGCTTGAAGAGAGCTTGAAGAGAGCTTGAAGAGAGCTTGAAG 3892
QY 3870 AAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3929
Db 3893 AAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3952
QY 3930 ATTGGGGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3989
Db 3953 ATTGGGGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4012
QY 3990 AAA 3992
Db 4013 AAA 4015

RESULT 11
ACCS8039
ID ACCS8039 standard; cDNA; 4015 bp.
XX
ACCS8039;
AC
XX
XX
DT 11-AUG-2003 (first entry)
XX

Db 601 TCAGGCCCCGCCCCGCGCAACGCTAGTGAACCCCGAGGCGTCTGAGATGCGAACGCGC 660
Qy 668 CTGGAACCATAGCGTCAAGGAGGCGGAGTCCCCCTGAGCTCCAGACCCCGGATGCGAG 727
Db 661 CTGGAACCATAGCGTCAAGGAGGCGGAGTCCCCCTGAGCTCCAGACCCCGGATGCGAG 720
Qy 728 GAGGCGGAGGAGGAGTCCAGCCGAGATCTGCGGTTGCCAAGAGCCAGAGCTGCGC 787
Db 721 GAGGCGGAGGAGGAGTCCAGCCGAGATCTGCGGTTGCCAAGAGCCAGAGCTGCGC 780
Qy 788 TGCCCTGAGCGGAGGAGGAGTCCAGCCGAGATCTGCGGTTGCCAAGAGCTGCGC 847
Db 781 TGCCCTGAGCGGAGGAGGAGTCCAGCCGAGATCTGCGGTTGCCAAGAGCTGCGC 840
Qy 848 GCGTGAACCGAGTGAACGCTGATTTCTGTGTGTGTCACTGCGAAGCCCGCGAGAGC 907
Db 841 GCGTGAACCGAGTGAACGCTGATTTCTGTGTGTGTCACTGCGAAGCCCGCGAGAGC 900
Qy 908 CACTCTTTGAGAGGAGTGAACGCTGATTTCTGTGTGTGTCACTGCGAAGCCCGCGAGAGC 967
Db 901 CACTCTTTGAGAGGAGTGAACGCTGATTTCTGTGTGTGTCACTGCGAAGCCCGCGAGAGC 960
Qy 968 GCACCAACGCGGAGCCCGCATCAATGCGGCGCAACAGCTGCTGAGAGCAAGCTTGTCC 1027
Db 961 GCACCAACGCGGAGCCCGCATCAATGCGGCGCAACAGCTGCTGAGAGCAAGCTTGTCC 1020
Qy 1028 CCGGCTGATGCGGAGGAGGAGTCCATCTCTGCTGAGGAGGAGGAGGAGGAGTGTG 1087
Db 1021 CCGGCTGATGCGGAGGAGGAGTCCATCTCTGCTGAGGAGGAGGAGGAGGAGTGTG 1080
Qy 1088 GCGCTCTCTCTACTAGCTCTCTGAGGCGGAGGAGGAGGAGGAGGAGGAGTGTG 1147
Db 1081 GCGCTCTCTCTACTAGCTCTCTGAGGCGGAGGAGGAGGAGGAGGAGGAGTGTG 1140
Qy 1148 GACCATCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1207
Db 1141 GACCATCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1200
Qy 1208 GCGGCGAGCGCTACTGCGAATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1267
Db 1201 GCGGCGAGCGCTACTGCGAATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1260
Qy 1268 GTGCGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1327
Db 1261 GTGCGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1320
Qy 1328 AGCGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1387
Db 1321 AGCGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1380
Qy 1388 CACAGACCCCGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1447
Db 1381 CACAGACCCCGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1440
Qy 1448 CCGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1507
Db 1441 CCGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1500
Qy 1508 CAGAGACCGCGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1567
Db 1501 CAGAGACCGCGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1560
Qy 1568 GCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1627
Db 1561 GCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1620
Qy 1628 GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1687
Db 1621 GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1680
Qy 1688 CAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1747
Db 1681 CAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1740

Qy 1748 TGTCAACGAGACCAAGCTTTCAAGAGGAGGAGGAGGAGGAGGAGTGTG 1807
Db 1741 TGTCAACGAGACCAAGCTTTCAAGAGGAGGAGGAGGAGGAGGAGTGTG 1800
Qy 1808 CAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1867
Db 1801 CAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1860
Qy 1868 GAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1927
Db 1861 GAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1920
Qy 1928 CTTATCCCAAGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1987
Db 1921 CTTATCCCAAGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 1980
Qy 1988 CAGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2047
Db 1981 CAGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2040
Qy 2048 CAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2107
Db 2041 CAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2100
Qy 2108 CCGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2167
Db 2101 CCGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2160
Qy 2168 GCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2227
Db 2161 GCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2220
Qy 2228 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2287
Db 2221 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2280
Qy 2288 TCGGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2347
Db 2281 TCGGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2340
Qy 2348 GCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2407
Db 2341 GCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2400
Qy 2408 GACCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2467
Db 2401 GACCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2460
Qy 2468 CAGTGTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2527
Db 2461 CAGTGTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2520
Qy 2528 CAGTGTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2587
Db 2521 CAGTGTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2580
Qy 2588 CAGCTGTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2647
Db 2581 CAGCTGTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2640
Qy 2648 GCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2707
Db 2641 GCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2700
Qy 2708 CTTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2767
Db 2701 CTTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2760
Qy 2768 GACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2827
Db 2761 GACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 2820

human or animal. (I) is also useful for treating wounds of other
epidermal surfaces including mucosal surfaces such as bronchus, mouth,
nose, oesophagus, stomach, or intestine. The present sequence encodes
human TERT (hTERT), which is given in the exemplification of the present
invention. hTERT is located to chromosome 5

Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 82.4%; Score 3306.6; DB 7; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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8  GCAGGCTGCGTCCGCTGCTGCGGACGTGGGAGACCTGGCCCGGCGCAACCCCGGATGCC 67
Db  1  GCAGGCTGCGTCCGCTGCTGCGGACGTGGGAGACCTGGCCCGGCGCAACCCCGGATGCC 60

QY  68  GCGGCTGCTCCCGCTGCGGACCGGTGCGCTCCCTGCTGCGGACCGCACTACCGGAGTGTCT 127
Db  61  GCGGCTGCTCCCGCTGCGGACCGGTGCGCTCCCTGCTGCGGACCGCACTACCGGAGTGTCT 120

QY  128  GCCGCTGCGCAAGTTCGTGGGCGGCGCTGGGCGCCGAGGCTGGGCGGTGTGTGACGCGCG 187
Db  121  GCCGCTGCGCAAGTTCGTGGGCGGCGCTGGGCGCCGAGGCTGGGCGGTGTGTGACGCGCG 180

QY  188  GGAACCGGCGGCTTTCGCGCGCTGTGTGCGCCAGTGTGCTGTGTGCTGTGCGGAGCGC 247
Db  181  GGAACCGGCGGCTTTCGCGCGCTGTGTGCGCCAGTGTGCTGTGTGCTGTGCGGAGCGC 240

QY  248  ACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
Db  241  ACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

QY  308  CCGAGTGTGCGAGAGTGTGTGCGAGCGCGCGCGCGAGAGAGTGTGTGCTGTGCGCTTCCG 367
Db  301  CCGAGTGTGCGAGAGTGTGTGCGAGCGCGCGCGCGAGAGAGTGTGTGCTGTGCGCTTCCG 360

QY  368  GCTGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
Db  361  GCTGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420

QY  428  CCTGCCCAACACGCTGTGACCGACGCACTGCGGAGGAGCGGCGCGCGCGCGCGCGCG 487
Db  421  CCTGCCCAACACGCTGTGACCGACGCACTGCGGAGGAGCGGCGCGCGCGCGCGCGCG 480

QY  488  CCGGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547
Db  481  CCGGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

QY  548  GCGTCCCAAGCTGCGCTACCAAGGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
Db  541  GCGTCCCAAGCTGCGCTACCAAGGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 600

QY  608  TCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
Db  601  TCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660

QY  668  CTGGAACCATATGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Db  661  CTGGAACCATATGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720

QY  728  GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 787
Db  721  GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 780

QY  788  TGCGCCCTGAGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db  781  TGCGCCCTGAGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840

QY  848  GCGTGAACCGAGTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
Db  841  GCGTGAACCGAGTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900

QY  908  CACTCTTTTGAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
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Db  901  CACTCTTTTGAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
QY  968  GCAGCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1027
Db  961  GCAGCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020

QY  1028  CCGGCTGTACCGCGAGCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCT 1087
Db  1021  CCGGCTGTACCGCGAGCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080

QY  1088  GCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1147
Db  1081  GCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140

QY  1148  GACCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1207
Db  1141  GACCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200

QY  1208  GCCCGCAGGCTACTGTGCAAAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
Db  1201  GCCCGCAGGCTACTGTGCAAAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260

QY  1268  GTGCCCTTACGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1327
Db  1261  GTGCCCTTACGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320

QY  1328  AGCGGCTGTCTGTGCGCGGAGAAAGCCCGAGGCTCTGTGTGTGTGTGTGTGTGTGTGT 1387
Db  1321  AGCGGCTGTCTGTGCGCGGAGAAAGCCCGAGGCTCTGTGTGTGTGTGTGTGTGTGTGT 1380

QY  1388  CACAGACCCCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1447
Db  1381  CACAGACCCCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440

QY  1448  CGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1507
Db  1441  CGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500

QY  1508  CAACGAGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1567
Db  1501  CAACGAGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560

QY  1568  GCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1627
Db  1561  GCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620

QY  1628  GAGCCCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1687
Db  1621  GAGCCCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680

QY  1688  CAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1747
Db  1681  CAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740

QY  1748  TGTCAAGGAGCGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1807
Db  1741  TGTCAAGGAGCGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1800

QY  1808  CAAGTGTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1867
Db  1801  CAAGTGTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860

QY  1868  GGAAGCAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1927
Db  1861  GGAAGCAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920

QY  1928  CTTATCTCCCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1987
Db  1921  CTTATCTCCCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980

QY  1988  CAGAGCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2047
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DE	Human telomerase reverse transcriptase gene.
XX	
XX	
KM	Gene; ds; human; telomerase reverse transcriptase; adipogenic capacity;
KW	primary preadipocyte cell; adipogenesis; obesity; adipocytokine;
KW	anorectic; adiponectin; insulin.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	56..3454
ET	//tag= a
FT	/product= "telomerase reverse transcriptase"
FN	
PD	WO2003031640-A2.
XX	
PD	17-APR-2003.
XX	
PF	07-OCT-2002; 2002MO-US031635.
XX	
PR	06-OCT-2001; 2001US-0327650P.
PR	06-OCT-2001; 2001US-0327651P.
XX	
PA	(BOST-) BOSTON MEDICAL CENT CORP.
XX	
PI	Kirkland U, Tchkonja T;
DR	WPI: 2003-421278/39.
DR	P-PDSB; ABR58045.
XX	
XX	New primary preadipocyte strain expressing telomerase reverse
PT	transcriptase, useful in research applications, screening assays,
PT	clinical applications, and in the administration of therapeutic agents,
PT	particularly for obesity.
XX	
PS	Disclosure; Page 11-13; 53pp; English.
XX	
CC	The invention relates to the generation of primary preadipocyte cell
CC	strains that express telomerase reverse transcriptase (TERT- the
CC	catalytic subunit of telomerase), and maintain and/or enhance replicative
CC	potential and maintain adipogenic capacity of the cell. This sequence
CC	represents the gene encoding the TERT protein. The cell strain can be
CC	used in research to study all aspect of adipogenesis, especially in
CC	relation to researching treatments for e.g. obesity. The cell can also be
CC	used to identify adipogenesis modulators for use as therapeutic agents
CC	such as hormones, growth factors, cytokines, enzymes, cholesterol binding
CC	proteins, cholesterol removing proteins or their combinations.
CC	Alternatively, the therapeutic agent may be an adipocytokine, preferably
CC	adiponectin, or insulin
XX	
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
XX	
Query March	82.4%; Score 3306.6; DB 7; Length 4015;
Best Local Similarity	89.9%; Pred. No. 0;
Matches 3618; Conservative	0; Mismatches 359; Indels 46; Gaps 5
OY	8 GCAGCGGTGCGTCCTGCTGCACAGTGGAAGCCCTGGCCCCCGGCAACCCCGCAGATGCC 67
Db	1 GCAGCGGTGCGTCCTGCTGCACAGTGGAAGCCCTGGCCCCCGGCAACCCCGCAGATGCC 60
OY	68 GCGGCGTCCCCCGTGCAGACCGGTGGCTCCCTGTCGACAGCACATACCGCAGAGTCT 127
Db	61 GCGGCGTCCCCCGTGCAGACCGGTGGCTCCCTGTCGACAGCACATACCGCAGAGTCT 120
OY	128 GCCGTGGCCACGATTGCTGCGCGGCTTGGAGGCCCGAGGCTGCGCGCTGTGTGACGCCG 187
Db	121 GCCGTGGCCACGATTGCTGCGCGGCTTGGAGGCCCGAGGCTGCGCGCTGTGTGACGCCG 180
OY	188 GAACCCCGCGCGCTTTTCCGCGCGCTGATGGCCACAAGTACTGATGACGTGCGCTGGACG 247
Db	181 GAACCCCGCGCGCTTTTCCGCGCGCTGATGGCCACAAGTACTGATGACGTGCGCTGGACG 240
OY	248 AGGAGCGCCCCCGCGCGCCCTCTCTTCGCGCAGGTATCTGCTGTAAGAAGTGTGATGC 307

[illegible]

QY 728 GAGGCGGGGGGCACTGCGCAAGCCGAACTCTGCGCTTGCCCAAGAGGCCCAAGGCTGCGCG 787
DB 721 GAGGCGGGGGGGAGTCCAGCGCGAAAGTCTGCGCTTGCCCAAGAGGCCCAAGGCTGCGCGCG 780
QY 788 TGCCCTTGAGCCGAGAGCGAGCGCCGCTTGAGGAGAGGCTCTGAGGCCCAAGCCGAGAGAG 847
DB 781 TGCCCTTGAGCCGAGAGCGAGCGCCGCTTGAGGAGAGGCTCTGAGGCCCAAGCCGAGAGAG 840
QY 848 GCGTGAGCCGAGAGTACCTGCTGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
DB 841 GCGTGAGCCGAGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 908 CAGCTCTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
DB 901 CAGCTCTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 968 GCAACAGCGGGGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1027
DB 961 GCAACAGCGGGGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1028 CCGGCTGTAAGCGGAGCAAGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1087
DB 1021 CCGGCTGTAAGCGGAGCAAGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1088 GCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1147
DB 1081 GCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1148 GACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1207
DB 1141 GACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1208 GCCCAGCGCTACTGCAATGCGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1267
DB 1201 GCCCAGCGCTACTGCAATGCGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1268 GTGCGCTTACGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1327
DB 1261 GTGCGCTTACGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1328 AGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1387
DB 1321 AGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1388 CAGAGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447
DB 1381 CAGAGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1448 CCGCTTCTGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1507
DB 1441 CCGCTTCTGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1508 CAGAGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1567
DB 1501 CAGAGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1568 GCTCTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1627
DB 1561 GCTCTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1628 GAGCCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1687
DB 1621 GAGCCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1688 CAGGTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1747
DB 1681 CAGGTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 1748 TGTCAAGAGCAAGCTTCAAAAGAGAGCTCTTTTCTTCAACCGAAGAGTGTCTGAG 1807
DB 1741 TGTCAAGAGCAAGCTTCAAAAGAGAGAGCTCTTTTCTTCAACCGAAGAGTGTCTGAG 1800
QY 1808 CAGGTTGCAAGCATTTGAAATCAGACAGACTTGAAAGAGGTGAGAGCTGCGGAGCTGTC 1867

DB 1801 CAGGTTGCAAGCATTTGAAATCAGACAGACTTGAAGAGGCTGACGTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTGAGGCGAGCTGCGGAGAGCCAGGCGCCGCTGCTGAGAGTCAACATCTCCG 1927
DB 1861 GGAAGCAGAGGTGAGGCGAGCTGCGGAGAGCCAGGCGCCGCTGCTGAGAGTCAACATCTCCG 1920
QY 1928 CTTCACTCCCAAGCTGAGCGGCTGCGGCGGATTTGTAACATGAGTACGTCTGAGAGC 1987
DB 1921 CTTCACTCCCAAGCTGAGCGGCTGCGGCGGATTTGTAACATGAGTACGTCTGAGAGC 1980
QY 1988 CAGAACCTTCCGAGAGAGAGAGAGGCGCCAGGCTGCTGCTGAGAGTGAAGGCTGTT 2047
DB 1981 CAGAACCTTCCGAGAGAGAGAGAGGCGCCAGGCTGCTGCTGAGAGTGAAGGCTGTT 2040
QY 2048 CAGGCTGCTCACTAGAGCGGCGCGCGCGCCGCTGCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCT 2107
DB 2041 CAGGCTGCTCACTAGAGCGGCGCGCGCGCCGCTGCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCT 2100
QY 2108 CTTGAGAGATATCAAGAGGCTGCTGCGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2167
DB 2101 CTTGAGAGATATCAAGAGGCTGCTGCGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
QY 2168 GCGGCTGAGCTGTAATTTGTAAGAGTGTGAAGGCGCGCTGCTGAGAGCAATCCCCCA 2227
DB 2161 GCGGCTGAGCTGTAATTTGTAAGAGTGTGAAGGCGCGCTGCTGAGAGCAATCCCCCA 2220
QY 2228 GGAAGAGCTCAGAGAGTCACTGCGAGCATCATCAAAAGGAGAGAGCTGCTGCTGCTGCTGCT 2287
DB 2221 GGAAGAGCTCAGAGAGTCACTGCGAGCATCATCAAAAGGAGAGAGCTGCTGCTGCTGCTGCT 2280
QY 2288 TCGGTAAGCGGTGCTGAGAGAGCGCGCTGCTGAGAGAGCTGCTGAGAGAGCTGCTGAGAGAG 2347
DB 2281 TCGGTAAGCGGTGCTGAGAGAGCGCGCTGCTGAGAGAGCTGCTGAGAGAGCTGCTGAGAGAG 2340
QY 2348 GGTCTTACCTTGAAGAGAGCTGCGAGCTGATGAGAGAGCTGCTGAGAGAGCTGCTGAGAGAG 2407
DB 2341 GGTCTTACCTTGAAGAGAGCTGCGAGCTGATGAGAGAGCTGCTGAGAGAGCTGCTGAGAGAG 2400
QY 2408 GACAGCGCGCTAGAGAGAGTGCCTGCTGATGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCT 2467
DB 2401 GACAGCGCGCTAGAGAGAGTGCCTGCTGATGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCT 2460
QY 2468 CAGTGCCTTCTGAGAGCTCTTCTGAGCTTCAATGAGAGAGAGCTGCTGAGAGAGCTGCTGAG 2527
DB 2461 CAGTGCCTTCTGAGAGCTCTTCTGAGCTTCAATGAGAGAGAGCTGCTGAGAGAGCTGCTGAG 2520
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DB 2581 CAGCTGCTGCTAGAGAGAGTGAAGAGAGAGCTGCTGAGAGAGCTGCTGAGAGAGCTGCTGAG 2640
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DB 2641 GCTCTGCGCTTGTGAGAGTATTTCTTGTGTGAGAGAGCTGCTGAGAGAGCTGCTGAGAGAG 2700
QY 2708 CTTCTCTAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2767
DB 2701 CTTCTCTAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
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QY 2888 GAGAGAGCTACTCAGAGTATGCGGAGCTTCCATCAGAGCAAGTCTTCAACCG 2947

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QY 3188 CTGCTACTCATCTGAAAGCCAGAGCAGATGT-----GCAGTGCCTGG 3237
Db 3181 CTGCTACTCATCTGAAAGCCAGAGCAGATGTCTGGGGGCGCAAGGGCGCGC 3240
QY 3238 CTTCACTGAGAGAGTGCCTGCTGCTGTGTGTAGTGTCAAGAGACTGAGTAACTG 3297
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QY 3358 GCTGCTGCTGCGCGCTCTGTGTGGGTGAGCAGAGCATCTGATGGAAGGACAGAGCTG 3417
Db 3361 GCTGAGTGGAGAGCTCCGAGGAGCAGCGTGACTGCTGAGAGCGCGCAGCCAGCCGAC 3420
QY 3418 TCTGAGAGCTGACCATCTTCCACCTTGCT-----GCCG 3454
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QY 3455 GGGAGAGCTGGGGGCTGTGTCTCTCTGTTTGGCCATGTGGGATTTGGGGGCTG 3514
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Db 3661 GAGTGTCAAGCAGCTGCGGTCTCACTTCCCAAGGCTGGGCTGCGCTCCACCC 3719
QY 3690 CCAGTACCGTCTTGCCTGTGACACTTGTCCAGCATCAGGAGGTTTCTGATCCGT 3749
Db 3720 AGGGCAGCTTTTCTCAGCAGAGCGCGCTTCCACTCCCAATAGGAATATGCAATC 3779
QY 3750 CTGAAATTCAAGCAGTGTGAACCTGCGGTCTGAGCTTACAGCTTCTACTTTGTTC 3809
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QY 3810 TTTCTGTGTGTGAGACCTTGAAGAGACCTGAGAGCTTGGAAATTTGAGTGAACA 3869
Db 3833 CACCATTCAGGTGAGACCTTGAAGAGACCTTGGAGTCTTGGAAATTTGAGTGAACA 3892
QY 3870 AAGGTGCGCTGTACAGAGGAGAGACCTTGAAGTGGGGTCTTGTGGGTCAA 3929
Db 3893 AAGGTGCGCTGTACAGAGGAGAGACCTTGAAGTGGGGTCTTGTGGGTCAA 3952
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Db 3953 ATTGGGGGAGGT 4012

QY 3990 AAA 3992
Db 4013 AAA 4015

Search completed: February 29, 2004, 21:01:07
Job time : 998.857 secs

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Db 901 AAGAACCACTCTTTGAGAGGGTGCGCTCTGTGGACGCGGCCACTCCACCCATCCGTG 960
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Db 961 GCCGACGAGACCAACGCGGGGCCCGCCATGCAATGCGGGCACAAGTCCCTGGGACAGC 1020
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QY 1561 ATGCCAGCTCTGCTGACAGAGCTGACGTGAGATGAGCGTGGGAGCTGCGCTTGGC 1620
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QY 1681 TCGTGGCCAGTTCTGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1740
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Db 1801 TCTGAGACAGTTGCAAGATGAGATGAGACAGCACTTGAAGAGGGTGGAGCTGGCGG 1860
QY 1861 AGCTGTCGAGACAGAGGTGAGGAGCTGAGGAGAGAGGCGCGCTCTGTACGTTCA 1920
Db 1861 AGCTGTCGAGACAGAGGTGAGGAGCTGAGGAGAGAGGCGCGCTCTGTACGTTCA 1920
QY 1921 GACTCGGCTTACCTCCCAAGCTGACGGGCTGCGGCGGATTTGTGACATGAGACTACGTCG 1980
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Db 2101 TCGTGGGCTGAGACATATCAGAGGCGCTGGGAGCACTTGTGTGTGCGGTGGGCGCC 2160
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 QY 3241 CAGTGCAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
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 DB 3301 TTGAGAGATTTCTTACCTCTTTTTCGATCAGAGAGTGTAACTCCACCACTGTAGGCT 3360
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RESULT 2

US-09-424-686B-1
 ; Sequence 1 Application US/09424686B

GENERAL INFORMATION:

; APPLICANT: Hagen, Gustav
 ; APPLICANT: Siegmund, Hans-Ulrich
 ; APPLICANT: Weichelt, Walter
 ; APPLICANT: Wick, Mareisa

APPLICANT: Zubov, Dmitry
 TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and
 ; FILE REFERENCE: Beyer 10,203
 ; CURRENT APPLICATION NUMBER: US/09/424,686B
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/EP98/03468
 ; NUMBER OF SEQ. ID NOS: 7
 ; SOFTWARE: Microsoft Word
 ; SEQ. ID NO. 1
 ; LENGTH: 4042
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-424-686B-1

Query Match 83.1%; Score 333.6; DB 20; Length 4042;

Best Local Similarity 90.0%; Pred. No. 0; Mismatches 359; Indels 46; Gaps 5;

Matches 3645; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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Qy 2161 AGGACCGGCGCTGAGAGTCTTGTCAAGGTGATGAGAGAGAGAGAGAGAGAGAG 2220
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Dp	3001	TGAATGTCAAGAGCTGTTTCTGGAATTGGACAGTAAAGAGCTCCAGACGGTGTGCACCA	3068
QY	3061	ACATTTACAAGATCTCTCTGCTGCAGGGGTACAGGTTTACGCAATGTGTGTGCAGCTCC	3120
Dp	3061	ACATTTACAAGATCTCTCTGCTGCAGGGGTACAGGTTTACGCAATGTGTGTGCAGCTCC	3120
QY	3121	CATTTCATCAGCAAGTTTGGAAAGAACCCCACTTTTCTGTGGGTCACTCTTCAGACGG	3180
Dp	3121	CATTTCATCAGCAAGTTTGGAAAGAACCCCACTTTTCTGTGGGTCACTCTTCAGACGG	3180
QY	3181	CTTCCTCTCTGTACTCTTCATCTCTGAAGCCAGACAGCAGATGT-----GCAGG	3220
Dp	3181	CTTCCTCTCTGTACTCTTCATCTCTGAAGCCAGACAGCAGATGT-----GCAGG	3240
QY	3231	TGCTGAGCTCAGTGGAGCAGAGTGCCTGCTGCTGTATGTATGTGTGAGGAGACTAGT	3290
Dp	3241	GGCGCGCGCGCCCTCTGCCCTCCAGAGGCCGTGTCAAGTGTGTGCACCAACATCTCTGC	3300
QY	3291	GAATCTGGAGCTTAGGAAGTTCTTACCCCTTTTCCGATCAGGAAGTGGTTTAAACCAACA	3350
Dp	3301	TCAACTACTCTGACACCGGTGCACCTTACGTGCCACTCTCTGGGTGCATCTCAGACAGCC	3360
QY	3351	CTGTGAGCTCGTCTGCCCGCCCTCTGTGGGGTATGACAGACACTGATAGGAAGGACA	3410
Dp	3351	AGAGCACTGATGTGGAAAGTCCCGGGGAGACAGCGTGAACGTCCCTGTGAGGCCCGACCA	3420
QY	3411	GGAGTGTCTGGAGCTCCATTCCTTCCACCTTGTCTT-----3449	
Dp	3421	ACCGGGCACTCCCTCAACATTTCAAGACATCTGTGACTGTATGGCCACCAGCCCGACACC	3480
QY	3450	--GCCTGGAGAAAGCGCTGGGGGGCGCTGTCTCTCTGTTTCCCCATGATGGATTGGG	3507
Dp	3481	AGCGCGAAGACAGACACCAAGACCGCTGTCAAGCGCGGCTCTAGTCCCGAGAGGAGAG	3540
QY	3508	GGGCTGAGCTCTCTCTGTTTGTGCGCTGTGTGTGGGATTTGGGTGTCTCCCTGCATGTCACT	3567
Dp	3511	GGCGGCCACACCCAGCGGCCCGACCGCTGGAGTCTGAGGCTGATGATGTTTGGCCG	3600
QY	3568	TAGGGCCCTTTGTGAAACCCAGGCCAAG-----GACTTAGAGAGAGGCCAGGCCCAAGCT	3622
Dp	3601	AGGCTGTGATGTCCGGCTGAAGGGGTGATGTCCGGCTGAGAGGCTGAGAGATGTCCAGCC	3660
QY	3623	ACCCACCCCTCTCAGAGAGCAGAGCGCGGTATACACACACAGAGCCCGCGCGCTCT	3682
Dp	3661	AAGGCTGAGTGTCCAGACACATGCGCGTCT-TCACTTCCCAAGAGCTGCGCTCGAGCT	3719
QY	3683	CTGCTTCCAGATCACGTCCTCTGCGCCCTGTGACACTTGTTCACAGATCAGAGGAGTTCT	3742
Dp	3720	CCAGCCCGAGGCGCAGCTTTTCTCTCACCGAGAGCCCGGCTTCACTCCGCACATGAGATA	3779
QY	3743	GATCCGTCTGAATTTCAAGCATGTGGAACCTGTGGGTCTGTAGGTTTACAGCTTCTACTT	3802
Dp	3780	GTCAATCCCAAGATTCGCCATTGTTCACCCCTC-----GCTGTGCCCTCTTGTGCTT	3832
QY	3803	TCTGTCTTCTTGTGTGTGTGTGAGACCCCTGAGAGAGACCTGTGGAGCTCTGGGAATTGGA	3862
Dp	3833	CCACCCCAACATCCAGGTGTGAGACCCCTGAGAGAGACCTGTGGAGCTCTGGGAATTGGA	3892
QY	3863	GTGACAAAGGTGTGCTCTGTATACACAGCGACAGACCTGTCACTGTAGTGGGGTCTCTGT	3922
Dp	3893	GTGACAAAGGTGTGCTCTGTATACAGCGACAGACCTGTCACTGTAGTGGGGTCTCTGT	3952
QY	3923	GGGTCAATTGGGGGAGGTGCTGTGGAGTAAATACTGATAATATAGATTTTCAGTT	3982
Dp	3953	GGGTCAATTGGGGGAGGTGCTGTGGAGTAAATACTGATAATATAGATTTTCAGTT	4012
QY	3983	TTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4012	
Dp	4013	TTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4042	

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RESULT 3
US-09-424-686F-1
/ Sequence 1, Application US/09424686F
/ GENERAL INFORMATION:
/ APPLICANT: Hagen, Gustav
/ APPLICANT: Siegmund, Hans-Ulrich
/ APPLICANT: Weichei, Walter
/ APPLICANT: Wick, Mareisa
/ APPLICANT: Zubov, Dmitry
/ TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and Thera
/ TITLE OF INVENTION: Use
/ FILER OF INVENTION: Bayer 10,203
/ FILE REFERENCE: Bayer 10,203
/ CURRENT APPLICATION NUMBER: US/09/424, 686F
/ CURRENT FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/EP98/03468
/ PRIOR FILING DATE: 1998-06-09
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: Microsoft Word
/ SEQ ID NO 1
/ LENGTH: 4042
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-424-686F-1

Query Match      83.1%; Score 333.6; DB 20; Length 4042;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY      1 GTTTCAGGCAAGCGCTGCGCTCTGCTGCGCAAGTGGAAAGCCCTGACCCCGGCAACCCCG 60
DB      1 GTTTCAGGCAAGCGCTGCGCTCTGCTGCGCAAGTGGAAAGCCCTGACCCCGGCAACCCCG 60

QY      61 CGATGCGCGCGCGCTCCCGCGCTGCGGAGCGGCGCTCCCTGCTGCGGACGCACTACGCG 120
DB      61 CGATGCGCGCGCGCTCCCGCGCTGCGGAGCGGCGCTCCCTGCTGCGGACGCACTACGCG 120

QY      121 AGGTGCTGCGCTGAGCAAGTTCGTGCGCGCGCTGCGGAGCGCGCGCAAGGCTGCGGCTGCTG 180
DB      121 AGGTGCTGCGCGCTGAGCAAGTTCGTGCGCGCGCTGCGGAGCGCGCGCAAGGCTGCGGCTGCTG 180

QY      181 AGCGCGGAGAACCGCGGCGGCTTTCGCGCGCGCTGCGGCGCGCAAGTGCCTGCTGCGTGCCT 240
DB      181 AGCGCGGAGAACCGCGGCGGCTTTCGCGCGCGCTGCGGCGCGCAAGTGCCTGCTGCGTGCCT 240

QY      241 GCGACGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB      241 GCGACGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

QY      301 TGGTGGCCCGAGTGTCTGACAGAGCTGTGCGAGCGCGCGCGCGCGCAAGAGAGTGTGCGCTTGC 360
DB      301 TGGTGGCCCGAGTGTCTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCAAGAGAGTGTGCGCTTGC 360

QY      361 GCTTGGCGCTGCTGCTGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB      361 GCTTGGCGCTGCTGCTGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420

QY      421 GCAAGTACTGCGCCCAACAGCGGTGACCGAGCACTGCGGAGGAGCGCGCGCGCGCGCGCGCG 480
DB      421 GCAAGTACTGCGCCCAACAGCGGTGACCGAGCACTGCGGAGGAGCGCGCGCGCGCGCGCGCG 480

QY      481 TGCTGCGCGCGCTGAGGAGAGAGAGTGTGCTTCACTGCTGCGCAAGCTGCGCGCGCTCTTTG 540
DB      481 TGCTGCGCGCGCTGAGGAGAGAGAGTGTGCTTCACTGCTGCGCAAGCTGCGCGCGCTCTTTG 540

QY      541 TGCTGCTGCGCTCCAGCTGCGCTTACAGAGTGTGCGGAGCGCGCGCGCTGACAGCTGCGCG 600
DB      541 TGCTGCTGCGCTCCAGCTGCGCTTACAGAGTGTGCGGAGCGCGCGCGCTGACAGCTGCGCG 600

QY      601 CTGCGCACTACAGCGCGCGCGCGCGCGCGCGCGCAAGCGCTGAGACCGCGCGCGCGCGCGCG 660
DB      601 CTGCGCACTACAGCGCGCGCGCGCGCGCGCGCGCAAGCGCTGAGACCGCGCGCGCGCGCGCG 660

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QY 661 AACGGGCTGGAAACATAGGCTCAGAGGAGGCGGGGTCCTCCGCTGGGCTGGCAAGCCCGG 720
Db 661 AACGGGCTGGAAACATAGGCTCAGAGGAGGCGGGGTCCTCCGCTGGGCTGGCAAGCCCGG 720
QY 721 GTGGAGAGAGGCGGCGGGGAGTGCAGAGGAGTGTGCGGTGGCCCAAGAGGCGGAGG 780
Db 721 GTGGAGAGAGGCGGCGGGGAGTGCAGAGGAGTGTGCGGTGGCCCAAGAGGCGGAGG 780
QY 781 GTGGCGGTGGCCCTGAGAGGCGGAGAGGCGGCTTGGGAGAGGAGTGTGCGGCGGAGG 840
Db 781 GTGGCGGTGGCCCTGAGAGGCGGAGAGGCGGCTTGGGAGAGGAGTGTGCGGCGGAGG 840
QY 841 GCAAGAGCGGTGAGACCGAGTGAACGAGTGTCTGTGAGTGTCTGTGAGAGGCGGAGG 900
Db 841 GCAAGAGCGGTGAGACCGAGTGAACGAGTGTCTGTGAGTGTCTGTGAGAGGCGGAGG 900
QY 901 AAGAGAGCACTCTTTGGAGAGGAGTGTCTGTGAGAGGCGGAGGCGGAGGCGGAGG 960
Db 901 AAGAGAGCACTCTTTGGAGAGGAGTGTCTGTGAGAGGCGGAGGCGGAGGCGGAGG 960
QY 961 GCGGCGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1020
Db 961 GCGGCGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1020
QY 1021 CTTGTGCGGAGTGTGAGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1080
Db 1021 CTTGTGCGGAGTGTGAGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1080
QY 1081 AGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1140
Db 1081 AGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1140
QY 1141 TCGTGGAGAGCACTTTCTGGAGTGTGAGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1200
Db 1141 TCGTGGAGAGCACTTTCTGGAGTGTGAGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1200
QY 1201 CCGGCGTGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1260
Db 1201 CCGGCGTGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1260
QY 1261 ACAGGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1320
Db 1261 ACAGGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1320
QY 1321 CCGGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1380
Db 1321 CCGGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1380
QY 1381 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1440
Db 1381 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1440
QY 1441 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1500
Db 1441 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1500
QY 1501 CCGGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1560
Db 1501 CCGGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1560
QY 1561 ATGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1620
Db 1561 ATGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1620
QY 1621 TGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1680
Db 1621 TGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1680
QY 1681 TCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1740
Db 1681 TCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1740
QY 1741 TCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1800

Db 1741 TCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1800
QY 1801 TCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1860
Db 1801 TCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1860
QY 1861 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1920
Db 1861 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1920
QY 1921 GAGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1980
Db 1921 GAGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 1980
QY 1981 TGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2040
Db 1981 TGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2040
QY 2041 CAGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2100
Db 2041 CAGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2100
QY 2101 TCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2160
Db 2101 TCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2160
QY 2161 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2220
Db 2161 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2220
QY 2221 TCGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2280
Db 2221 TCGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2280
QY 2281 GCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2340
Db 2281 GCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2340
QY 2341 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2400
Db 2341 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2400
QY 2401 TCGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2460
Db 2401 TCGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2460
QY 2461 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2520
Db 2461 AGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2520
QY 2521 TCGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2580
Db 2521 TCGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2580
QY 2581 TCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2640
Db 2581 TCGTGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2640
QY 2641 ACAGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2700
Db 2641 ACAGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2700
QY 2701 CGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2760
Db 2701 CGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2760
QY 2761 TCGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2820
Db 2761 TCGGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2820
QY 2821 TCGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 2880

Db	2821	TTCAATGCGCGCCACACGGCCCTAATTCCTCGGTGGCGCTGCTGCTGAATACCCGGACCC	2881
QY	2881	TGGAGGTGCAAGCGCACTACTCCAGCTATGCCCGGACCTCCATCAAGACGACTCTACCT	2940
Db	2881	TGGAGGTGCAGAGCCACTACTCCAGCTATGCCCGGACCTCCATCAAGACGACTCTACCT	2940
QY	2941	TCACCGGCGCTTCAAGGCTGGGAGAAATCGCTCGGAAATCTCTTGGGGGCTTGGGGGCG	3000
Db	2941	TCACCGGCGCTTCAAGGCTGGGAGAAATCGCTCGGAAATCTCTTGGGGGCTTGGGGGCG	3000
QY	3001	TGAAGTGTCAAGCCTGTCTTGAATTTGCAAGTGAACAAGCTCTCAGACGCTGTGACCA	3060
Db	3001	TGAAGTGTCAAGCCTGTCTTGAATTTGCAAGTGAACAAGCTCTCAGACGCTGTGACCA	3060
QY	3061	ACATCTACAAGATTCCTCGCTGCGAGGGGGTACAGGTTTCAAGCATGTGTGCTGACGCTCC	3120
Db	3061	ACATCTACAAGATTCCTCGCTGCGAGGGGGTACAGGTTTCAAGCATGTGTGCTGACGCTCC	3120
QY	3121	CATTTCATCAGCAAGTTTGGAAAGAACCCCAATTTTCTCGCGCTCACTCTGACAGG	3180
Db	3121	CATTTCATCAGCAAGTTTGGAAAGAACCCCAATTTTCTCGCGCTCACTCTGACAGG	3180
QY	3181	CCTCCCTCTGCTACTCTCCATCTGAAAGCCAGAAAGCGAGGTGTG-----GCAGG	3230
Db	3181	CCTCCCTCTGCTACTCTCCATCTGAAAGCCAGAAAGCGAGGTGTG-----GCAGG	3230
QY	3231	TGCTGGGCTCAGTGGCGAGAGTGGCTGCTGCTGATGTAGTGTAGTGTGAGGAGACTAGT	3290
Db	3241	GCGCGCGCGCCCTCTGCCCTCCGAGGCGGTGACGTGCTGTGACCAAGACATCTCTGCG	3300
QY	3291	GAATCTGGAGCTTAAAGAAAGTCTTTACCCCTTTTGCATCAGAAAGTGTGTTAAACCAACA	3350
Db	3301	TCAAGCTACTCAGACACCGGTGCACCTACGTGTCACCTCTCGGGGTCACTCAGACAGGCC	3360
QY	3351	CTGTAGGCTGTCTGCGCGCCCTCTGCTGTGGGTGTAGAGAGCAACCTATGAAAGGACA	3410
Db	3351	AGAGCGACCTGAGTGTGAAGCTCCCGGGAGACACCTGACTGCTCGGAGCGCGAGCCA	3420
QY	3411	GGAAGCTGTGTGGAGCTGCCATCTCTTCCACCTTGCTCT-----	3449
Db	3421	AACCGGCACTGCCCTCAGACTTTCAAGACCATCTGTGACTGATGGCCACCGGCCACAGCC	3480
QY	3480	--GCTGGGGAAGCGCTGGGGGCGCTGTCTCTCTGTTGCCCATGTGTGGATTTGGG	3507
Db	3481	AGCGCGAAGAGACAGACAGCAGCCCTGTCAAGCGGAGCTTACCTCCAGAGAGGAGG	3540
QY	3508	GCGCTGGGCTCTCTGTTTGGCCGTGTGTGGAAATGGAGCTGTCTCCGTCATATGGACCT	3567
Db	3541	GGCGGCCACACCCAGGCGCCGACCGCTGGAGTGTAGGCGCTAGTGAAGTGTTTGGCGG	3600
QY	3568	TAGGCGCTTGTGCAACCCAGGCCAAG-----GGCTTAAAGAGAGCGCAGGCCCAAGCT	3622
Db	3601	AGGCTGTGATGTCCGCTGAAAGGCTGAGTGTCCGCTAGGCTGTGAGGTGCACTGTCAAGCC	3660
QY	3623	AACCCACCCCTCTCAAGAGCAGAGGCGCGATATCAACAGACAGAGCCCGCGCGCTCT	3682
Db	3661	AAGGCGTGAAGTGTCCAGACACACTGCTGCT--TCACTTCCCAAGGTGAGCGCTCGGCT	3719
QY	3683	CTGCTTCCCAAGTCAACGCTCTCTGCGCCCTGAGCACTTGTGTCAAGATCAGGAGAGTTCCT	3742
Db	3720	CCACCCCAAGGCGCAGCTTTTCTCTCAACAGAGCCGAGGCTTCACTCCCAATAGGAATA	3779
QY	3743	GATCGGTGTGAATTCAGAGCATGTGCAACCTGCGGCTCTGAGCTTAAACACTTCTACTT	3802
Db	3780	GTCAATCCCGAGATTTCGCAATTGTCAACCCCTC-----GCCCTGCCCTCTTGTGCTT	3832
QY	3803	TCTGTTCTTTCTGTGTTTGTGAGAACCTTGAAGAGACCCTGGAGCTCTTGGAAATTTGGA	3862
Db	3833	CCACCCCAACCATCAAGGTGAGGACCTTGAAGAGACCCTGGAGCTCTTGGAAATTTGGA	3892
QY	3863	GTGACCAAAAGTGTGCTCTGTACACAGGCGAGACCTCTGACCTCTGATGTGGGGGTCTCTGT	3922
Db	3893	GTGACCAAAAGTGTGCTCTGTACACAGGCGAGACCTCTGACCTCTGATGTGGGGGTCTCTGT	3952

QY	3923	GGGTCAAATTTGGGGGAGAGTCTGTGGAGAGTAAATCTGAATATATGAGTTTCACTT	3982
Db	3953	GGGTCAAATTTGGGGGAGAGTCTGTGGAGTAAATCTGAATATATGAGTTTCACTT	4012
QY	3983	TTGAAAAAAAAAAAAAAAAAAAAA	4012
Db	4013	TTGAAAAAAAAAAAAAAAAAAAAA	4042

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? Sequence 2, Application US/05582246
? GENERAL INFORMATION:
? APPLICANT: Bayer Aktiengesellschaft
? APPLICANT: Hagen, Gustav
? APPLICANT: Wick, Mareisa
? APPLICANT: Zubov, Dmitry
? TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic Re
? TITLE OF INVENTION: Subunit, and their Diagnostic and Therapeutic Use
? FILE REFERENCE: Lea 32 805
? CURRENT APPLICATION NUMBER: US/09/582,246
? CURRENT FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: PCT/EP98/08216
? PRIOR FILING DATE: 1998-12-22
? PRIOR APPLICATION NUMBER: DE19757984.1
? PRIOR FILING DATE: 1997-12-24
? NUMBER OF SEQ ID NOS: 44
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 2
? LENGTH: 4042
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-562-246-2

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Query Match	83.1%;	Score 3333.6;	DB 24;	Length 4042;
Best Local Similarity	90.0%;	Pred. No. 0;		
Matches 3645;	Conservative 0;	Mismatches 359;	Indels 46;	Gaps 5

QY	1	GTTTCAGGACAGCGCTGCTCCGTGCTGGCAAGTGTGGAAAGCCCTGAGCCCGGACACCCCG	60
Db	1	GTTTCAGGACAGCGGCTGCTCCGTGCTGGCAAGTGTGGAAAGCCCTGAGCCCGGACACCCCG	60
QY	61	CGATGCGCGCGCTCCCGCTCCCGAGCCGTGGCTTCTGTCGGADGCACTACCGG	120
Db	61	CGATGCGCGCGCTCCCGCTCCCGAGCCGTGGGCTTCTGTCGGCACTACCGG	120
QY	121	AGGTGTGTCGCTGGGCAAGTTCGTGGGGGGGCGTGGGGCCCCCAGGGGCTGGCGCTATGGC	180
Db	121	AGGTGTGTCGCTGGGCAAGTTCGTGGGGGGGCGTGGGGCCCCCAGGGGCTGGCGCTATGGC	180
QY	181	AGCGCGGGAGCCCGCGGCTTTCGCGCGGTGTGGGCCAGTGCCTGTGTGGTGGCCCT	240
Db	181	AGCGCGGGAGCCCGCGGCTTTCGCGCGGTGTGGGGCAGTGCCTGTGTGGTGGCCCT	240
QY	241	GGGACGCAACGGCGGCCCCCGCGCGCCCTTCCTTCGCGCAGAGTGTCTTGCCTGAAGAGAC	300
Db	241	GGGACGCAACGGCGGCCCCCGCGCGCCCTTCCTTCGCGCAGAGTGTCTTGCCTGAAGAGAC	300
QY	301	TGTGTGCCCCAGTGTCTGCAGAGGTGTGGCAGAGCGCGGCGGAAGAACTGTGTGACCTTCG	360
Db	301	TGTGTGCCCCAGTGTCTGCAGAGGTGTGGCAGAGCGCGGCGGAAGAACTGTGTGACCTTCG	360
QY	361	GCTTGCGCTGTGGACGGGGCCCGCGGGGGCCCCCCAGAGGCTTCACACCAACGTCGC	420
Db	361	GCTTGCGCTGTGGACGGGGCCCGCGGGGGCCCCCCAGAGGCTTCACACCAACGTCGC	420
QY	421	GCAGCTACCTGCCCCAACAAGGTGAACGACGCACTGGCGGGGAGCGGGGCGGTGGGGGCTGC	480
Db	421	GCAGCTACCTGCCCCAACAAGGTGAACGACGCACTGGCGGGGAGCGGGGCGGTGGGGGCTGC	480
QY	481	TGCTGCGCGCGTGGGCGACGACTGTGTGATTCACTGTGCGACGCTGCGGCTCTTTTG	540

[illegible]

2701 CGAAGCTTCTCAGAGACCTGAGCGAGGTGCTCCCTGAGTATGAGTGGGTGAGTACT 2760
2701 CGAAGCTTCTCAGAGACCTGAGCGAGGTGCTCCCTGAGTATGAGTGGGTGAGTACT 2760
2761 TCGGAGAGACAGTGTGTAATCTTCCCTGTAGAAAGACAGAGGCTTGGGTGAGACGAGCTTTTG 2820
2761 TCGGAGAGACAGTGTGTAATCTTCCCTGTAGAAAGACAGAGGCTTGGGTGAGACGAGCTTTTG 2820
2821 TTCAAGATCCGGGCGGAGGAGGCTTATCCCTGAGTGGGCTGAGTGGTATACCGAGAGCC 2880
2821 TTCAAGATCCGGGCGGAGGAGGCTTATCCCTGAGTGGGCTGAGTGGTATACCGAGAGCC 2880
2881 TGGAGGTGAGAGGAGCTTACTTCCAGATATGCTCCGAGCTCCATGAGAGGAGTCTACCT 2940
2881 TGGAGGTGAGAGGAGCTTACTTCCAGATATGCTCCGAGCTCCATGAGAGGAGTCTACCT 2940
2941 TCAACCGGCGGCTTCAAGGCTGGAGAGGACATGCGTCCGAACTCTTTGGGGTCTTTGGGCG 3000
2941 TCAACCGGCGGCTTCAAGGCTGGAGAGGACATGCGTCCGAACTCTTTGGGGTCTTTGGGCG 3000
3001 TGAAGTGTACAGCCTGTTTGTGAGTTCAGAGTGAACAGCCTCCAGACGAGTGTACCA 3060
3001 TGAAGTGTACAGCCTGTTTGTGAGTTCAGAGTGAACAGCCTCCAGACGAGTGTACCA 3060
3061 ACATGTAGAAATCCTCTGCTGAGAGGTACAGTTCAGAGTTCAGAGTTCAGAGTTC 3120
3061 ACATGTAGAAATCCTCTGCTGAGAGGTACAGTTCAGAGTTCAGAGTTCAGAGTTC 3120
3121 CATTTATCAGAGATTTTGAAGAAACCCACATTTTCTGCGGCTGATCTGACAGAG 3180
3121 CATTTATCAGAGATTTTGAAGAAACCCACATTTTCTGCGGCTGATCTGACAGAG 3180
3181 CCTCCTCTGCTACTCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
3181 CCTCCTCTGCTACTCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
3241 TGCCTGAGCTGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3290
3241 TGCCTGAGCTGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3290
3291 GAATGTGGGCTTGAAGATTTCTTACCCCTTTTCCAGTACAGAGTGTATACCAACCA 3350
3291 GAATGTGGGCTTGAAGATTTCTTACCCCTTTTCCAGTACAGAGTGTATACCAACCA 3350
3301 TCAAGTACTGAGACAGGAGTGTACAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3360
3301 TCAAGTACTGAGACAGGAGTGTACAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3360
3351 CTGTGAGGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3410
3351 CTGTGAGGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3410
3361 AGAGCAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3420
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3411 GAGAGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3449
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3421 ACCCGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
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3450 --GCGTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3507
3450 --GCGTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3507
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3508 GAGGCTGAGCTGCTCTGTTTGGGCTGAGTGTGAGGAGTGTGAGTGTGAGTGTGAGTGT 3567
3541 GCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3600
3541 GCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3600
3568 TAGGCGGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3622
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3623 ACCCGAGGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3682
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3661 AAGGCTGTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3719
3683 CTGCTTCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3742
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3720 CACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3779
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RESULT 5
US-08-974-549-343
Sequence 343, Application US/08974549
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OR INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997

QY 1748 TGTCAAGAGACACGCTTCAAAAGACAGGCTCTTTTCTAACCGGAGAGTGTCTGAG 1807
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QY 1808 CAAGTTCGAAGACATTTGAATGACACAGCACTTGAAGAGGATGACGCTGCGGAGCTGTC 1867
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QY 1868 GGAAGCAGAGATCAGGACAGCATCGGAAAGCCAGGCGCCCTGCTGACGTCAGACTCCG 1927
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QY 1928 CTTTCATCCCAAGCTTGAAGGAGCTGCGGCGGATTTGTGAACATGACTGCTGTGGAGC 1987
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Db 2101 CCTGACAGATATCCACAGGAGCTGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
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QY 2288 TGGATATGCGGATGTCAGAAAGCGCCATGAGCAGCTGCGAAGGCTTCAAGAGCA 2347
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QY 2348 GGTCTCTACCTTGAAGACCTTCAAGCGGATCATGAGAAAGTGTGAGTCACTGAGAG 2407
Db 2341 GGTCTCTACCTTGAAGACCTTCAAGCGGATCATGAGAAAGTGTGAGTCACTGAGAG 2400
QY 2408 GACCAAGCGCTGAGAGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2467
Db 2401 GACCAAGCGCTGAGAGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
QY 2468 CAGTGGCTCTTCAAGCTTCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2527
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Db 2581 CAGCTGTGCTACGCGCAGATGAGAGCAAGCTGTTGCGGAGATTCGCGGAGCGGCT 2640
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Db 2761 GACAGTGTGAATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
QY 2828 GCGGAGCCAGGCTATTCCTCTGAGTGGCGCTGCTGAGTATCCCGAGCTTGAAGT 2887

Db 2821 GCGGAGCCAGGCTATTCCTCTGAGTGGCGCTGCTGAGTATCCCGAGCTTGAAGT 2880
QY 2888 GAGAGCGATCTACAGATGAGCGGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2947
Db 2881 GAGAGCGATCTACAGATGAGCGGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2940
QY 2948 CCGCTTCAAGGCTGAGAGAGATGAGTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 3007
Db 2941 CCGCTTCAAGGCTGAGAGAGATGAGTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 3000
QY 3008 TCAAGCTTCTGAGATTTGAGATGAGTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 3067
Db 3001 TCAAGCTTCTGAGATTTGAGATGAGTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 3060
QY 3068 CAAGATCTCTGAGTCAAGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 3127
Db 3061 CAAGATCTCTGAGTCAAGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 3120
QY 3128 TCAAGATTTGAG 3187
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QY 3188 CTGCTACTCATCTGAG 3237
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QY 3238 CCTCAAGTGAAG 3297
Db 3241 CCGCTCTGAGCTTCAAG 3300
QY 3298 GAGCTTGAAGATTTTACCTTCAAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 3357
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QY 3358 GCTGCTGAG 3417
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QY 3418 TGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3454
Db 3421 TGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3480
QY 3455 GGAAGCGCTGAG 3514
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QY 3515 GGTCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3574
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QY 3575 CTTGTCAAG 3629
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QY 3630 CCTCTGAG 3689
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QY 3690 CAGTCAAGCTCTGAG 3749
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QY 3750 CTAAGATTTCAAG 3809
Db 3780 CTAAGATTTCAAG 3832
QY 3810 TTTCTGAGTGTGAG 3869
Db 3833 TTTCTGAGTGTGAG 3892
QY 3870 AAGTGTGCTGTAACAG 3929

Db 3993 AAGGTGTCCTGTACACAGCAGGACCTGCACTGATGGGGTCCCTGTGGCTCA 3952
QY 3930 ATTGGGGGAGGAGTGTGGAGTAAATCTGAATATGATTTTTCAGTTTGA 3989
Db 3953 ATTGGGGGAGGAGTGTGGAGTAAATCTGAATATGATTTTTCAGTTTGA 4012
QY 3990 AAAAAAAAAAAAAAAAAAAAAA 4012
Db 4013 AAAAAAAAAAAAAAAAAAAAAA 4035

RESULT 6
US-09-432-503-343

Sequence 343, Application US/09432503

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Linsner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17685

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 343:

SEQUENCE CHARACTERISTICS:

LENGTH: 4037 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note="refined sequence of hTERT CDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 343:
US-09-432-503-343

Query Match 82.8%; Score 3320.2; DB 20; Length 4037;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 3638; Conservative 3; Mismatches 356; Indels 46; Gaps 6;

QY 8 GCAGCGCTGCGCTCTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAACCCCGGATGCC 67
Db 1 GCAGCGCTGCGCTCTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAACCCCGGATGCC 60
QY 68 GCGCGCTCTCCCGCTGCGCGAGCCGTGCGCTCTGTGTCGCAAGTGGAGAGCCCTGCGCCG 127
Db 61 GCGCGCTCTCCCGCTGCGCGAGCCGTGCGCTCTGTGTCGCAAGTGGAGAGCCCTGCGCCG 120
QY 128 GCGCGCTCTCCCGCTGCGCGAGCCGTGCGCTCTGTGTCGCAAGTGGAGAGCCCTGCGCCG 187
Db 121 GCGCGCTCTCCCGCTGCGCGAGCCGTGCGCTCTGTGTCGCAAGTGGAGAGCCCTGCGCCG 180
QY 188 GGAACCCGCGGCTTTCCGCGCGCTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGC 247
Db 181 GGAACCCGCGGCTTTCCGCGCGCTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGC 240
QY 248 ACG 307
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QY 308 CCGAGTCTCTCAAGAGTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGCCTGCGCCG 367
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QY 428 CTTGCCCAACAGAGTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGCCTGCGCCG 487
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QY 488 CCGCGTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGCCTGCGCCGCGGCAAGC 547
Db 481 CCGCGTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGCCTGCGCCGCGGCAAGC 540
QY 548 GCGTCCAGCTGCGCTCAAGTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGCCTG 607
Db 541 GCGTCCAGCTGCGCTCAAGTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGCCTG 600
QY 608 TCAAGCCG 667
Db 601 TCAAGCCG 660
QY 668 CTGAAACATAGGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGCCTGCGCCGCGG 727
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QY 728 GAGCG 787
Db 721 GAGCG 780
QY 788 TGCCTCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
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QY 848 GCGTGAACCGAGTGAACCGTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGC 907
Db 841 GCGTGAACCGAGTGAACCGTGTGTCGCAAGTGGAGAGCCCTGCGCCGCGGCAAGC 900

QY 68 GCGCGCTCCCGCTGCGAGCCGCTGCTGCTGCGAGCACTACGCGAGGCT 127
DB 61 GCGCGCTCCCGCTGCGAGCCGCTGCTGCTGCGAGCACTACGCGAGGCT 120
QY 128 GCGCGCTGCGAGCTGCTGCGAGCCGCTGCGAGCCGCTGCGAGCCGCT 187
DB 121 GCGCGCTGCGAGCTGCTGCGAGCCGCTGCGAGCCGCTGCGAGCCGCT 180
QY 188 GCGCGCTGCGAGCTGCTGCGAGCCGCTGCGAGCCGCTGCGAGCCGCT 247
DB 181 GCGCGCTGCGAGCTGCTGCGAGCCGCTGCGAGCCGCTGCGAGCCGCT 240
QY 248 AGCG 307
DB 241 AGCG 300
QY 308 CGGAGTGTGAGAGGCTGTGAGAGCGCGCGCGCGAGAGAGGCTGTGAG 367
DB 301 CGGAGTGTGAGAGGCTGTGAGAGCGCGCGCGAGAGAGGCTGTGAG 360
QY 368 GCTGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
DB 361 GCTGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 428 CTTGCGCAACAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 487
DB 421 CTTGCGCAACAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 488 CGCGCTGAGAGCGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCG 547
DB 481 CGCGCTGAGAGCGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCG 540
QY 548 GCGTCCAGAGCTGCGCTACAGAGTGTGAGAGCGCGCGCGCGCGCGCG 607
DB 541 GCGTCCAGAGCTGCGCTACAGAGTGTGAGAGCGCGCGCGCGCGCGCG 600
QY 608 TAAAGCG 667
DB 601 TAAAGCG 660
QY 668 CTGGAACCACTAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 727
DB 661 CTGGAACCACTAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGGCGCGCGCGCGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCG 787
DB 721 GAGGCGCGCGCGCGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCG 780
QY 788 TGCCTCTGAGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
DB 781 TGCCTCTGAGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 848 GGTGAGCGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 907
DB 841 GGTGAGCGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 908 CACCTCTTGTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 967
DB 901 CACCTCTTGTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 968 GAGACAGCG 1027
DB 961 GAGACAGCG 1020
QY 1028 CCGGCTGTAGCGCGAGAGCACTTCTCTCTCTCTCTCTCTCTCTCTCT 1087
DB 1021 CCGGCTGTAGCGCGAGAGCACTTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1088 GCGCT 1147
DB 1081 GCGCT 1140
QY 1148 GACCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1207

DB 1141 GACCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1208 GCGCGCTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
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QY 1268 GGTGCGCTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1327
DB 1261 GGTGCGCTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1328 AGCGCGTGTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387
DB 1321 AGCGCGTGTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 1388 CACAGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447
DB 1381 CACAGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
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QY 1508 CAAAGAGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1567
DB 1501 CAAAGAGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560
QY 1568 GCTTCTGCTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1627
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DB 1621 GAGCGCGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1680
QY 1688 CAAAGTCTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1747
DB 1681 CAAAGTCTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1740
QY 1748 TGTCAAGAGAGCAAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 1807
DB 1741 TGTCAAGAGAGCAAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 1800
QY 1808 CAAAGTCTGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1867
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QY 1868 GGAAGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1927
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QY 1928 CTTCAATCCCGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 1987
DB 1921 CTTCAATCCCGAGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 1980
QY 1988 CAAAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2047
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QY 2048 CAGCGTGTCT 2107
DB 2041 CAGCGTGTCT 2100
QY 2108 CTTGAGAGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2167
DB 2101 CTTGAGAGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2160
QY 2168 GCGCGCTGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2227
DB 2161 GCGCGCTGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220
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QY 3575 CTGTGCAAAACCCAGGCAAG-----GGCTTAGAGAGAGCCAGGCCAGCTACCCAC 3629
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 QY 3930 ATTGGGGGAGGTGCTGTGGAGTAAATAGTAATATGAGTTTTCAGTTTGA 3989
 Db 3953 ATTGGGGGAGGTGCTGTGGAGTAAATAGTAATATGAGTTTTCAGTTTGA 4012
 QY 3990 AAAAAAAAAAAAAAAAAAAAAA 4012
 Db 4013 AAAAAAAAAAAAAAAAAAAAAA 4035

RESULT 9 US-10-325-810-343

Sequence 343, Application US/10325810

GENERAL INFORMATION:

APPLICANT: Czech, Thomas R.

Lininger, Joachim

Nakamura, Toru

Chapman, Karen B.

Morlin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181

FILING DATE: 29-Sep-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-Oct-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 23-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenhus, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 343:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4037 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 56..3454
 OTHER INFORMATION: /note="refined sequence of hTERT cDNA"
 US-10-325-810-343
 SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Query Match 82.8%; Score 3320.2; DB 49; Length 4037;
 Best Local Similarity 90.0%; Pred. No. 0;
 Matches 3638; Conservative 3; Mismatches 356; Indels 46; Gaps 6;

QY 8 GCAGCGGTGCTCTCTCTGCGACGCGGAGAGCCCTGCGCCCGCCAGCCGCTGCG 67
 Db 1 GCAGCGGTGCTCTCTCTGCGACGCGGAGAGCCCTGCGCCCGCCAGCCGCTGCG 60
 QY 68 GCAGCGGTGCTCTCTCTGCGACGCGGAGAGCCCTGCGCCCGCCAGCCGCTGCG 127
 Db 61 GCAGCGGTGCTCTCTCTGCGACGCGGAGAGCCCTGCGCCCGCCAGCCGCTGCG 120
 QY 128 GCAGCGGTGCTCTCTCTGCGACGCGGAGAGCCCTGCGCCCGCCAGCCGCTGCG 187
 Db 121 GCAGCGGTGCTCTCTCTGCGACGCGGAGAGCCCTGCGCCCGCCAGCCGCTGCG 180
 QY 188 GCAGCGGTGCTCTCTCTGCGACGCGGAGAGCCCTGCGCCCGCCAGCCGCTGCG 247
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QY 2768 GACAGTGTGAGTCTTCCCTGTAGAGACAGAGCCCTGGTGGACAGGCTTTTGTTCAT 2827
Db 2761 GACAGTGTGAGTCTTCCCTGTAGAGACAGAGCCCTGGTGGACAGGCTTTTGTTCAT 2820
QY 2828 GCGGCGCCACAGGCTTTTCCCTGTGGGCGGCTGTGCTGTGATACCCGACCTTGGAGT 2887
Db 2821 GCGGCGCCACAGGCTTTTCCCTGTGGGCGGCTGTGCTGTGATACCCGACCTTGGAGT 2880
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Db 3421 ACTGCTCTGAGACTTCAAGACATCTGAGCTGATGAGCCACCCGCCACAGCCAGCCGA 3480
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Db 3541 CAACCCAGGCGCGACCCCTGTGAGTCTGAGGCTGTGAGTGTGTGTGTGTGTGTGT 3600
QY 3575 CTGTGTCAAAACCCAGGCGAG-----GCTGTGAGAGAGGCGCCAGGCTTACCCAC 3629
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QY 3630 CCTCTCAGAGAGAGAGGCGGCTATACACAGACAGAGCCCGGCGGCTCTGTGTCTC 3689
Db 3661 GAGTGTGACAGACACTGTGCGCTT-TCAATTTCCCAAGGCTGGCGCTGCTTCAACCC 3719
QY 3690 CCAGTACAGCTCTCTGTGCGCTGTGACACTTGTTCAGATCAAGAGGTTTCTGTATCGT 3749
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QY 3750 CTGAATTTCAAGCATGTGAACTGTGGGTCTGTAGCTTAAAGCTTTTCTGTCTTC 3809
Db 3780 CCGAGATTC--GCCATTTGTCAACCCCTGCGCTGCTT-----CCTTGGCTTCCACCCC 3832
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Db 3833 CACATCCAGTGTGAGACCTGTGAGAGAGACCTGTGAGAGTGTGGAATTTGAGTGAACA 3892
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Db 3893 AAGTGTGCGCTGTATACACAGAGAGACCTGTGACCTGTGATGGGCTTCCCTGTGGGTCA 3952
QY 3930 ATTGGGGGAGTGTGTGTGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3989
Db 3953 ATTGGGGGAGTGTGTGTGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 4012
QY 3990 AAAAAAAAAAAAAAAAAAAAAA 4012
Db 4013 AAAAAAAAAAAAAAAAAAAAAA 4035

RESULT 10
US-08-974-524E-117
Sequence 117, Application US/08974524E
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 477
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,524E
FILING DATE: 19-Nov-1997
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elinhorn, Gregory P.
REGISTRATION NUMBER: 36,440
REFERENCE/DOCKET NUMBER: 015389-002950US
TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 576-0300

QY 1088 GCCCTCTTCTACTAGCTCTCTGAGGCCAGCTGACTGAGGCTCTGAG 1147
DB 1081 GCCCTCTTCTACTAGCTCTCTGAGGCCAGCTGACTGAGGCTCTGAG 1140
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DB 1921 CTTCAATCCCAAGCTCTGAGGCTCTGAGCAATGAGGCTCTGAG 1980
QY 1988 CAGAAAGCTCTGAGGCTCTGAGCAATGAGGCTCTGAGGCTCTGAG 2047
DB 1981 CAGAAAGCTCTGAGGCTCTGAGCAATGAGGCTCTGAGGCTCTGAG 2040
QY 2048 CAGGCTCTGAGGCTCTGAGCAATGAGGCTCTGAGGCTCTGAG 2107
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 Qy 3630 CCTCTCAGAGAGAGAGGCGCGCTATCAGACAGACAGAGCGCGCGCTCTGTGCTTC 3689
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 Db 3953 ATTGGGGGAGAGTGTGTGTGAGATTAATATGATATATGATTTTCAATTTTGAATA 4012
 Qy 3990 AAAAAAAAAAAAAAAAAAAAAA 4012
 Db 4013 AAAAAAAAAAAAAAAAAAAAAA 4035

RESULT 12
US-09-026-981-35

Sequence 35: Application us/09026981

GENERAL INFORMATION:

APPLICANT: Counter, Christopher M.

APPLICANT: Meyerson, Matthew

APPLICANT: Weinberg, Robert A.

TITLE OF INVENTION: Telomerase Catalytic Subunit Gene and

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/026,981
 FILING DATE: 20-FEB-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/064,322
 FILING DATE: 30-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/055,762
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/054,549
 FILING DATE: 01-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/047,151
 FILING DATE: 20-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/038,750
 FILING DATE: 20-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION/DOCKET NUMBER: 32,227
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4023 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-026-981-35

Query Match 82.5%; Score 3311.4; DB 14; Length 4023;

Best Local Similarity 89.9%; Pred. No. 0;

Matches 3624; Conservative 0; Mismatches 361; Indels 46; Gaps 5;

Qy 5 CAGGACGCGCTGCTCTGTGCTGAGCAGTGGAGAGCCCTGCGCCAGCCCGCGAT 64
 Db 1 CAGGAGGCGCTGCTCTGTGCTGAGCAGTGGAGAGCCCTGCGCCAGCCCGCGAT 60
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 Qy 185 CCGGAGACCCGCGGCTTTCGCGCGCTGTGTGCGCAGTGTGCTGTGCTGAGAGAGCTGT 244
 Db 181 CCGGAGACCCGCGGCTTTCGCGCGCTGTGTGCGCAGTGTGCTGTGCTGAGAGAGCTGT 240
 Qy 245 CGCAGCGCGCGCGCGCGCGCGCGCTTCTTCCGCGCAGTGTCTGTGCTGAGAGAGCTGT 304
 Db 241 CGCAGCGCGCGCGCGCGCGCGCGCTTCTTCCGCGCAGTGTCTGTGCTGAGAGAGCTGT 300
 Qy 305 GCGCGAGTGTGTGAGAGCTGTGTGAGAGCGGCGGAGAGAGAGTGTGCTTGGCTT 364
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 Qy 365 CCGCTGTGTGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 424
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 Qy 425 CTACCTGTGTGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 484
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QY 3988 AAAA 3992
Db 4737 AAAA 4741

RESULT 14

US-08-911-312A-1

Sequence 1, Application US/08911312A

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,312A

FILING DATE: 14-AUG-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Einhorn, Gregory P.

REGISTRATION NUMBER: 38,440

REFERENCE/DOCKET NUMBER: 015389-002500US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 7029 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 782..4177
OTHER INFORMATION: /product= "human telomerase reverse
transcriptase (hTERT)"
OTHER INFORMATION: /note= "cDNA contained in plasmid
pGRN121"
US-08-911-312A-1

Query Match 82.4%; Score 3307; DB 13; Length 7029;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3619; Conservative 0; Mismatches 360; Indels 46; Gaps 5;

QY 6 AGGAGAGGCTGCTCTCTCTGCGCAGTGGAAAGCCCTTGCCGCCGCGGAGTG 65
Db 725 ACGAGAGGCTGCTCTCTCTGCGCAGTGGAAAGCCCTTGCCGCCGCGGAGTG 784
QY 66 CCGGAGGCTCTCTCTCTGCGCAGTGGAAAGCCCTTGCCGCCGCGGAGTG 125
Db 785 CCGGAGGCTCTCTCTCTGCGCAGTGGAAAGCCCTTGCCGCCGCGGAGTG 844
QY 126 CTGCGGCTGAGCAGCTTCTGCGCGCTTGGGAGCCCGGAGGCTGAGGCTGAGCGC 185
Db 845 CTGCGGCTGAGCAGCTTCTGCGCGCTTGGGAGCCCGGAGGCTGAGGCTGAGCGC 904
QY 186 GGGGAGCCCGGAGGCTTCTGCGCGCTTGGGAGCCCGGAGGCTGAGGCTGAGCGC 245
Db 905 GGGGAGCCCGGAGGCTTCTGCGCGCTTGGGAGCCCGGAGGCTGAGGCTGAGCGC 964
QY 246 GCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 305
Db 965 GCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1024
QY 306 GCGGAGGCTGAGAGGCTTCTGCGCGCTTGGGAGCCCGGAGGCTGAGGCTGAGCGC 365
Db 1025 GCGGAGGCTGAGAGGCTTCTGCGCGCTTGGGAGCCCGGAGGCTGAGGCTGAGCGC 1084
QY 366 GCGGCTGAGCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 425
Db 1085 GCGGCTGAGCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1144
QY 426 TACCTGCGGCAACAGTGAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 485
Db 1145 TACCTGCGGCAACAGTGAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1204
QY 486 CGCGGCTGAGGAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 545
Db 1205 CGCGGCTGAGGAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1264
QY 546 GTGGCTCCAGCTGCGCTTACAGAGTGGGCGGCGGCTGTAACAGCTCGGCGTGC 605
Db 1265 GTGGCTCCAGCTGCGCTTACAGAGTGGGCGGCGGCTGTAACAGCTCGGCGTGC 1324
QY 606 ACTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 665
Db 1325 ACTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1384
QY 726 AGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 785
Db 1445 AGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1504
QY 786 GCTGCGCTGAGCGGAGCGGAGCGGCGGCTTGGGAGGCTGAGGCTGAGGCTGAGG 845
Db 1505 GCTGCGCTGAGCGGAGCGGAGCGGCGGCTTGGGAGGCTGAGGCTGAGGCTGAGG 1564
QY 846 ACGGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 905
Db 1565 ACGGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1624
QY 906 GCCACCTCTTGGAGGCTGCTCTCTGCGCAGGCGCACTCCACCATCGTGGCGCGC 965

Db 1625 GCCACCTCTTGAAGGAGTGGCTCTGGAACGGCCACTCCACCCATCCGTGAGCCG 1684
QY 966 CAGACACAGCGGAGCCGCCCATCAACATCGGGGCAACACGTCCTGAGAGCAGCCCTGT 1025
Db 1685 CAGACACAGCGGAGCCGCCCATCAACATCGGGGCAACACGTCCTGAGAGCAGCCCTGT 1744
QY 1026 CCCCCGGTGAAGCGGAGACCAAGCACTTCTCTACTCTTCAAGCGACAGAGAGCACTG 1085
Db 1745 CCCCCGGTGAAGCGGAGACCAAGCACTTCTCTACTCTTCAAGCGACAGAGAGCACTG 1804
QY 1086 CCGCCCTCTCTCTACTCTGAGCTCTGAGGCGGAGCGGAGCTGAGGAGGCTGAG 1145
Db 1805 CCGCCCTCTCTCTACTCTGAGCTCTGAGGCGGAGCGGAGCTGAGGAGGCTGAG 1864
QY 1146 GAGACCATCTTCTGAGGCTTCCAGGCTTGAATGCGAGGAGCTCCCGCAGGTTGCCCG 1205
Db 1865 GAGACCATCTTCTGAGGCTTCCAGGCTTGAATGCGAGGAGCTCCCGCAGGTTGCCCG 1924
QY 1206 CTGGCCCAAGCGCTAAGGCAAAAGCGGCGCTGTTCTGAGAGCTGCTGAGAAACAGCG 1265
Db 1925 CTGGCCCAAGCGCTAAGGCAAAAGCGGCGCTGTTCTGAGAGCTGCTGAGAAACAGCG 1984
QY 1266 CAGTGCCTTACAGGAGTGTCTCTCAAGACGACCTGCGCGCTGAGAGCTGAGTCAACCCA 1325
Db 1985 CAGTGCCTTACAGGAGTGTCTCTCAAGACGACCTGCGCGCTGAGAGCTGAGTCAACCCA 2044
QY 1326 GCAAGCCGCTGTCTGTGCTCCGAGAGAGAGCCCGCAGGCTGTGTGAGCGGCGCCGAGAGAG 1385
Db 2045 GCAAGCCGCTGTCTGTGCTCCGAGAGAGAGCCCGCAGGCTGTGTGAGCGGCGCCGAGAGAG 2104
QY 1386 GACACAGACCCCGCTGCTGTGTGAGCTGTCTCGGACAGACAGCAGCCCTGAGAGAG 1445
Db 2105 GACACAGACCCCGCTGCTGTGTGAGCTGTCTCGGACAGACAGCAGCCCTGAGAGAG 2164
QY 1446 TACGAGCTTGTGTGCGGAGCTGCTGCGCGGAGTGTGTGCGGAGCTGTGTGAGAG 1505
Db 2165 TACGAGCTTGTGTGCGGAGCTGCTGCGCGGAGTGTGTGCGGAGCTGTGTGAGAG 2224
QY 1506 CACAAAGAACGCGCTTCTCTCAAGAAACCAAGAGTTCATCTCTCTGAGAGAGCATGCG 1565
Db 2225 CACAAAGAACGCGCTTCTCTCAAGAAACCAAGAGTTCATCTCTCTGAGAGAGCATGCG 2284
QY 1566 AAGCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1625
Db 2285 AAGCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2344
QY 1626 AGAAGCCAGAGGAGTGTGTGCTGCGCGGAGAGACCGCTGTCTGTGAAGAGATCTG 1685
Db 2345 AGAAGCCAGAGGAGTGTGTGCTGCGCGGAGAGACCGCTGTCTGTGAAGAGATCTG 2404
QY 1686 GCCAAGTCTGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1745
Db 2405 GCCAAGTCTGACACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2464
QY 1746 TATGTCAAGGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTG 1805
Db 2465 TATGTCAAGGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTG 2524
QY 1806 AGAAGTTCGAAAGCAATGGAATCAGACAGCACTTGAAGAGGAGTGAAGTGAAGAGTGA 1865
Db 2525 AGAAGTTCGAAAGCAATGGAATCAGACAGCACTTGAAGAGGAGTGAAGTGAAGAGTGA 2584
QY 1866 TCGAAGCAGAGGTCAAGGACATCGGAGAACCGAGGCGCGCTGTGTGAGTCAAGCTC 1925
Db 2585 TCGAAGCAGAGGTCAAGGACATCGGAGAACCGAGGCGCGCTGTGTGAGTCAAGCTC 2644
QY 1926 CGCTTATCTCCCAAGCTGACGCGGCTGCGCGGCTGAGTGAATGAGTGAATGAGTGAATG 1985
Db 2645 CGCTTATCTCCCAAGCTGACGCGGCTGCGCGGCTGAGTGAATGAGTGAATGAGTGAATG 2704
QY 1986 GCCAGAAAGTTCGAG 2045
Db 2705 GCCAGAAAGTTCGAG 2764

QY 2046 TTCAAGGCTCAATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2105
Db 2765 TTCAAGGCTCAATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2824
QY 2106 GGCCTGAGAGATATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2165
Db 2825 GGCCTGAGAGATATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2884
QY 2166 CCGCGGCTGAGGAGTATTTGTGAAGTGAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 2225
Db 2885 CCGCGGCTGAGGAGTATTTGTGAAGTGAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 2944
QY 2226 CAGGACAGGCTCACAGAGGAGTATGCGAGATCATCAACCCAGAAACAGCTACTGCGTG 2285
Db 2945 CAGGACAGGCTCACAGAGGAGTATGCGAGATCATCAACCCAGAAACAGCTACTGCGTG 3004
QY 2286 CGTGGTATGCGGAGTGTCAAGAGGCGGCGCATGAGGAGCTTCCGAGAGGCTTCAAGAGC 2345
Db 3005 CGTGGTATGCGGAGTGTCAAGAGGCGGCGCATGAGGAGCTTCCGAGAGGCTTCAAGAGC 3064
QY 2346 CACGCTCTACCTTGAAGAGCTTCAAGGCTGATCAATGAGCAGATTGATGAGCTCACCTGAG 2405
Db 3065 CACGCTCTACCTTGAAGAGCTTCAAGGCTGATCAATGAGCAGATTGATGAGCTCACCTGAG 3124
QY 3125 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3184
Db 3185 AGCAGTGGCTCTTCAAGGCTTCTCAAGCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 3244
QY 3245 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3304
Db 3305 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3364
QY 3365 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3424
Db 3425 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3484
QY 3484 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3544
Db 3545 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3604
QY 3604 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3664
Db 3665 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3724
QY 3725 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3784
Db 3785 GAGACCAAGCCGCTGAGAGGAGTGCCTGCTCATCAGAGAGAGCTCTCCCTGAATGAGGCC 3844

Search completed: March 1, 2004, 22:58:46
Job time : 8185.61 secs

Db 2941 CGGCTCAGAGCTGGAGGAGAACATGGCTCCGAAACTTTGGGGTCTTGCGGCTGAATG 3000
QY 3008 TCACAGCCTGTTTCTGATTTGAGGTTGAACAGCTTCACAGCGGTGACCAACATCTA 3067
Db 3001 TCACAGCCTGTTTCTGATTTGAGGTTGAACAGCTTCACAGCGGTGACCAACATCTA 3060
QY 3068 CAAGATCCTGCTGAGGAGGTTGACAGTTTCAAGATGTTGCTGAGCTCCATTTC 3127
Db 3061 CAAGATCCTGCTGAGGAGGTTGACAGTTTCAAGATGTTGCTGAGCTCCATTTC 3120
QY 3128 TCAGCAAGTTTGAAGAAGCCCAATTTTCTGCGGTGATCTGACACGCTCCCT 3187
Db 3121 TCAGCAAGTTTGAAGAAGCCCAATTTTCTGCGGTGATCTGACACGCTCCCT 3180
QY 3188 CTGCTACTCATCTGAAAGCCCAAGAGGATGT-----GAGGTGCTGG 3237
Db 3181 CTGCTACTCATCTGAAAGCCCAAGAGGATGT-----GAGGTGCTGG 3240
QY 3238 CTTAGTGGAGAGAGTGTCTGCTGCTGTTAGTTAGTTGACAGAGTGAATCTG 3297
Db 3241 CGGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCAACAGCATTCCTGCTCAGCT 3300
QY 3298 GGTCTAGGAAGTTCTTACCTCTTTGACATCAGGAAGTGTTTAACCAACATCTG 3357
Db 3301 GACTCGACACCGTGTACCTTACGTGCACTCTGCGGTCACTAGAGACAGCCAGACGA 3360
QY 3358 GCTGCTGCTCCGCTCTCTGTTGGGTGAGCAGACCTGATGGAAGGACAGAGCTG 3417
Db 3361 GCTGAGTGGAGAGTCTCCGAGGAGCAGAGCTGAGCTGAGGCGGACCAACCGGCT 3420
QY 3418 TCTGGAGAGTGCATCTTCCACCTTGCT-----GCTG 3454
Db 3421 ACTGCCCTCAGACTTCAAGACATCTGAGCTGATGAGCACCGCCACAGCCAGCCGA 3480
QY 3455 GGGAGAGCTGGGGGCTGTGCTCTCTGTTTGGCCCATGATGAGGATTTGGGGGCTG 3514
Db 3481 GAGCAGACACAGACAGCTCTGTACGCGGCTTACGTCCAGAGGAGAGGCGGCT 3540
QY 3515 GCCTCTCTGTTTCCCTGTGTGAGGATTTGGGCTGTCTCCGTCATGCACTTAGGCT 3574
Db 3541 CACACCCAGGCGCGCACCGGTGGAGTGTGAGGCTGAGTGAATTTGGCCAGGCTG 3600
QY 3575 CTTGTGCAAGCCAGGCTAAG-----GGTTAGAGAGGAGCCAGGCCATCCCAAC 3629
Db 3601 CATGTCCGCTGAAGCTGATGTGCGGTGAGGCTGAGCGATGTCCAGCCAGGCT 3660
QY 3630 CCCTCTCAGAGAGAGAGCGGATATCACACAGAGCCCGCGCTCTGCTTC 3689
Db 3661 GAGTGTCCAGACACCTGCTGT-TCATTTCCCAAGGCTGGGCTGCTCCACCC 3719
QY 3690 CCAGTACCGTCTGCTGCTGAGACATTTGTCCAGCATCAGGAGTTTCTGATCGT 3749
Db 3720 AGGCGCAGCTTTCTCACAGAGCCGCTTCCATCCCATAGGAATAGTCATC 3779
QY 3750 CTGAATTCAGGCAATGCAAGCTGCGGTCCGAGCTTAACGCTTCACTTCTGTC 3809
Db 3780 CCGAGTTTGCATTTTCACTCT-----GCTGCTCTCTTTCCTCCACCC 3832
QY 3810 TTTCTGTGTGTGAGACCTTGAAGAGACCTGAGAGCTCTGGAATTTGAGTGACA 3869
Db 3833 CACCATCCAGTGAAGACCTTGAAGAGACCTTGAAGAGCTTGAAGTGACA 3892
QY 3870 AAGGTGTGCTGTGACAGAGGAGAGACCTGACCTGATGAGGCTCTGTGGTCAA 3929
Db 3893 AAGGTGTGCTGTGACAGAGGAGAGACCTGACCTGATGAGGCTCTGTGGTCAA 3952
QY 3930 ATTGGGGGAGGTGCTGTGGAGTAATAATGAAATATATATAGTTTCAAGTTTGA 3989
Db 3953 ATTGGGGGAGGTGCTGTGGAGTAATAATGAAATATATAGTTTCAAGTTTGA 4012
QY 3990 AAA 3992
Db 4013 AAA 4015

QY 168 TGGCGCTGATGAGCGCGGAGACCCGCGCTTTCCGCGCGCTGATGAGCCAGTGCCTG 227
DB 126 TCCGCGCTGACACCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 185
QY 228 GTGTGATGCGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 287
DB 186 CGGCGGACAGCG 245
QY 288 TGGCTTGAAGAGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 347
DB 246 CCG 305
QY 348 GTGTGCGCGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 407
DB 306 TGTGCG 364
QY 408 ACCACGAGCGTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 467
DB 365 CTGCG 424
QY 468 GCGTGGGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 527
DB 425 CCG 484
QY 528 TGGCGCGCTTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 567
DB 485 TCCGCGCTTGTGTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 524

RESULT 5

US-10-767-471-10913/c
; Sequence 10913, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10913
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(40000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-767-471-10913

Query Match 1.4%; Score 56.8; DB 6; Length 40000;
Best Local Similarity 48.2%; Pred. No. 0.0042;
Matches 160; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

QY 1 GTTTAGAGCAGCGCTGCTGTGCGAGCGTGAAGACCCCTGAGCCCGGCAACCCCG 60
DB 24768 GTGCG 24709
QY 61 CGATGCGCGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 24708 CGGTGAGAGCG 24649
QY 121 AGGTGCG 180
DB 24648 GCG 24589
QY 181 AGCG 240
DB 24588 CCTTACCTGCTT 24529
QY 241 GGGAGCAGCG 300

DB 24528 CGCGGCGCTTGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24469
QY 301 TGTGCG 332
DB 24468 CGCGGCGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24437

RESULT 6

US-10-767-701-4866
; Sequence 4866, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21 (53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4866
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS92278_1
US-10-767-701-4866

Query Match 1.4%; Score 54.6; DB 6; Length 666;
Best Local Similarity 46.8%; Pred. No. 0.0025;
Matches 240; Conservative 0; Mismatches 269; Indels 4; Gaps 2;

QY 228 GTGTGCGCGCTTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 287
DB 38 GCGCGCGCTTGTGAGAGCGCTTCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 97
QY 288 TGGCTTGAAGAGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 347
DB 98 GCGCGCGAGCG 157
QY 348 GTGTGCGCGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 407
DB 158 GCGCGCGAGCG 217
QY 408 ACCACGAGCGTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 467
DB 218 TCCCTCCG 274
QY 468 GCGTGGGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 527
DB 275 CCGCGCGCGCGCTTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 334
QY 528 TGGCGCGCTTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 587
DB 335 GTGCG 394
QY 588 TACCACTGCG 647
DB 395 TCCG 453
QY 648 GGTGTGAAGTGCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 707
DB 454 CCG 513
QY 708 CTGCGAGCG 740
DB 514 CCGGCGCGCTTCCGAGAGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546

RESULT 7

US-10-767-701-4186
; Sequence 4186, Application US/10767701
; GENERAL INFORMATION:

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 4186
LENGTH: 584
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS75356_1
US-10-767-701-4186

Query Match 1.4%; Score 54.2; DB 6; Length 584;
Best Local Similarity 45.7%; Pred. No. 0.0029;
Matches 188; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

QY 20 CTTGCTGCGAGCGTGGGAAACCTTGGCCCGGACACCTCCCGGATGCGCGCTCCCG 79
DB 144 CCCCCCCCCCGCCGACCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 203
QY 80 CTGCGGAGCGCGTGGCGCTCCCGTGGCGAGCACTACCGGAGTGGCTGGCGCGCGCG 139
DB 204 CCGCCCG 263
QY 140 GTTGTGCGCGCGCTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 199
DB 264 GCG 323
QY 200 TTTCGCGCGCGCGTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 259
DB 324 CCG 383
QY 260 CCG 319
DB 384 GCTCCCG 443
QY 320 GAGGCTGTGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 379
DB 444 CCGCGAGGCGTCACTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 503
QY 380 GCG 430
DB 504 CGACCG 554

RESULT 8
US-10-767-701-2473/c
Sequence 2473, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 2473
LENGTH: 570
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
NAME/KEY: unsure
LOCATION: (1) - (570)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41826_1

US-10-767-701-2473

Query Match 1.3%; Score 53.4; DB 6; Length 570;
Best Local Similarity 52.3%; Pred. No. 0.0042;
Matches 137; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

QY 574 GCGGCG 633
DB 260 GCGGCG 201
QY 634 GTG-GACCCGAGAGCGTGTGGATGCGGAGCGCGCGCGCGCGCGCGCGCGCGCG 692
DB 200 GTGCG 141
QY 693 GGGGTCCCGTGGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 752
DB 140 GGGGCG 81
QY 753 AGTCTGCGGTGCG 812
DB 80 CCG 21
QY 813 GTTGGCGAGGCGTCTGGG 831
DB 20 CCGGCG 2

RESULT 9
US-10-767-701-4466
Sequence 4466, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 4466
LENGTH: 580
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS80039_1
US-10-767-701-4466

Query Match 1.3%; Score 53.4; DB 6; Length 580;
Best Local Similarity 52.3%; Pred. No. 0.0043;
Matches 147; Conservative 0; Mismatches 126; Indels 8; Gaps 1;

QY 12 CCGTGCCTCTGCGCGAGCGTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 71
DB 125 CCG 184
QY 72 GCTCCCGCTGCGGAGCGTGGCGCTCCCTGCTGCGGAGCGCACTACCGCGAGTGTGCGG 131
DB 185 CCG 244
QY 132 CTGCGGAGCGTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 191
DB 245 GGGGCG 304
QY 192 CCGGCGCGCTTCCGCGCGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 251
DB 305 CTTGCTCTCT-----GCTGCTGCGCGCGTCTCCCGCGCGCGCGCGCGCGCGCG 356
QY 252 CCG 292
DB 357 CTCCCG 397

RESULT 10
US-10-767-701-9739
; Sequence 9739, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 9739
; LENGTH: 1092
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAV03-CLUS33367_1
US-10-767-701-9739

Query Match 1.3%; Score 53.4; DB 6; Length 1092;
Best Local Similarity 45.0%; Pred. No. 0.0055;
Matches 201; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

QY 39 GCGCTGCGCCCGCCGACCCCGGATGCGCGCGCTCCCGCTGCGGACCGTGGCTTC 98
DB 177 GCGCTGCGCGCGCGCGCTCCCGACCCCTCCCGCGCGCGCTCCCGCTCCCGCGCC 236
QY 99 CTGCTGCGACGACCTACCGGAGTGTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 158
DB 237 CG 296
QY 159 CCG 218
DB 297 CCG 356
QY 219 CAGTGTGCTGTGCTGCG 278
DB 357 CG 416
QY 279 CAGTGTGCTGTGCTGAGGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 338
DB 417 CCG 476
QY 339 GCGAAGAGTGTGCTGCG 398
DB 477 GTGCTGTGCTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 536
QY 399 GAGGCTTACACACGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 458
DB 537 CCG 596
QY 459 GCGAGCG 485
DB 597 GCG 623

RESULT 11
US-10-767-701-30024
; Sequence 30024, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 30024
; LENGTH: 522

TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: 9848339
US-10-767-701-30024

Query Match 1.3%; Score 53.2; DB 6; Length 522;
Best Local Similarity 49.4%; Pred. No. 0.0045;
Matches 167; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

QY 122 GGTGTGCG 181
DB 56 GAGCG 115
QY 182 GCG 238
DB 116 GCG 175
QY 239 CTGAGACGACG 298
DB 176 GCTGT 235
QY 299 GCTGT 358
DB 236 CATGCG 295
QY 359 CAGCTTGTGCG 418
DB 296 CGACCTGCG 355
QY 419 GCGGAGT 456
DB 356 GCTGT 393

RESULT 12
US-10-767-701-8805
; Sequence 8805, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 8805
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAV03-CLUS56975_1
US-10-767-701-8805

Query Match 1.3%; Score 53.2; DB 6; Length 667;
Best Local Similarity 45.0%; Pred. No. 0.005;
Matches 199; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

QY 126 CTGCG 185
DB 23 CTCTCTGT 82
QY 186 GCGGACCG 245
DB 83 CACCAACCG 142
QY 246 GCAAGCG 305
DB 143 GCGT 202
QY 306 GCGGAGT 365

QY 40 CCGTCGAGCCCGAGCAACCCCGAGAAAGCGCGGCTCCCGCTGCAGACCCTGAGCTCC 99
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QY 100 TGTGTGGCAGCCACTACCGGAGGTGTGTCGCTGGCCACGTTGTGCGGCGCTTGGAGC 159	
74 CCGCGCGCGCGCGCGCAAGCCCGCGCGCGCGCGCGCGCGCAAGCTCCCGCGCGCTCCCGCGCGCGC 133	
QY 160 CCGAGGAGCTGAGCGGCGCTGTGTGCAAGCGCGGAGAACCGCGGCGCGTTTCCGCGCGTGTGTGCGCC 219	
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QY 220 AGTGCCTGTGTGTGCGCTGTGCTCTTGAGACGACAGCGCGCGCGCGCGCGCGCTCTTCCGCC 279	
194 CGCGCTGCGCGCGCGCGCGCTCG 253	
QY 280 AGGTGTCTGTGCTGAAAGAGAGCTGTGTGCGCCCAAGTGTGTGCAAGGCTGTGTGAGAGCGGCG 339	
Db 254 CGCGCGCGCGCGCAACCGAGTGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTGCC 313	
340 CGAAGAACGTGTGTGCGCTTTCGCGCTTTCGCGCTTGTG---GACGAGGCGCGCGAGGAGCGCC 395	
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5668 TGGGCTTCGCGGAGTTCGCGGACGACCGGCTCGGCGCGCGTCTCC 5693
548 GGCTCCAGCTGGGCTTACAGGTGTGGGGCGCGCGGTATACAGCTTGGCGGTGCAC 607

Db 5608 GCGCCGCTCTTCCCTGAGGAGCTG---CCGCTCCGCTTGGCTCTTCCGCGAGGAC 5552
QY 608 TCAGGC--CCGCCCCCGCCACAGCTATGAGACCCCGAGAGGGCTGTGGATGCGAACGG 665
Db 5551 GCAGCGGGGGGCTCTCTCCGCGAGCTGCGGAAACGGCCGCTCTGAGCTTCCAGCTCT 5492
QY 666 GCTTGAAACATAGGCTGAGGAGGCGGGGTCCTCCCTGAGCTGCTG 712
Db 5491 GCTTGACTTCTGCTGTGAGGCGAGCTCTCTCAGCTTCCGCTG 5445

RESULT 15

US-10-767-471-603/c
; Sequence 603, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 603
; LENGTH: 11409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-603

Query Match

1.3%; Score 52; DB 6; Length 11409;
Best Local Similarity 44.2%; Pred. No. 0.028;

Matches 184; Conservative 6; Mismatches 226; Indels 0; Gaps 0;

QY 17 CGTCTGCTGCGCAGTGGAGACCTTGGCCCGCCGACCCCGCGATGCGCGCTCC 76
Db 1943 CTTCTTCACAGACTGCTGCTGCTCTCCCTGCTCTGCTGCGCCGACCGGATCA 1884
QY 77 CCGCTGCGGAGCGGTGCTCCCTGCTGCGGAGCACTACCGGAGGTGCTCCGCTGAG 136
Db 1883 ACTCTGCTCCGCGGCGGAGCGCTGCTGCGGAGCTTCCGCGAGCTGCGCTGCTCT 1824
QY 137 CAGCTTGTGCGGCGCTGCGGCGCCGAGGAGCTGCGGAGTGAAGCGGAGACCGAGC 196
Db 1823 CAGCTTGTGCTGAGCAGCTCCGCTGCGGAGCGGCTGCTCTGCGGAGCTGCTCT 1764
QY 197 GGTCTTCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256
Db 1763 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1704
QY 257 CCGCGCGCGCGCTCTCTCTGCGGAGGAGTGTCTGCTGAGAGAGTGTGAGCCGAGTGT 316
Db 1703 TCTGCTGCGSACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1644
QY 317 GCGAGAGCTGTGAGAGCGGCGGCGGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCT 376
Db 1643 GCGAGGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1584
QY 377 CCGGCG 432
Db 1583 GTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1528

Search completed: March 1, 2004, 23:56:49
Job time: 60.9188 secs

JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1584)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Cvello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Source location/Qualifiers
1..1584
/organism="Pan troglodytes"
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ORIGIN
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Best Local Similarity 83.1%; Pred. No. 4.3e-154;
Matches 1317; Conservative 0; Mismatches 267; Indels 0; Gaps 0;
QY 1636 GGGTTGCTGTTGTTCCGGCCGAGAGACCGCTCTGGCTAGAGATCTTGGCCAACTTCC 1695
DB 1 GGGTTGCTGTTGTTCCGGCCGAGAGACCGCTCTGGCTAGAGATCTTGGCCAACTTCT 60
QY 1696 TGCACTGCTGATGAGTGTGTAGCTGCTGAGCTGCTGAGTCTTTTATATGACAG 1755
DB 61 TGCACTGCTGATGAGTGTGTAGCTGCTGAGCTGCTGAGTCTTTTATATGACAG 120
QY 1756 AGACCAAGTTTCAAAAAGAGAGCTCTTTTCTACCGGAAGAGTGTCTGAGCAAGTTGC 1815
DB 121 AGACCAAGTTTCAAAAAGAGAGCTCTTTTCTACCGGAAGAGTGTCTGAGCAAGTTGC 180
QY 1816 AAAGCATTTGATTCAGACAGCACTTGAAGAGAGTGTGAGCTGGGAGAGTGTGGAAGAG 1875
DB 181 AAAGCATTTGATTCAGACAGCACTTGAAGAGAGTGTGAGCTGGGAGAGTGTGGAAGAG 240
QY 1876 AGGTCAAGCAGCATTCGGAAAGCCAGCCCGCTCTGCTGACGTCCAGACTTCGCTTATCC 1935
DB 241 AGGTCAAGCAGCATTCGGAAAGCCAGCCCGCTCTGCTGACGTCCAGACTTCGCTTATCC 300
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DB 301 CCAAGCTGACGGGCTGCGGCGCATTTGTGAACATGACTAAGTGTGGGAGCCAGAACGT 360
QY 1996 TCCGACAGAAAAGAGGCGCAGCGTCTCACTCGAGGGTGAAGCACTGTTCAACGCTGC 2055
DB 361 TCCGACAGAAAAGAGGCGCAGCGTCTCACTCGAGGGTGAAGCACTGTTCAACGCTGC 420
QY 2056 TCAACTACGAGCGGCGCGGCGCGCTCTGAGAGCTCTGAGTGTGGGCTGGAGCG 2115
DB 421 TCAANNACAGCGGCGCGGCGCGCTCTGAGAGCTCTGAGTGTGGGCTGGAGCG 480
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DB 481 ATATTCACAGGCTCTGAGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 2176 AGCTGACTTTGTCAAGTGTGATGTGACGGGCGCGTACAGACCATCCCCACAGACAGG 2235
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DB 601 NNN 660
QY 2296 CCGTGTTCAGAGGCGCGCATGTGGGCAAGTCCGGAAGGCTTCAAGAGCCAGCTCTCTA 2355
DB 661 NNN 720

QY 2356 CCTTGACAGACCTCCAGCGGTACATGAGCAGTTGCTGCTCACTCGAGGACCAAGCC 2415
DB 721 CCTTGACAGACCTCCAGCGGTACATGAGCAGTTGCTGCTCACTCGAGGACCAAGCC 780
QY 2416 CGCTGAGGAGTCCGCTGCTCATTCAGACAGAGCTCTCCCTGAATGAGGCGAGAGTGGCC 2475
DB 781 CACTGAGGAGTCCGCTGCTCATTCAGACAGAGCTCTCCCTGAATGAGGCGAGAGTGGCC 840
QY 2476 TCTTGAAGTCTCTTACGCTTACATGAGCAGCAAGCGCGTGGCATCAGGGGCAAGTCT 2535
DB 841 NNN 900
QY 2536 AGCTCAGTGCAGAGGAGTCCCGAGAGGCTCATCTCTCCAGCTGCTGAGAGCTGT 2595
DB 901 AGCTCAGTGCAGAGGAGTCCCGAGAGGCTCATCTCTCTCCAGCTGCTGAGAGCTGT 960
QY 2596 GCTACGGGAGATGAGAGACAGCTGTTTGGGGGATTCGGCGGAGCGGGTCTCTCTGC 2655
DB 961 GCTACGGGAGATGAGAGACAGCTGTTTGGGGGATTCGGCGGAGCGGGTCTCTCTGC 1020
QY 2656 GTTGTGATGATTTCTTGTGTGACACCTCACTCACCCAGCAAAACCTTCTCA 2715
DB 1021 GTTGTGATGATTTCTTGTGTGACACCTCACTCACCCAGCAAAACCTTCTCA 1080
QY 2716 GACCTCTGTCAGAGTGTCTCTGATGATGAGTGTGATGAGTGTGATGAGTGTGATGAG 2775
DB 1081 NGACCTCTGTCAGAGTGTCTCTGATGATGAGTGTGATGAGTGTGATGAGTGTGATGAG 1140
QY 2776 TGAATCTCTCTGTAAGACAGAGGCTGGGTGACAGGCTTTTGTTCAGATGCGGCGCC 2835
DB 1141 TGAATCTCTCTGTAAGACAGAGGCTGGGTGACAGGCTTTTGTTCAGATGCGGCGCC 1200
QY 2836 ACGGCTATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2895
DB 1201 ACGGCTATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 2896 ACTACTCAGCTATGCGCGAGCTCCATCAGAGCAGTCTCACTTCAACCGGCGCTTCA 2955
DB 1261 ACTACTCAGCTATGCGCGAGCTCCATCAGAGCAGTCTCACTTCAACCGGCGCTTCA 1320
QY 2956 AGCTGAGGAGACATGCTGTGCAAACTTTTGGGAGTCTTGGGCTGAGTGTCAAGCC 3015
DB 1321 AGCTGAGGAGACATGCTGTGCAAACTTTTGGGAGTCTTGGGCTGAGTGTCAAGCC 1380
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DB 1381 TGTTCCTGAGTTTGCAGTGAAGAGCTCCAGACGAGTGTGACCAATCTTACAGAGTCC 1440
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QY 3136 TTTGGAAGAACCCCAATTTTCTGCGGCTGATCTTGAAGAAGCTCTCTGCTACT 3195
DB 1501 TTTGGAAGAACCCCAATTTTCTGCGGCTGATCTTGAAGAAGCTCTCTGCTACT 1560
QY 3196 CCATCTCTGAAGCAAGACGAG 3219
DB 1561 CCATCTCTGAAGCAAGACGAG 1584

RESULT 3
AY407351 1835 bp DNA linear GSS 15-DEC-2003
LOCUS Mus musculus TERT gene, VIRUTAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY407351
VERSION AY407351.1 GI:39763322
KEYWORDS GSS,
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1835)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tannenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.
inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL
PUBMED
14671302
2 (bases 1 to 1835)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tannenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
source
1.1835
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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ORIGIN
Query Match 20.2%; Score 810.2; DB 29; Length 1835;
Best Local Similarity 64.5%; Pred. No. 6,7e-92;
Matches 1088; Conservative 0; Mismatches 560; Indels 7; Gaps 2;

1636 GGGTGGCTGTGTGTCGCGCCGAGACACCGTCTGCGTGAAGAGATCTGCGCAAGTTC
1696 TGCACTGCGTGAATGATGTGTGATGCTGCTGAGCTGCTGCTTTTATATGCAAG
61 TGTTCGCTGATGACACATATAGTGTACAGCTGTTAGTCACTTTTATCATCAG 120
1756 AGACACGTTTAAAGAAACAGGCTTTTCTACCGAAGAGTCTGAGCAAGTTC 1815
121 AGAGCATTCCAGAGAAACAGGCTTTTCTACCGTAAAGTGTGAGCAAGTTC 180
1816 AAGCATTGGAATACACAGCACTTGAAGAGGTGAGCTGGGAGAGCTTCGAGAG 1875
181 AGAGCATTGAGTACAGCAACCTTGAAGAGTGTGAGAGAGCTGTACAAAGAG 240
1876 AGGTCAAGGAGCATCGGAGAGCCGAGCCGCTGCTGACGTCAAGCTTCGCTTCA 1935
241 AGGTCAAGGAGCATCGGAGAGCCGAGCCGCTGCTGACGTCAAGCTTCGCTTCA 300
1936 CCAAGCTTACAGGAGCTGCGCGGATGTGTAATGATGATGATGATGATGATGAT 1995
301 CCAAGCTTACAGGAGCTGCGCGGATGTGTAATGATGATGATGATGATGATGAT 360
1996 TCCGAG-AGAAAAGAGGCGAGAGCTTCACTCGAGAGGTGAAGCACTGTCAGCTG 2054
361 TGGGAGAGAGAGAGAGAGGCGGAGATTTCAACAGAGCTCTCAAGAGCTTCGAG 420
2055 CTCAATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2114
421 CTCAATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
2115 GATATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2174
481 GACATCTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
2175 GAGCTGATCTTTGTCAAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2234
541 AGGATGATCTTTGTGAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 600

2235 CTACAGAGGTGATTCGAGAGATCATCAACCCAGAACGTAAGTGGCTGGTAT 2294
601 NNN 660
2295 GCCGTGTCCAGAGAGGCGGCGCATGGGCAAGTCCGAGAGGCTTCAAGAGCCAG 2354
661 NNN 720
2355 ACCGTGACAACTCCAGAGGCTGATGCAAGTGTGTGCTGATGCTGAGGAGGAGG 2408
721 ACCGTGACAACTCCAGAGGCTGATGCAAGTGTGTGCTGATGCTGAGGAGGAGG 780
2409 ACCAGCCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2468
781 GCCAGTGCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
2469 AGTGGCTCTTCAAGCTTCTTCAAGCTTCTTCAAGCTTCTTCAAGCTTCTTCAAG 2528
841 NNN 900
2529 AAGTCTACGTCAGAGTGCAGAGGAGATCCGAGAGGCTCAGTCTTCAAGCTTCTG 2588
901 NNGTGTATAGAGAGTGCAGAGGAGATCCGAGAGGCTCAGTCTTCAAGCTTCTG 960
2589 AGCTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2648
961 AGTGTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
2649 CTCTGCGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2708
1021 CTCTGCGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
2709 TTCTCAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2768
1081 TTCTCAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
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1141 ACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
2829 CCGAGCCAGGCTATTTCCCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2888
1201 CCGAGCCAGGCTATTTCCCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
2889 CAGAGGAGTACTCAGAGTATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2948
1261 TTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
2949 GAGTTCAGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3008
1321 GTCCTCAAGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
3009 CAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3068
1381 CAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
3069 AAGATCTCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3128
1441 AAGATCTCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
3129 CAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3188
1501 CAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
3189 TGCTACTCATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3223
1561 TGCTACTCATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1595

RESULT 4
BM453198
LOCUS
BM453198 925 bp mRNA linear EST 05-FEB-2002

DEFINITION	AGENCOURT_6387556 NIH_MGC_1 Homo sapiens cDNA clone IMAGE:552984					
ACCESSION	5', mRNA Sequence.					
VERSION	BM453198					
KEYWORDS	BM453198.1 GI:16502238					
SOURCE	EST.					
ORGANISM	Homo sapiens (human)					
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 925) NIH-MGC http://mgs.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)					
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)					
COMMENT	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LLM12208 row: p column: 01 High quality sequence stop: 646. Location/Qualifiers 1. 925 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5529840" /feature_type="leiomysarcoma" /lab_host="DH10B (phage-resistant)" /clone_1ib="NIH MGC 71" /note="Organ: uterus; Vector: PCMV-SPORE6; Site 1: Notif; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."					
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Best Local Similarity	99.2%; Pred. No. 2.7e-91;					
Matches 821; Conservative	0; Mismatches 5; Indels 2; Gaps 1					
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Oy	2	GCGCCAGAACCGGCGCCTGAGCTGTACTTTGTCAAGTGATGACGGGCGGTACGA	61			
Oy	2216	CACCATCCCCAAGACAGGCTCACGAGAGTCATGCCAGATCATCAAACCAGAAC	2277			
Dn	62	CACCATCCCCAAGACAGGCTCACGAGAGTCATGCCAGATCATCAAACCAGAAC	121			
Oy	2276	GTACTCGTGCCTGGTATGCGGTGATCGGTGATCAAGAGCGGCCATGGGAGTTCGCAAGG	2333			
Dn	122	GTACTCGTGCCTGGTATGCGGTGATCGGTGATCAAGAGCGGCCATGGGAGTTCGCAAGG	181			
Oy	2336	CTTCAAGAGCACGCTCTTAATTGACAGACCTCAAGCTTCAATGCGACATTTGCTGCG	2399			
Dn	182	CTTCAAGAGCACGCTCTTAATTGACAGACCTCAAGCTTCAATGCGACATTTGCTGCG	241			
Oy	2396	TCACTCGACAGAGACCAAGCGCGCTAGAGAGATGCGGTGATCATGACAGAGCTCCCT	2455			
Dn	242	TCACTCGACAGAGACCAAGCGCGCTAGAGAGATGCGGTGATCATGACAGAGCTCCCT	301			
Oy	2456	GAATGAGGCGACAGTGGGCTTTTGACAGCTTTCTTACGCTTCAATGTCACAAGCGCGT	2511			
Dn	302	GAATGAGGCGACAGTGGGCTTTTGACAGCTTTCTTACGCTTCAATGTCACAAGCGCGT	361			
Oy	2516	GCGCATCAAGGAGCAAGTCTCAAGTCAATGCAATGCAAGGATCCCGCAGGAGCTCATCTTC	2575			
Dn	362	GCGCATCAAGGAGCAAGTCTCAAGTCAATGCAATGCAAGGATCCCGCAGGAGCTCATCTTC	421			
Oy	2576	CACGCTGCTCTGACAGCTGTGTGATAGGAGCATAGAGAAACAAGCTGTTGGCGGATTCG	2633			
Dn	422	CACGCTGCTCTGACAGCTGTGTGATAGGAGCATAGAGAAACAAGCTGTTGGCGGATTCG	481			

QY	2636	GCGGGACGGGTGTGCTTCCTGCGTGTGGAGGATGATTTCTCTGTGGTGGACACTCACTCAAC	2659
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QY	2656	CCAGCGGAAAACCTTCTCTCAAGAACCTTGCTCCAGGTGTCTCTAGATATGGCTCGTGT	2755
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Db	662	TTTTGTTCAGATGCGGCGCCACAGGCGCTATTCCTCCGTGTGCGGCGCTGTGCTGATACCG	721
QY	2876	GACCTTGAAGGTGTGAAGAGCAGATCTCTCAGCTATGCCCCGGAACCTCCATCAGAGCACTCT	2935
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QY	2936	CACCTTCACACCGCGCTTCAA--GGCTGGAGGAACAATGCGTCCGAAA	2981
Db	782	CACCTTCACACCGCGCTTCAAAGGCTGGAGGAACAATGCGTCCGAAA	829
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DEFINITION	RS117589 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BG198331		
VERSION	BG198331.1	GI:13720018	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 813)		
AUTHORS	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,		
	Cain,S., Lerventhal,C., Thornton,M., Ramachandran,R.,		
	Whittington,J., Lermer,L., Costanzo,D., McElligott,K., Boorer,S.,		
	Mays,R., Smith,E., Veloso,N., Kliska,A., Hess,J., Cothren,K., Lo,K.,		
	Offendackher,J., Danzig,J. and Ducat,M.		
	Creation of genome-wide protein expression libraries using random		
	activation of gene expression		
	Nat. Biotechnol. 19 (5), 440-445 (2001)		
JOURNAL	Nat. Biotechnol.		
MEDLINE	21227151		
PIRBASE	11329013		
COMMENT	Contact: Scott J. Cain		
	Atherys, Inc.		
	3201 Carnegie Ave, Cleveland, OH 44115, USA		
	Tel: 216 431 9900		
	Fax: 216 361 9596		
	Email: scain@atherys.com		
FEATURES	High quality sequence stop: 533.		
Source	Location/Qualifiers		
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	/note="See 'Creation of Genome-wide Protein Expression		
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	method was used, these sequence tags are not necessarily		
	expressed in HT1080 under normal circumstances."		
ORIGIN			
Query Match	17.6%	Score 706	DB 12; Length 813;
Best Local Similarity	98.2%	Prid. No. 8,6e-79;	
Matches 723;	Conservative	0;	Mismatches 12;
			Indels 1; Gaps 1;

QY 3090 TACAGTTTACGATGTGTGTCAGCTCCCATTTTCATCAGCAAGTTTGAAGAACCC 3149
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 QY 3150 ACATTTTCTGCGCGCTGATCTCTGACAGCGCTCCCTCTGCTACTTCCATCTGAAAGCC 3209
 DB 689 ACATTTTCTGCGCGCTGATCTCTGACAGCGCTCCCTCTGCTACTTCCATCTGAAAGCC 630
 QY 3210 AAGACGACAGTATGTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3269
 DB 629 AAGACGACAGTATGTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 570
 QY 3270 TAGTGTGTGTCAGAGACTGATGTAATCTGGGCTTACGAAAGTTCTTACCCCTTTTGCATCA 3329
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 DB 209 CCTCTGAGAGAGAGAGGCGCGATATCCAGCAGAGAGGCGCGCGCTGCTGCTGCTGCTGCTGCT 150
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 DB 149 CCACTGACCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 90
 QY 3750 CTGAATTTCAAGCATTCGACACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3809
 DB 89 CTGAATTTCAAGCATTCGACACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 30
 QY 3810 TT-TCTGTGTGTGGA 3824
 DB 29 TTAACGTGTGTGGA 14
 RESULT 6 851 bp mRNA linear EST 15-JUL-2003
 BUI02370
 LOCUS
 DEFINITION UT-M-F10-bx-f-12-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA clone
 IMAGE:6400523 5, mRNA sequence.
 ACCESSION BUI02370.1 GI:23627105
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST.
 Mus musculus (house mouse)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 851)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: gsabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa

FEATURES

source

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIN at:
<http://image.lnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pyx-5.

Location/Qualifiers

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 /tissue_type="whole brain"
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 /lab_host="DH10B (T1 phage resistant)"
 /clone_id="NIH_BMAP_F10"
 /note="Organ: Brain; Vector: pyx-Anc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 to the protocol of Benton and Davis (1978) using a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pyx-Anc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is GAGCCAGGAC. This library was created for the University
 Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Query Match 12.5%; Score 500.2; DB 13; Length 851;
 Best Local Similarity 75.1%; Pred. No. 4.1e-53;
 Matches 638; Conservative 0; Mismatches 206; Indels 6; Gaps 1;

QY 2269 AGAAGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2328
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 QY 2329 GCAAGGCTTCAAGAGCAGCGCTCTACTGACAGAGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2388
 DB 61 ACAAGTCTTTAGAGAGAGAGTCAACACCTCTCTGACCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 120
 QY 2389 TGTGGCTCACTGAG-----GAGACAGCCCGCTGAGGAGATGCGTGTGATGAGC 2442
 DB 121 TCTTAAGCATCTGACAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 2443 AGAGCTCTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2502
 DB 181 AGAGCATCTCTATGATGAG 240
 QY 2503 GCCACACGCGCTGCGATAGAGGAGCAAGTCTTACGTCAGTGCAGAGGAGATCCCGCAGG 2562
 DB 241 GTCAAGATGCTGTAAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 2563 GCTCATCTCTCTGACAGCTGCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2622
 DB 301 GCTCAGACCTATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
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QY 2743 ATGCTCTGCTGTGACCTTGGGAGAGACAGTGTGAACTTCCCTGTAGAGACGAGGCC 2802
 Db 481 ATGGGTGATGATTAACCTTGACAGAGACAGTGTGAACTTCCCTGTAGAGACCTGTACCC 540
 QY 2803 TGGGTGACGAGGCTTTTGTTCAGATGCGGGCCCAACGGCCCTATCCCTGTGTGGGCTCG 2862
 Db 541 TGGGTGATGACCTTCCATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 2863 TGCTGATACCCGAGCCCTGAGAGTGCAGAGCACTACTCCAGCTATGCGGAGCTTCCA 2922
 Db 601 TGCTGACACTCAACTTTGGAGGTGTTCTGTGACTACTCAGGTTATGCCAGACTTCAA 660
 QY 2923 TCAGAGCAGTCTCACTTCAACCGGCTTCAAGGTGGAGGAGGAGGAGGAGGAGGAGG 2982
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 QY 2983 TCTTTGGGCTCTTGGGCTGAGAGTGTTCAGAGTGTTCAGAGTGTTCAGAGTGTTCAGAG 3042
 Db 721 TCTGTGCTGCTTGGGCTGAGAGTGTTCAGAGTGTTCAGAGTGTTCAGAGTGTTCAGAG 780
 QY 3043 TCCAGAGCTGTGACCAATCTACAAATCTCTCTGCTGACGAGGCTGACAGTGTTCAGAG 3102
 Db 781 TCCAGAGCTGTGACCAATCTACAAATCTCTCTGCTGACGAGGCTGACAGTGTTCAGAG 840
 QY 3103 CATGTGTCT 3112
 Db 841 CATGTGTCT 850

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 DEFINITION 5', mRNA sequence.

ACCESSION BM824748
 VERSION BM824748.1 GI:19181161
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS

Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongseung@mail.kribb.re.kr
 Plate: 99 row: E column: 07
 High quality sequence stop: 492.
 Location/Qualifiers

FEATURES

source

1. 492
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 /note="Organ: Stomach; Vector: pT773-Pac; Site 1: EcoRI;
 Site 2: NotI. The S22SNU16 library was contributed by the
 Soares laboratory and it was constructed as described by
 Bonaldo, M.F., Lemon, G. and Soares, M.B. (1996), Genome
 Research 6(5): 791-806. RNA was prepared from harvested

ORIGIN

Query Match 11.1%; Score 445; DB 12; Length 492;
 Best Local Similarity 100.0%; Pred. No. 3,7e-46;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

cells of SNU-16 culture. SNU-16 cell was obtained from
 Korean Cell Line Bank (KCLB). SNU-16 was established from
 ascitic fluids of Korean patients by Park J.G. et al.
 (1990), Cancer Res 50: 2773-2780."

QY 2775 GTGAATCCCTGAG 2834
 Db 1 GTGAATCCCTGAG 60
 QY 2835 CACGGCTATTCCTCTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2894
 Db 61 CACGGCTATTCCTCTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
 QY 2895 GACTACTCAGCTATGCGGAGCTCCTGATACCGGAGCTTCAACCGGAGCTTC 2954
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 QY 2955 AAGGCTGGAG 3014
 Db 181 AAGGCTGGAG 240
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 QY 3135 GTTGGAG 3194
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 QY 3195 TCCATCTGAG 3219
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RESULT 8
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 mRNA sequence.

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 VERSION AA281296.1 GI:1924194
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE 1 (bases 1 to 389)
 JOURNAL NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncigap>.
 COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: gsapbs-remail.nih.gov
 This clone is available royalty-free through LBNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.
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 Location/Qualifiers

FEATURES

source

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 /clone="IMAGE:712562"

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 VERSION CF531121.1
 KEYWORDS EST
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 ORGANISM Mus musculus
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 1 (bases 1 to 688)
 REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mouse1.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES

source
 Location/Qualifiers

1..688
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 /note="Organ: Brain; Vector: pYX-Asc; Site:1: EcoR I; Site:2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., Program coordinator."

ORIGIN

Query Match 8.6%; Score 346.2; DB 14; Length 688;
 Best Local Similarity 73.9%; Pred. No. 7.3e-34;
 Matches 438; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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 Db CAGCCGATACCGGAGGTGTGCGCGCTGCGCACTTGTGCGCGCGCTGCGCGCG 182
 123 CAGCGCATACCGGAGGTGTGCGCGCTGCGCACTTGTGCGCGCGCTGCGCGCG 182
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 LOCUS U1-M-FYO-cgp-19-0-U1.r1 NIH-BMAP FYO Mus musculus cDNA clone
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 VERSION CF531069.1 GI:34583033
 KEYWORDS EST
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 649)
 REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mouse1.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES

source

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
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 /clone_lib="NIH-BMAP FYO"
 /note="Organ: Brain; Vector: pYX-Asc; Site:1: EcoR I; Site:2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National

Information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
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Location/Qualifiers

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ORIGIN

Query Match 7.2%; Score 287.4; DB 9; Length 303;
Best Local Similarity 98.7%; Pred. No. 2e-26; Mismatches 1; Gaps 1;
Matches 299; Conservative 0; Indels 3;

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QY 3232 GCCTGGCCTCAGTGGCAGCAGTGGCTGCTGCTGTGTAGTGTCTCAGAGACTGAGTG 3291
Db 61 GCTTGGCCTCAGTGGCAGCAGTGGCTGCTGCTGTGTAGTGTCTCAGAGACTGAGTG 120
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Db 301 CCT 303
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Search completed: March 1, 2004, 03:42:23
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Qy 1268 GTGCCCCCAAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1327
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Db 1321 AGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
Qy 1388 CACAGACCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1447
Db 1381 CACAGACCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
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Db 1441 CCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
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Db 1501 CAAGAAACGCGCTTCTCTCAAGAAACACCAAGAAATCATCTCTGTGTGTGTGTGTGTGT 1560
Qy 1568 GCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1627
Db 1561 GCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
Qy 1628 GAGCCCAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1687
Db 1621 GAGCCCAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
Qy 1688 CAAGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1747
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Qy 1808 CAAGTCTCAAAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1867
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Qy 1868 GGAAGCAGAGGTCAAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1927
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Qy 1928 CTTGATCCCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1987
Db 1921 CTTGATCCCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
Qy 1988 CAGAACGTTTCGACAGAAAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2047
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2641 GCTCTGTGCTGAGGATGTTCTTGTGTGAGACCTCACTCAACCCAGCGGAAAC 2700
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2701 CTTCTCAGAGACCTGTGTCGAGGCTGCTGAGTATGCTGCTGAGTAACTTGCAGGA 2760
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2821 GCCGCGCCACGCGCTTATCCCTGTGAGAGAGAGCCCTGGGTGGAGAGCTTTGTGAAGT 2880
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2941 CGGCTTCAAGGCTGAGAGAAAGAGCTGCGCAAACTTTGGGGGTCTTGGCGCTGAAGT 3000
3008 TCACAGCTGTTTGTGATTTGAGTGAAGAGCTTCAAGAGCTTGTGACCAACATCTA 3067
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3181 CTGCTATCTCATCTGAGAGAGCTTCTTCTGCGGTCTTGAAGAGCTTCTCTCT 3240
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3421 ACTGCTTCAAGCTTCAAGAGAGCTTGAAGTATGAGCAACCCGCAAGCCAGCGGA 3480
3455 GGAAGAGCTGAGAGAGAGCTTGTCTCTGTTTGGCCATGATGATGATGATGATGATG 3514
3481 GAGAGAGAGAGAGAGAGAGCTTGTCAAGCGGAGCTTCAAGTCCAGAGAGAGAGAGAG 3540
3515 GCTTCTCTTGTGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3574
3541 CACAG 3600
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3630 CTTGTGCAAG 3689
3661 GAGTGTCAAG 3719
3690 CAGTCAAG 3749
3720 AG 3779
3750 CTGAATTCAG 3809
3780 CCAGATTCAG 3832
3810 TTTCTGTGTGTGAG 3869
3833 CACATTCAG 3892
3870 AAGGTGCTCTGTACAG 3929
3893 AAGGTGCTCTGTACAG 3952
3930 ATTGGGGGAG 3989
3953 ATTGGGGGAG 4012
3990 AAA 3992
4013 AAA 4015

RESULT 2
US-09-990-080-1
; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT) cDNA
US-09-990-080-1
Query Match 82.4%; Score 3306.6; DB 9; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY	8	GCAGGCTGCGCTCTCTGCTGCGCAGCATGTGGAGAGCCCTGGACCCCGGCACACCCCGGAAATGCG	67
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QY	68	GCAGGCTCTCCCGCTGCGCAGATCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGATGCT	127
Db	61	GCAGGCTCTCCCGCTGCGCAGATCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGATGCT	120
QY	128	GCCGCTGGCGCAAGTTGCTGCGAGCGCTGAGCGGCCCAAGGAGCTGAGCGGCTGATGCGACGCG	187
Db	121	GCCGCTGGCGCAAGTTGCTGCGAGCGCGCTGAGCGGCCCAAGGAGCTGAGCGGCTGATGCGACGCG	180
QY	188	GGACCCCGGCGCTTCCGCGCGCTGATGAGCCCAATGCTCGTATGCTGCTGCTGGAAGCG	247
Db	181	GGACCCCGGCGCTTCCGCGCGCTGATGAGCCCAATGCTCGTATGCTGCTGCTGGAAGCG	240
QY	248	ACGCGCGCGCCCCCGCGCGCCCTCTCCGTCAGAGTGTCTGCTCTGAAAGAGCTGATGCG	307
Db	241	ACGCGCGCGCCCCCGCGCGCCCTCTCCGTCAGAGTGTCTGCTCTGAAAGAGCTGATGCG	300
QY	308	CCGATGCTGTGAGAGAGCTGTGCGAGCGCGGCGCAAGAAAGTGTGCTTCCGCTTCCG	367
Db	301	CCGATGCTGTGAGAGAGCTGTGCGAGCGCGGCGCAAGAAAGTGTGCTTCCGCTTCCG	360
QY	368	GCTGCTGAGACGAGGCGCCCGCGAGGCGCCCGCGAGGCTTTCACCAACAGCGTGCAGAGTA	427
Db	361	GCTGCTGAGACGAGGCGCCCGCGAGGCGCCCGCGAGGCTTTCACCAACAGCGTGCAGAGTA	420
QY	428	CCTGCGCCCAACAGGTGACCGACACTGCGGGGAGAGCGGGGCGTGGGGGCTGCTGCTGCG	487
Db	421	CCTGCGCCCAACAGGTGACCGACACTGCGGGGAGAGCGGGGCGTGGGGGCTGCTGCTGCG	480
QY	488	CCGCGTGGGCGACGAGCTGTGCTGATTCACTCTGCGCAGCTGAGCGCGCTTTTGTGCTGAT	547
Db	481	CCGCGTGGGCGACGAGCTGTGCTGATTCACTCTGCGCAGCTGAGCGCGCTTTTGTGCTGAT	540
QY	548	GCGCTTCCACGCTGCGCTTACAGAGTGTGCGGGCGCGCGTGTATCCAGACTCGGCGCTGCCAC	607
Db	541	GCGCTTCCACGCTGCGCTTACAGAGTGTGCGGGCGCGCGTGTATCCAGACTCGGCGCTGCCAC	600
QY	608	TCAGGCGCGGCGCCCGCGCACAAGCTAATGAGAACCCCGAAGAGCGTCTGAGATTCGAAACGGAG	667
Db	601	TCAGGCGCGGCGCCCGCGCACAAGCTAATGAGAACCCCGAAGAGCGTCTGAGATTCGAAACGGAG	660
QY	668	CTGGAACCATAGCTCAGGGAAGCGCGGAGTCCCTTGGGCTTGCCAGCGCCCGGAGTGGAG	727
Db	661	CTGGAACCATAGCTCAGGGAAGCGCGGAGTCCCTTGGGCTTGCCAGCGCCCGGAGTGGAG	720
QY	728	GAGGCGCGGAGGAGATGTGCAGCGCAAGTCTGCGCTTGGCCCAAGAGGCGCAGAGCTGAGCG	787
Db	721	GAGGCGCGGAGGAGATGTGCAGCGCAAGTCTGCGCTTGGCCCAAGAGGCGCAGAGCTGAGCG	780
QY	788	TGCGCTTGAAGCGGAGCGGAGCGCGCTTGGGAGAGGATCTGAGGCTCCACCCGGGAGAGAC	847
Db	781	TGCGCTTGAAGCGGAGCGGAGCGCGCTTGGGAGAGGATCTGAGGCTCCACCCGGGAGAGAC	840
QY	848	GCGTGAACCGAGTGAACGATGATTTCTGTGTGTGTCACTGCGCAGACCCCGCGGAGAGAGC	907
Db	841	GCGTGAACCGAGTGAACGATGATTTCTGTGTGTGTCACTGCGCAGACCCCGCGGAGAGAGC	900
QY	908	CACCTCTTTTGAAGGATGCGCTCTCTGGAGACGCGCACTTCCACCCATTCGGTGGGCGCGCA	967
Db	901	CACCTCTTTTGAAGGATGCGCTCTCTGGAGACGCGCACTTCCACCCATTCGGTGGGCGCGCA	960
QY	968	GCACCAACGCGGCGCCCGCATTCACATCGCGGCGCACAGCTCCCTTGGGACAGCGCTTGTCC	1027
Db	961	GCACCAACGCGGCGCCCGCATTCACATCGCGGCGCACAGCTCCCTTGGGACAGCGCTTGTCC	1020
QY	1028	CCCGGTATACGCGGAGACCAAGCACTTCTCTTACTCTTCAAGCGCAAGAGAGCAAGCTGCG	1087
Db	1021	CCCGGTATACGCGGAGACCAAGCACTTCTCTTACTCTTCAAGCGCAAGAGAGCAAGCTGCG	1080

QY	1088	GCCTCCCTCTCACTCAAGCTCTCTGAGAGCCCAAGCTCACTGAGCCTCGAGAGCTCTGTGGA	1147
Db	1081	GCCTCTCTCTCACTCAAGCTCTCTGAGAGCCCAAGCTCACTGAGCCTCGAGAGCTCTGTGGA	1140
QY	1148	GACCACTTTCTTGAGGTTCCAGAGCCCTGAGATGCCAGGACCTCCCGCAGATTGTCCCGCT	1207
Db	1141	GACCACTTTCTTGAGGTTCCAGAGCCCTGAGATGCCAGGACCTCCCGCAGATTGTCCCGCT	1200
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Db	1201	GCCTCAGAGCTCACTGAGAAATGCGAGCCCTGTTTCTGAGAGCTGTTGAGAAACAAGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGCTCCTCAAGACGACTGCGCGCTGCGAGCTGCGCTCACCCACAGC	1327
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QY	1328	AGCGGATGTCTGTACCAGGAGAGAGCCCAAGAGCTCTGTGAGCGAGCCCCGAGAGAGAGGA	1387
Db	1321	AGCGGATGTCTGTACCAGGAGAGAGCCCAAGAGCTCTGTGAGCGAGCCCCGAGAGAGAGGA	1380
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QY	1448	CGAGTCTGTGAGGAGCTGCTGACAGCGAGTGTGTCCCGCAGGCTCTGTGAGGCTCCAGGCA	1507
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QY	1628	GAGCCCAAGGGTTTGGCTGTGTTCGGGCGGACAGACACCTGTGGGTAGAGAAATCTGGGC	1687
Db	1621	GAGCCCAAGGGTTTGGCTGTGTTCGGGCGGACAGACACCTGTGGGTAGAGAAATCTGGGC	1680
QY	1688	CAAGTTCCTGACATGAGTGTGATGTGTATCGTGTGAGAGTGTCAAGTCTTTCTTTTA	1747
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QY	1748	TGTCACGAGAACCAAGTTTCAAAGAACAGGCTTTTTCACCGGAAAGATGTCTGGAG	1807
Db	1741	TGTCACGAGAACCAAGTTTCAAAGAACAGGCTTTTTCACCGGAAAGATGTCTGGAG	1800
QY	1808	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTTGAGCTGCGGAGCTGTCTC	1867
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Db	1861	GGAAGCAGAGGTCAGGACAGCATGGGGAAGCAGGCGCGGCTGTGACGTGCACAATCTCG	1920
QY	1928	CTTCACTCCCAAGCCTGACGGGCTGTGCGGCTCGATTGTGAACAATGACACTACGTGTGGAGC	1987
Db	1921	CTTCACTCCCAAGCCTGACGGGCTGTGCGGCTCGATTGTGAACAATGACACTACGTGTGGAGC	1980
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Db	1981	CAGAAAGTTCCGACAGAGAAAGAGAGGCGAGCGCTCACTCAGAGGGTGAAGGACACTGTT	2040
QY	2048	CAGCGTGCTCACTACAGAGCGAGCGCGCGCTCCGCGCTCTGTGGCGCTCTGTGTGGGG	2107
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Db 3953 ATTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4012
Qy 3990 AAA 3992
Db 4013 AAA 4015

RESULT 3

US-09-843-676-224

Sequence 224, Application US/09843676

Patent No. US20020164786A1

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Moxin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20020164786A1 Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hprt"
/note= "human telomerase reverse
transcriptase (hprt) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-843-676-224
Query Match 82.4%; Score 3306.6; DB 9; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 368 GCTGCTGAGCGGAGCCCGCGGAGGCCCCCGGAGGCTTTCACCAACGAGCTGCGAGCTA 427
DB GCTGCTGAGCGGAGCCCGCGGAGGCCCCCGGAGGCTTTCACCAACGAGCTGCGAGCTA 420
QY 428 CCGGCGCAACAGGTGACCGACCACTGCGGAGGAGAGCGGAGCGTGTGCTGCTGCG 487
DB CCGGCGCAACAGGTGACCGACCACTGCGGAGGAGAGCGGAGCGTGTGCTGCTGCG 480
QY 421 CCGGCGCAACAGGTGACCGACCACTGCGGAGGAGAGCGGAGCGTGTGCTGCTGCG 480
DB CCGGCGCAACAGGTGACCGACCACTGCGGAGGAGAGCGGAGCGTGTGCTGCTGCG 480
QY 488 CCGGCGGAGGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
DB CCGGCGGAGGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 548 GCGTCCGAGTGGCGCTACCAAGGTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 607
DB GCGTCCGAGTGGCGCTACCAAGGTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 600
QY 608 TCAAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 667
DB TCAAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 660
QY 668 CTGGAACCATAGGTGAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 727
DB CTGGAACCATAGGTGAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 720
QY 661 CTGGAACCATAGGTGAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 720
DB CTGGAACCATAGGTGAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 720
QY 728 GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 787
DB GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 721 GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 788 TGCCCTTGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 847
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DB GCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
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DB GCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
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QY 1261 GTGCGCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
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DB CACAGAGCCCGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
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Db 1561 GCTTCGCTGAGAGCTGACGTGGAAGATGAGAGTGGGAGTGGGCTTGGCTGGCAG 1620
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Db 1621 GAGCCGAGG33GTTGGCTGTGTCCGCGCAGAGCAACCTGTGAGAGATCTGGC 1680
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Db 1681 CAAGTTCCTGCACTGGCTGATGATGTGTACGTGTGTGAGCTGCTAGAGTCTTTT 1740
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Db 1801 CAAGTTCGAAGCTTGGATTCAGACAGCACTTGAAGAGGTGCACTGCGGAGAGTGTG 1860
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Db	541	GGTCTCCAGTGGGCTTACAGAGTTGTGGGCGCGGCTGTATCCAGTGGGCGCTGCAC	600
Qy	608	TCAAGCCCGGCCCGCCACACACGCTAGTGAACCCGAAGGCTGTGGATATGCAGAGGC	667
Db	601	TCAAGCCCGGCCCGCCACACGCTAGTGAACCCGAAGGCTGTGGATATGCAGAGGC	660
Qy	668	CTGGAAACATAGGCTCAAGGAGGCGCGGAGTCCCCCTGGGCTGCACGCCCGGCTGCAG	727
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Qy	728	GAGGCGCGGAGGAGTGCAGCGCGGAAGTCTGCAGTTGCCCAAGAGCCAGAGGTGGCGG	787
Db	721	GAGGCGCGGAGGAGTGCAGCGCGGAAGTCTGCAGTTGCCCAAGAGCCAGAGGTGGCGG	780
Qy	788	TGCGCTTGAAGCCGGAAGGACGCGCCGTTGGGACGAGGAGTCTGGGCCACCCGAGCAGAC	847
Db	781	TGCGCTTGAAGCCGGAAGGACGCGCCGTTGGGAGCGAGGAGTCTGGGCCACCCGAGCAGAC	840
Qy	848	GCGTGAACCGAGTGAACCGTGTCTTGTGTGTGTCACTGTGCCAGCCGCGAAGAGC	907
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Qy	968	GCAACACGCGGGCGCCCCCATCCACATGCGGACCAACGCTCCTGGAGACAGCTTTGTTC	1022
Db	961	GCAACACGCGGGCGCCCCCATCCACATGCGGACCAACGCTCCTGGAGACAGCTTTGTTC	1021
Qy	1028	CCGAGGTATAGCGCGAGACCAAGACCTTCCTCACTCTCAGGAGGACAAAGAGAGGTGG	108
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Qy	1088	GCGCTCTTCTCTACTCAGCTCTTGTAGGCCCAAGCTGACTGGGAGCTGGAGGCTCGTGA	114
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Qy	1148	GACCATCTTCTGGGGTTCAGAGCCCTGGATATGCCAGGAGATCCCCGAGAGTTGCCCGCT	120
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Qy	1208	GCCCCAGCGCTATGCGCAATGCGGCCCTGTCTTGTAGAGCTGCTTGGAGACCAACGCGCA	126
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Qy	1268	GTGCCCCCTACGGGGTCTCTCAAGCGCATATGCCGCTGCGAGCTGCGGTCACCCACG	132
Db	1261	GTGCCCCCTACGGGGTCTCTCAAGCGCATATGCCGCTGCGAGCTGCGGTCACCCACG	132
Qy	1328	AGCCGAGTGTGTGCGCCGAGAGAGGCCCAAGGAGCTGTGTGGCGGCCCGAGAGAGAGA	138
Db	1321	AGCCGAGTGTGTGCGCCGAGAGAGGCCCAAGGAGCTGTGTGGCGGCCCGAGAGAGAGA	138
Qy	1388	CACAGACCCCCGCTGCGCTGTGTGAGTGTCTCCGACAGCACAGAGGCCCTGTGACAGGTGA	144
Db	1381	CACAGACCCCCGCTGCGCTGTGTGAGTGTCTCCGACAGCACAGAGGCCCTGTGACAGGTGA	144
Qy	1448	CGGCTTGTGCGGAGCGCTGCTGCGCGAGCTGGTGCCCCAGAGGCTGTGGGGTCCAGAGCA	150
Db	1441	CGGCTTGTGCGGAGCGCTGCTGCGCGAGCTGGTGCCCCAGAGGCTGTGGGGTCCAGAGCA	150
Qy	1508	CAACGAGCGCGCTTCTCAGAGACCAAGAAATTCACTCTCGGGAGACATGCCAA	156
Db	1501	CAACGAGCGCGCTTCTCAGAGACCAAGAAATTCACTCTCGGGAGACATGCCAA	156
Qy	1568	GCTTCGCGTGAAGAGCTGACGTGAAGATGAGCGGTGGGACTGCGCTTGTGTGCGCAG	162
Db	1561	GCTTCGCGTGAAGAGCTGACGTGAAGATGAGCGGTGGGACTGCGCTTGTGTGCGCAG	162

QY	1628	GAGCCAGGGGTTGGCTGTGTTCCGGCCGAGAGACCGCTGCGTGAAGAGATCTCGC	1687
Db	1621	GAGCCAGGGGTTGGCTGTGTTCCGGCCGAGAGACCGCTGCGTGAAGAGATCTCGC	1686
QY	1688	CAAGTCTTCGACCTGGCTGATGATGTGTACGTGTGAGGTGCTCAAGTCTTTCTTTA	1747
Db	1681	CAAGTCTTCGACCTGGCTGATGATGTGTGTACGTGTGAGGTGCTCAAGTCTTTCTTTA	1740
QY	1748	TGTCAAGAGACACGTTTCAAAAGAAACAGGCTCTTTTCTACCGGAAAGAGTCTGAG	1807
Db	1741	TGTCAAGAGACACGTTTCAAAAGAAAGAGGCTCTTTTCTACCGGAAAGAGTCTGAG	1800
QY	1808	CAAGTTGCAAAGCATTTGAAATCGACAGCACTTGAAGAGGTGCACTGGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAGCATTTGAAATCGACAGCACTTGAAGAGGTGCACTGGCGGAGCTGTC	1860
QY	1868	GGAAACAGAGGTCAAGGACGATCCGGAAAGCCAGGCGCCGCTGTGACGTGCAGCTCG	1927
Db	1861	GGAAACAGAGGTCAAGGACGATCCGGAAAGCCAGGCGCCGCTGTGACGTGCAGCTCG	1920
QY	1928	CTTCATCCCCAAAGCCTGACGAGGCTGCGGCGCATTTGTGAACATGACATACGTGTGAGAC	1987
Db	1921	CTTCATCCCCAAAGCCTGACGAGGCTGCGGCGCATTTGTGAACATGACATACGTGTGAGAC	1980
QY	1988	CAGAACGTTCCGACAGAAAGAGGGGCGAGCGTCAACCTCAGAGGGTGAAGGACATGTT	2047
Db	1981	CAGAACGTTCCGACAGAAAGAGGGGCGAGCGTCAACCTCAGAGGGTGAAGGACATGTT	2040
QY	2048	CAGCGTCTCAACTACGAGCGGGGCGGCGCCCGGCTCTTGAGGCGCTTGTGCTGAGG	2107
Db	2041	CAGCGTCTCAACTACGAGCGGGGCGGCGCCCGGCTCTTGAGGCGCTTGTGCTGAGG	2100
QY	2108	CCTGAGCATATCCACAGAGGCTGAGGCGCACTTCTGTGCTGTGCGGCGCCAGAGACC	2167
Db	2101	CCTGAGCATATCCACAGAGGCTGAGGCGCACTTCTGTGCTGTGCGGCGCCAGAGACC	2160
QY	2168	GCGCGCTAGCTGACTTTGTACAGGTGATGTGACGAGGCGCGTACGACACCATCCCCA	2227
Db	2161	GCGCGCTAGCTGACTTTGTACAGGTGATGTGACGAGGCGCGTACGACACCATCCCCA	2220
QY	2228	GGAACAGGCTCAGAGAGTCACTGCGACGATCATAAACCAGAAACAGTACTCGTGGCG	2287
Db	2221	GGAACAGGCTCAGAGAGTCACTGCGACGATCATAAACCAGAAACAGTACTCGTGGCG	2280
QY	2288	TGGGATACCGTGGTCCAGAAAGGCGCGCCATGGGCACTCTCGAAAGCTTCAAGAGCCA	2347
Db	2281	TGGGATACCGTGGTCCAGAAAGGCGCGCCATGGGCACTCTCGAAAGCTTCAAGAGCCA	2340
QY	2348	CGTCTCACTCTTGACAGACCTCCAGACCGTACATGCGACAGTTCGTGGCTCACTGACAGA	2407
Db	2341	CGTCTCACTCTTGACAGACCTCCAGACCGTACATGCGACAGTTCGTGGCTCACTGACAGA	2400
QY	2408	GACCAAGCCCGCTGAGAGGATGCCGTGCTATCGACACAGTCTCTTCTGAAATGAGCCAG	2467
Db	2401	GACCAAGCCCGCTGAGAGGATGCCGTGCTATCGACACAGTCTCTTCTGAAATGAGCCAG	2460
QY	2468	CAGTGGCTCTTGACAGCTCTTCTACACCTTCACTGTGCAACAACGCGCTGCGCATCAGAGG	2527
Db	2461	CAGTGGCTCTTGACAGCTCTTCTACACCTTCACTGTGCAACAACGCGCTGCGCATCAGAGG	2520
QY	2528	CAAGTCTCAAGTCCAGTGCACAGGGGATCCCGCAGAGGCTCCATCTCTTCACGCTGTCTG	2587
Db	2521	CAAGTCTCAAGTGCAGTGCACAGGGGATCCCGCAGAGGCTCCATCTCTTCACGCTGTCTG	2580
QY	2588	CAGCCTGTGCTACCGCACATGAGAAACAAGCTGTTTTCGCGGAGTTTGGCGGAGCAGGCT	2647
Db	2581	CAGCCTGTGCTACCGCACATGAGAAACAAGCTGTTTTCGCGGAGTTTGGCGGAGCAGGCT	2640
QY	2648	GCTCCTGCGTTGGTGGATGATTTCTTGTGTGACACCTCACTCAACCCACGGAAC	2707
Db	2641	GCTCCTGCGTTGGTGGATGATTTCTTGTGTGACACCTCACTCAACCCACGGAAC	2700

QY 2708 CTTCTCAGAGACCTGCTGAGAGTCCCTGAGTATGCGTGGTGAACCTTGGGAA 2767
Db 2701 CTTCTCAGAGACCTGCTGAGAGTCCCTGAGTATGCGTGGTGAACCTTGGGAA 2760
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Db 2761 GACAGTGTATGATCTTCCCTGTATGAGACGAGGCTGGGAGGAGGCTTTTGTCAAT 2820
QY 2828 GCGGAGGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 2887
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QY 2948 GCGGAGGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3007
Db 2941 GCGGAGGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3000
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Db 3001 TCAAGAGGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3060
QY 3068 CAAGAGGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3127
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QY 3188 CTGCTATCTCAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3237
Db 3181 CTGCTATCTCAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3240
QY 3238 CTTCTCAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3297
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Db 3301 GCGTATGAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3360
QY 3358 GCTGCTGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3417
Db 3361 GCTGCTGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3420
QY 3418 TCTGAGAGGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3454
Db 3421 TCTGAGAGGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3480
QY 3455 GCGAGAGGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3514
Db 3481 GCGAGAGGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3540
QY 3515 GCGTATGAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3574
Db 3541 GCGTATGAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3600
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Db 3601 CTTGTGAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3660
QY 3630 CTTGTGAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3689
Db 3661 CTTGTGAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3719
QY 3690 CAGTATGAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3749
Db 3720 CAGTATGAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3779
QY 3750 CAGTATGAGAGGAGGCTTATCCCTGTATGAGAGGCTGGGAGGAGGCTTTTGTCAAT 3809

Db 3780 CCGAGATTCGCAATTTTCAACCCCT-----GCCCCGCCCCCTTGTGCTTCAACCCC 3832
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Db 3833 CACCATTCAGGTGAGAGACCTTGTAGAGAGACCTTGTAGAGGCTTGTGAAATTTGAGATGACA 3892
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Db 3893 AAGGTGTGCCCTGTACACAGAGGAGACCTTGTAGAGGCTTGTAGAGGCTTGTGAAATTTGAGATGACA 3952
QY 3930 AATGGGGGAGGAGGCTTGTGAGAGGAGGCTTGTAGAGGCTTGTAGAGGCTTGTGAAATTTGAGATGACA 3989
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QY 3990 AAA 3992
Db 4013 AAA 4015

RESULT 5
US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Moxin, Greg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224
Query Match 82.4%; Score 3306.6; DB 14; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;
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Db 301 CCGAGGTGCTGAGAGGTGTGCGAGCGCGCGCGAGAGAGAGTGTGCTGCTGCTGCTGCTG 360
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Db 1201 GCGCGAGCGCTACTGTGGAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1268 GTGCGCGCGTACGAGGAGTCTCTCAAGAGCACTGCGCGCGCGCGCGCGCGCGCGCGCG 1327
Db 1261 GTGCGCGCGTACGAGGAGTCTCTCAAGAGCACTGCGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1388 AGCGGTGTCTGTGCG 1387
Db 1381 AGCGGTGTCTGTGCG 1380
QY 1388 CACAGACCG 1447
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QY 1448 CCGCTGTGTGCG 1507
Db 1441 CCGCTGTGTGCG 1500
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Db 1501 CAAGGAAGCGCGCTTCTCTGAGAAACCAAGAAAGTATCTTCTCTGCGGAGAGATGCGCA 1560
QY 1568 GCTCTGCTGTGAGAGCTGACGTGTGAGAGATGAGGCTGCGGAGCTGTGCTGCGCGAG 1627
Db 1561 GCTCTGCTGTGAGAGCTGACGTGTGAGAGATGAGGCTGCGGAGCTGTGCTGCGCGAG 1620
QY 1628 GAGCGCGAGGGTGTGCTGTGTTCCGCGCGCGAGAGACGCTGTGCTGAGAGATCTGCG 1687
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RESULT 6
US-10-208-243-1
; Sequence 1, Application US/10208243

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Db 4013 AAA 4015

RESULT 8
US-10-054-611-224
Sequence 224, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Linsner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase

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NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hprt"
/note= "human telomerase reverse
transcriptase (hprt) catalytic protein
component"
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US-10-054-611-224

Query Match 82.4%; Score 3306.6; DB 14; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

Query 8 GCAGCGCTGCGCTCTGCTGCGCAGTGGAGAAAGCCCTGAGCCCGGACCAAGCCCGCGATGCC 67
Db 1 GCACCGCTGCGCTCTGCTGCGCAGTGGAGAAAGCCCTGAGCCCGGACCAAGCCCGCGATGCC 60

Query 68 GCGGCGTCCCCGCGCGCGAGCGCGCGGCGCTCCCTGCTGCGAGCGACCTACGACGAGGATGCT 127
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Db 121 GCCCGTGGCCAGTTCGTGTCGCGCGCGCTGGAGGCCCCAGAGGCTGCGGCTGATGCAAGCGCG 180

Query 188 GGAACCGAGCGCTTTCGCGCGCGCTGATGCGCCAGATGCGCTGATGTCGTCCTCGGAGCGC 247
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QY	368	GCTTCTGGAACGGAGGCCCGCGGGAGGCCCGCCCGAGAGCTTTCACCAACAGAGTGTCCAGCTA	427
Db	361	GCTGTCTGGAACGGAGGCCCGCGGGAGGCCCGCCCGAGAGCTTTCACCAACAGAGTGTCCAGCTA	420
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QY	848	GCGTGTGACCGAGTGAACCTGTGTCTGTGTGTGTGTCACTTGTGCAGACCCGCGCAAGAAAGC	907
Db	841	GCGTGTGACCGAGTGAACCTGTGTGTCTGTGTGTGTGTCACTTGTGCAGACCCGCGCAAGAAAGC	900
QY	908	CACCTCTTTGAGAGGGTGTGCTCTGTGACGCGACACTCCCAACCANTCCTGTGGGCGCGCA	967
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QY	1148	GACCATCTTTCTAGGGATTACAGGCCCTGTGATGTGCAGAGACTCCCGGCAAGTTGTGCCCGGCT	1207
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QY	1208	GCCCCAGCGCTACTGTGGCAATGTGGGCCCTCTGTTTCTGTGAGCTGTCTTGGAAACACAGCGCA	1267
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QY	1328	AGCCGGTGTCTGTGTGCGCGGAGAAAGCCCAAGGCTCTGTGTGTGTGCGGCCCTCCAGAGAGAGGA	1387
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QY	1388	AACGAGCCCCGTCGCGTGGAGCGTGTCCGACAGACAGAGCCCTGGACAGGTGA	1447
Db	1381	CACGAGCCCCGTCGCGTGGAGCGTGTCCGACAGACAGAGCCCTGGACAGGTGA	1440
QY	1448	CGGCTTCGTGGGGCTGCGCTGGCGCGCTGGTCCCCAGGCTCTGGGGCTCCAGCA	1507
Db	1441	CGGCTTCGTGGGGCTGCGCTGGCGCGCTGGTCCCCAGGCTCTGGGGCTCCAGCA	1500
QY	1508	CAACGAACGCGCGCTTCCTCCAGGAACACCAAGATTATCTCCCTGGAGAAAGATGCCA	1567
Db	1501	CAACGAACGCGCGCTTCCTCCAGGAACACCAAGATTATCTCCCTGGAGAAAGATGCCA	1566
QY	1568	GCTTCGCTGCAGAGAGCTGACGTGGAAGATGACGTGCGGAGCTGGCTTGGCTGCAG	1627
Db	1561	GCTTCGCTGCAGAGAGCTGACGTGGAAGATGACGTGCGGAGCTGGCTTGGCTGCAG	1620
QY	1628	GAGCCCAAGGGGTTGGCTGTGTTCCGCGCGAGACACGCTGCGGTAGAGAGATCTGGC	1687
Db	1621	GAGCCCAAGGGGTTGGCTGTGTTCCGCGCGAGACACGCTGCGGTAGAGAGATCTGGC	1680
QY	1688	CAAGTTCCTGCATCGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAAGTCTTTCTTTA	1747
Db	1681	CAAGTTCCTGCATCGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAAGTCTTTCTTTA	1740
QY	1748	TGTCAACGAGACACAGTTTCAAAAGAACAGGCTCTTTTTCACACGGAAGATGTCTGAG	1807
Db	1741	TGTCAACGAGACACAGTTTCAAAAGAACAGGCTCTTTTTCACACGGAAGATGTCTGAG	1800
QY	1808	CAAGTTGCMAAGCATTGGATCAGATCAGACACTTGAAGAGGTGACGTGCGGGAGCTGT	1867
Db	1801	CAAGTTGCMAAGCATTGGATCAGATCAGACACTTGAAGAGGTGACGTGCGGGAGCTGT	1860
QY	1868	GGAAGCAAGAGTCAAGGACGACATCGGAAAGCAGGCGCGGCTGTGACGTCAACACTCG	1927
Db	1861	GGAAGCAAGAGTCAAGGACGACATCGGAAAGCAGGCGCGGCTGTGACGTCAACACTCG	1920
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Db	1921	CTTCAATCCCAAGCCTTACGCGGCTGCGCGCGATTTGTAACTGACATGACATGCTGTGGAGC	1980
QY	1988	CAGAACGTTCCGACAGAGAAAGAGGCGAGACGTCTCACTCAGAGGTGAAGGACACTGT	2047
Db	1981	CAGAACGTTCCGACAGAGAAAGAGGCGAGACGTCTCACTCAGAGGTGAAGGACACTGT	2040
QY	2048	CAGCGTGTCAACTACGAGCGGGGCGCGGCGCTCCGCGCTCTTGCGGCGCTCTGTGTGGG	2107
Db	2041	CAGCGTGTCAACTACGAGCGGGGCGCGGCGCTCCGCGCTCTTGCGGCGCTCTGTGTGGG	2100
QY	2108	CCTGAGCAATATCACAAGGCGCTGAGCGACCTTGTGTCGTGTGCGAGGCCACAGAACCC	2167
Db	2101	CCTGAGCAATATCACAAGGCGCTGAGCGACCTTGTGTCGTGTGCGAGGCCACAGAACCC	2160
QY	2168	GCCGCTGAGCTGTACTTTGTACAGGTGAGATGTACGCGGCGCGCTACACACATCTCCCA	2227
Db	2161	GCCGCTGAGCTGTACTTTGTACAGGTGAGATGTACGCGGCGCGCTACACACATCTCCCA	2220
QY	2228	GGAACAGGCTCAGAGAGTCACTGCGACAGATCATAAACCCAGAACACGTACTGCGTGGC	2287
Db	2221	GGAACAGGCTCAGAGAGTCACTGCGACAGATCATAAACCCAGAACACGTACTGCGTGGC	2280
QY	2288	TGCGTATGCGGTGTCCAGAAAGCGCCGCCATGGGCAAGTCCGCAAGGCTTCAAGAGCCA	2347
Db	2281	TGCGTATGCGGTGTCCAGAAAGCGCCGCCATGGGCAAGTCCGCAAGGCTTCAAGAGCCA	2340
QY	2348	GCTCTCTACTTGAACAGACTCTCAGACCGTACATCGACAGTTCGTGCTCACTTCAGAGA	2407
Db	2341	GCTCTCTACTTGAACAGACTCTCAGACCGTACATCGACAGTTCGTGCTCACTTCAGAGA	2400
QY	2408	GACCAAGCCCGCTGAGAGGATGCCGTGTCTATGACACAGACTCTTCCCTGAAATGAGGCCAG	2467
Db	2401	GACCAAGCCCGCTGAGAGGATGCCGTGTCTATGACACAGACTCTTCCCTGAAATGAGGCCAG	2460
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4013 AAA 4015

RESULT 10
US-10-044-692-1
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Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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Db 2287 ATGCGGTGTCAAGAGAGCG 2346
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RESULT 14

US-09-843-676-173 ; Sequence 173, Application US/09843676
Patent No. US20020164786A1

GENERAL INFORMATION:

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Inventor: Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20020164786A1el Telomerase

NUMBER OF SEQUENCES: 225

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CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-APR-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY:
LOCATION: 1..4029
OTHER INFORMATION: /note= "preliminary sequence for human TRF cDNA insert of plasmid pGRN121"
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US-09-843-676-173
Query Match 78.8%; Score 3159.8; DB 9; Length 4029;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 3577; Conservative 0; Mismatches 412; Indels 55; Gaps 13;
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RESULT 15
US-09-438-486-173
; Sequence 173, Application US/09438486
; Publication No. US2003009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US2003009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429

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? REFERENCE/OCKET NUMBER: 015389-0029931US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO.: 173:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4029 base pairs
? TYPE: nucleic acid
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? MOLECULE TYPE: cDNA
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IS-09-438-486-173

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Tue Mar 2 09:53:28 2004

us-09-424-686f-12.rnpb

Page 35

Db 4006 AAAAAAAAAAAAAAAAAAAAAA 4029

Search completed: March 1, 2004, 23:55:01
Job time : 924.576 secs

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

17262.293 Million cell updates/sec

Perfect score: 3411

Sequence: 1 ggcgatgcgcgcgtccccc.....tcctggaactgatgccaacc 3411

Scoring table: IDENTITY_NUC

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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2	3411	100.0	4015	6	AF175848	AR175848 Sequence
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4	3411	100.0	4015	6	AR182321	AR182321 Sequence
5	3411	100.0	4015	6	AR224455	AR224455 Sequence
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ALIGNMENTS

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VERSION	AR104587.1	GI:12817295	
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 4015)		
TITLE	Cech, T.R. and Langner, J.		
JOURNAL	Telomerase		
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QY 61 GAGGTGCTGCGCGCTGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB GAGGTGCTGCGCGCTGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 172
QY 121 CAGCGCGCGCGAGCCCGCGCTGCTGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB CAGCGCGCGCGAGCCCGCGCTGCTGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 232
QY 181 TGGGACG 240
DB TGGGACG 292
QY 241 CTGCTGCGCGCGAGCTGCTGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB CTGCTGCGCGCGAGCTGCTGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352
QY 301 GGGCTTCCGCGCTGCTGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB GGGCTTCCGCGCTGCTGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGGAGCTACCTGCGCGAGCACTGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB CGGAGCTACCTGCGCGAGCACTGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 472
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DB CAGGTGACCGGCTTCTGCGCGAGCTGCTGCGCGAGCTGCTGCGCGAGCTGCTGCGAG 1492
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VERSION AR175848.1 GI:17917147
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech, T.R. and Nakamura, T.
TITLE Telomerase
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 QY 2701 TTGCGAAGACAGTGTGATCTTCCCTGTAGAGACGAGGCCCTGGTGTGACGCTTTT 2760
 DB 2753 TTGCGAAGACAGTGTGATCTTCCCTGTAGAGACGAGGCCCTGGTGTGACGCTTTT 2812
 QY 2761 GTTGAATGCGGGCCACAGGCTTATCCCTGTAGAGACGAGGCCCTGGTGTGATACCGGAC 2820
 DB 2813 GTTGAATGCGGGCCACAGGCTTATCCCTGTAGAGACGAGGCCCTGGTGTGATACCGGAC 2872
 QY 2821 CTGAGGTGACAGAGGCTACTCCAGCTATGCGGACCTTCATCAAGCCAGTCTCAC 2880
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 DB 3053 AACATCTACAGATCTCTCTGTGACAGGCTTACAGATGTGCTGTGACGCTC 3112
 QY 3061 CCATTTCATCAGAGTGTGAGAACCCACATTTTTCGCGCGTATCTGTGACAG 3120
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 DB 3233 GCGCGCGCGCGGCTCTGCGCCGAGGCGGTGACAGTGTGCTGTGACCAAGCATTTCTG 3292
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RESULT 3

LOCUS E36793 4015 bp DNA linear PAT 18-JUN-2001
 DEFINITION Human telomerase catalytic subunit promoter.
 ACCESSION E36793
 VERSION E36793.1 GI:13022756
 KEYWORDS JP 1999253177-A/1.
 SOURCE unclassified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 4015)
 AUTHORS Thomas,R.S., Jochims,R., Toru,N., Karen,B.C., Greg,B.M.,
 Calvin,B.H. and William,H.A.
 TITLE Human telomerase catalytic subunit promoter
 JOURNAL Patent: JP 1999253177-A 1 21-SEP-1999;
 JERON CORP, UNIVERSITY TECHNOLOGY CORP
 COMMENT OS Unidentified
 PN JP 1999253177-A/1
 PD 21-SEP-1999
 PF 15-OCT-1998 JP 1998320169

ORIGIN

Query Match 100.0%; Score 3411; DB 6; Length 4015;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

source

Location/Qualifiers
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PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
 25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
 09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
 14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503, PI THOMAS
 R SECHI,JOCHIMU RINGER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
 MORIN,
 PI CALVIN B HAREI,WILLIAM H ANDREWS
 PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
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OY	721	CGTGGCGCTGCCCTTGAGCCGAGAGCGCCCGTTTGAGAGAGAGTCTTGAGCCACCCG	780
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OY	781	GGCAGAGACGCGTGAACCGAGTGAACCGATGTTCTGTGTGTGTGAATCACTTGCCAGACCGCC	840
Db	833	GGCAGAGACGCGTGAACCGAGTGAACCGATGTTCTGTGTGTGTGAATCACTTGCCAGACCGCC	892
OY	841	GAAGAAGCCACCTCTTTTGAAGAGTGGCTCTTGACAGCGCCACTGCCACCCATCCGTTG	900
Db	893	GAAGAAGCCACCTCTTTTGAAGAGTGGCTCTTGACAGCGCCACTGCCACCCATCCGTTG	952
OY	901	GGCGCGCCAGACACACGCGGGGGCCCCCATTCACATGCGGGCCACACACGCTCCCTGGAGACAG	960
Db	953	GGCGCGCCAGACACACGCGGGGGCCCCCATTCACATGCGGGCCACACACGCTCCCTGGAGACAG	1012
OY	961	CTGTGTCCCCCGGTGTAGCGCGAGACCAAGACATTCCTCTACCTCTCAAGCGACAGAGAG	1020
Db	1013	CTGTGTCCCCCGGTGTAGCGCGAGACCAAGACATTCCTCTACCTCTCAAGCGACAGAGAG	1072
OY	1021	CAGCTGGAGGCGCCTCTTCTCTACTAGCTCTGTAGAGGCGCCAGCTGACGTGGCGCTCGAGAG	1080
Db	1073	CAGCTGGAGGCGCCTCTTCTCTACTAGCTCTGTAGAGGCGCCAGCTGACGTGGCGCTCGAGAG	1132
OY	1081	CTCGTGAAGACCATCTTCTTGAGGTTCCAGGCGCTTGATGCGAGGACTCCCGCAGAGTTG	1140
Db	1133	CTCGTGAAGACCATCTTCTTGAGGTTCCAGGCGCTTGATGCGAGGACTCCCGCAGAGTTG	1192
OY	1141	CCCCGCGCCCGCCAGCGCTACTGCGAAATGCGGCGCCCGTTTCTGAGACCTGTTGGAGAC	1200
Db	1193	CCCCGCGCGCCCGCCAGCGCTACTGCGAAATGCGGCGCCCGTTTCTGAGACCTGTTGGAGAC	1252
OY	1201	CACGCGCAGTGCCTCTACGAGGATGCTCTCAAGACGACCTGCGCGTGGAGCTCGGCTC	1260
Db	1253	CACGCGCAGTGCCTCTACGAGGATGCTCTCAAGACGACCTGCGCGTGGAGCTCGGCTC	1312
OY	1261	AACCCAGACGCGGATGCTGTAGCCCGGGAGAAAGCCCGAGGCTCTGTAGGCGCGCCCGAG	1320
Db	1313	AACCCAGACGCGGATGCTGTAGCCCGGGAGAAAGCCCGAGGCTCTGTAGGCGCGCCCGAG	1372
OY	1321	GAGAGAGACACAGACCCCGTGGCTGTGTCAGTGTCTCGCCACAGACAGCGAGCCCTGG	1380
Db	1373	GAGAGAGACACAGACCCCGTGGCTGTGTCAGTGTCTCGCCACAGACAGCGAGCCCTGG	1432
OY	1381	CAGGTGTAGGCTTGTAGCGGGGCTGCGCGCGGCTGGAGGCCCGCCAGGCGCTCTGAGGGC	1440
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OY	1441	TCCAGAGCAACAGAACCGCGCTTCTCTCAAGAAACACAGAAAGTTGATTCCTCTGGAGAG	1500
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OY	1501	CATGCAAGCTCTCGCTCAGAGAGTGACGTGAGAAATGACGTGGCGGGACTGGCGCTTGG	1560
Db	1553	CATGCAAGCTCTCGCTCAGAGAGTGACGTGAGAAATGACGTGGCGGGACTGGCGCTTGG	1612
OY	1561	CTGGCGCAGAGAGCCAGAGGGTTGGCTGTGTTCCGGCCGACAGACACGCTCTGCGTGAAGAG	1620
Db	1613	CTGGCGCAGAGAGCCAGAGGGTTGGCTGTGTTCCGGCCGACAGACACGCTCTGCGTGAAGAG	1672
OY	1621	ATCTGAGCAAGTTCTCTCAGCTGGCTGATGATGTGTACGTGTGCGAGCTCTCAGAGCT	1680
Db	1673	ATCTGAGCAAGTTCTCTCAGCTGGCTGATGATGTGTACGTGTGCGAGCTCTCAGAGCT	1732
OY	1681	TTCTTTTATGTACGAGAGACACGTTTCAAAAAGACAGGCTTTTCTTACACCGAAGAGT	1740
Db	1733	TTCTTTTATGTACGAGAGACACGTTTCAAAAAGACAGGCTTTTCTTACACCGAAGAGT	1792

QY	1741	GTCTGGAGCAAGTTGGCAAGATTTGGATTCAGACAGCATTTGAAAGGGTCAAGCTGGG	1800
Db	1793	GTCTGGAGCAAGTTGGCAAGATTTGGATTCAGACAGCATTTGAAAGGGTCAAGCTGGG	1855
QY	1801	GAGCTGTGGAGCAAGGTCAAGCAGCATTTGGGAATCAGAGCCCGCTGTGACCTTC	1866
Db	1853	GAGCTGTGGAGCAAGGTCAAGCAGCATTTGGGAATCAGAGCCCGCTGTGACCTTC	1912
QY	1861	AGACTCGCTTCATCCCCAAGCTCAGAGGCGTGGCGCGCATTTGTGAATGATGACTACGTC	1920
Db	1913	AGACTCGCTTCATCCCCAAGCTCAGAGGCGTGGCGCGCATTTGTGAATGATGACTACGTC	1972
QY	1921	GTGGGAGCCAGAAAGTTTCGGAGAGAAAGAGGGCCAGAGCTCTACCTCGAGGGTGAAG	1988
Db	1973	GTGGGAGCCAGAAAGTTTCGGAGAGAAAGAGGGCCAGAGCTCTACCTCGAGGGTGAAG	2033
QY	1981	GCACGTGTCAAGCGTGTCAACTAGAGCGGGCGCGCGCCCGAGCTCTCTGGCGCTCT	2040
Db	2033	GCACGTGTCAAGCGTGTCAACTAGAGCGGGCGCGCGCCCGAGCTCTCTGGCGCTCT	2092
QY	2041	GTGCTGGGCTCTGACGATATTCACAGGGCTCTGGCGACCTTCGTGTCTGTGTGGGCTC	2100
Db	2093	GTGCTGGGCTCTGACGATATTCACAGGGCTCTGGCGACCTTCGTGTCTGTGTGGGCTC	2152
QY	2101	CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGCGGCGCTACAGACAC	2160
Db	2153	CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGCGGCGCTACAGACAC	2212
QY	2161	ATCCCCCAGACAGGCTTCAGGAGGTCACTGCTCAGCATCATCAAACCCAGAACAGTAC	2222
Db	2213	ATCCCCCAGACAGGCTTCAGGAGGTCACTGCTCAGCATCATCAAACCCAGAACAGTAC	2272
QY	2221	TGCGTGGCTCGGTATGCGGTGTCCAGAGAGCCCGCATGGGCGACGTCCGAGAGGCTTTC	2280
Db	2273	TGCGTGGCTCGGTATGCGGTGTCCAGAGAGCCCGCATGGGCGACGTCCGAGAGGCTTTC	2333
QY	2281	AAGAGCCACGCTCTTACTTTGACAGACTCCAGCGCTACATGCGACAGTTGTGGCTTAC	2340
Db	2333	AAGAGCCACGCTCTTACTTTGACAGACTCCAGCGCTACATGCGACAGTTGTGGCTTAC	2392
QY	2341	CTGACAGAGACACAGCCCGCTGAGAGGATGCGGTCTCATGACAGAGCTCTCCCTGAT	2400
Db	2393	CTGACAGAGACACAGCCCGCTGAGAGGATGCGGTCTCATGACAGAGCTCTCCCTGAT	2452
QY	2401	GAGGCTCAGAGTGGCTCTTGAGAGTCTTCTAAGCTTCAATGTGACACAGGCGGTGGC	2460
Db	2453	GAGGCTCAGAGTGGCTCTTGAGAGTCTTCTAAGCTTCAATGTGACACAGGCGGTGGC	2512
QY	2461	ATCAGGGGCAAGTCTTACATGTCAGATGCGAGGGATCCCGCAGGGCTCATCTCTCACG	2520
Db	2513	ATCAGGGGCAAGTCTTACATGTCAGATGCGAGGGATCCCGCAGGGCTCATCTCTCACG	2572
QY	2521	CTGCTCTGACGCTGTGTCTAGAGGACATGAGAAACAAGCTTTTGGCGGGATTCGGCGG	2588
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QY	2581	GACGCGGCTGCTCCCTGCGCTTTGGTGGATGATTTCTTGTGTGACACCTCACTCACCCAC	2640
Db	2633	GACGCGGCTGCTCCCTGCGCTTTGGTGGATGATTTCTTGTGTGACACCTCACTCACCCAC	2692
QY	2641	GCGAAACCTTCTCTCAGAGACCTGTGTCCAGAGTTCCTCTAGATATGTGTGTGTGAC	2700
Db	2693	GCGAAACCTTCTCTCAGAGACCTGTGTCCAGAGTTCCTCTAGATATGTGTGTGTGAC	2753
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Db	2753	TTGGCGAAGACAGTGTGAATTTCCCTGTGAGAGACAGAGGCTGGGTGGACGGCTTTT	2812
QY	2761	GTTTCAAGATGCGCGGCCACAGGCTATTTCCCTGTGTGGGCTGTGTGTGTGAATCCCGAAC	2820
Db	2813	GTTTCAAGATGCGCGGCCACAGGCTATTTCCCTGTGTGGGCTGTGTGTGTGAATCCCGAAC	2872
QY	2821	CTGAGAGTGCAGAGCACTACTCCAGCTATGCGCGGACCTTCATCAAGGCCAGTCTCAC	2880

Db	2873	CTGAGGATGACAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAC	2932
Qy	2881	TTCAACCGGGGTTTAAAGCTGAGAGAAACATGCTCGCAACTCTTTGGGGTCTTGGG	2944
Db	2933	TTCAACCGGGGTTTAAAGCTGAGAGAAACATGCTCGCAACTCTTTGGGGTCTTGGG	2992
Qy	2941	CTGAAGTGCACAGCCTGTTTCTGAGTTTGCAGTGAACAGCCTCACAAGGTTGCACC	3000
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Qy	3001	AACATCTACAAGATCTCTCTGTGTGAGAGGTACAGTTTCAACGATGTGTGTGAGTCC	3066
Db	3053	AACATCTACAAGATCTCTCTGTGTGAGAGGTACAGTTTCAACGATGTGTGTGAGTCC	3112
Qy	3061	CCATTTCATCAGCAAGTTTGAAGAACCCACATTTTTCCTGCGGCTATCTGCACAG	3120
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Qy	3121	GCTCTCCCTCTGTACTCCATCCTGAAGACGAAAGCAGAGGATGCTGTGGGGCCAA	3180
Db	3173	GCTCTCCCTCTGTACTCCATCCTGAAGACGAAAGCAGAGGATGCTGTGGGGCCAA	3222
Qy	3181	GAGGCTGCGGCGGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCACCAAGATTCTG	3240
Db	3233	GAGGCTGCGGCGGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCACCAAGATTCTG	3292
Qy	3241	CTCAAGCTGACCTGCACACCGTGTACCTACGCGGACCTCTGGGGTCACTCAGACACC	3300
Db	3293	CTCAAGCTGACCTGCACACCGTGTACCTACGCGGACCTCTGGGGTCACTCAGACACC	3352
Qy	3301	CAGACGACAGTGAAGTCCCGGGGACGACGCTGACATGCTCCCTGAGAGCGGACACC	3360
Db	3353	CAGACGACAGTGAAGTCCCGGGGACGACGCTGACATGCTCCCTGAGAGCGGACACC	3412
Qy	3361	AACCGGACACTGCTCCTCAGACTTCAAGACCAATCTCGACTAGTAGGCCAACCC	3411
Db	3413	AACCGGACACTGCTCCTCAGACTTCAAGACCAATCTCGACTAGTAGGCCAACCC	3463
Db	3413	AACCGGACACTGCTCCTCAGACTTCAAGACCAATCTCGACTAGTAGGCCAACCC	3463
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VERSION	AR182221.1	GI:20225137	
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SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 4015)		
AUTHORS	Morin,G.B.		
TITLE	Human telomerase catalytic subunit variants		
JOURNAL	Patent: US 6337200-A 1 08-JAN-2002;		
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Qy	61	GAGGTGCTGCGCTGACGCTTGTGTGCGGCGGCTGAGGCGCCCAAGGCTGCGGCTGATG	120
Db	113	GAGGTGCTGCGGCTGACGCTTGTGTGCGGCGGCTGAGGCGCCCAAGGCTGCGGCTGATG	172
Qy	121	CAGGCGGAGACCGGCGGCTTTTCCGCGGCTGTGATGCCCAAGTGCATGATGTGCTGACC	180

Db	173	CAGCGCGGGAGACCGGGGGCTTTTCGGCGCGCTGGTGGCCAGTGCCTGATGTGGCTGCGC	232
QY	181	TGGACGCACGACCGCGCCCCCGCGGCCCTTCCTTCGGCCAGGTGTCTTGCTTGAAGAG	240
Db	223	TGGACGCACGACCGCGCCCCCGCGGCCCTTCCTTCGGCCAGGTGTCTTGCTTGAAGAG	292
QY	241	CTGGTGGCCGAGTGTCTCAGAGCGCTGTGGCAGCGCGCGCGGAAGAACTGTGTGCCTTC	300
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QY	301	GCGTTCCGGCTGTCTGAGAGGGGGCCCCCGGGGGCCCCCGAGGCTTACCAACAGCGTG	360
Db	353	GCGTTCCGGCTGTCTGAGAGGGGGCCCCCGGGGGCCCCCGAGGCTTACCAACAGCGTG	412
QY	361	CGCAGCTACTGCGCCAAACAGGTACCGACCACTGCGGGGGAGCGGGGGCGCTGGGGGCTG	420
Db	413	CGCAGCTACTGCGCCAAACAGGTACCGACCACTGCGGGGGAGCGGGGGCGCTGGGGGCTG	472
QY	421	CTGCTGCGCGCGGTGGGCGAGAGGTGTCTGGTTCACTCTGTGGACAGCTGCGCGTCTTT	480
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QY	481	GTGCTGTGTGCTCCAGCTGCGCTTACCAAGGTGTGCGGGCGCGCGCTGTACAGCTCGGC	540
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Db	593	GCTGCGACTGAGCGCGCGCGCCCCCGCCACACGCTGTGTGAACCCCGAAGGCGTCTGGAGTGC	652
QY	601	GAAACGGGCTTGAACCAATAGCGGTAGAGGAGCGGAGGTCCCCCTGGGCTTCCACAGCCCG	660
Db	653	GAAACGGGCTTGAACCAATAGCGGTAGAGGAGCGGAGGTCCCCCTGGGCTTCCACAGCCCG	712
QY	661	GGTCCGAGAGAGCGCGGGGGGAGTGGCCAGAGTCTGCGCGTTGGCCCAAGGCGCCACG	720
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QY	781	GGCAGAGACGCGTGGACCGAGTGAACCGGTGTCTGTGTGTGTGTGAACCTGGCCAGACCGGC	840
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QY	841	GAAAGAGCACTCTTTTGAAGAGGTGCCTCTTGACAGCGGCACTCCACCACTCCGTG	900
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QY	901	GGCGCGCAGACCAACGCGGGGGCCCCCATTCACATCGGGGCGACACAGTCCCTGGAGACAG	960
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QY	961	CTTTGTCCCCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCACTGAGCGCAAGAGAG	1020
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QY	1021	CAGCTGGGGGCGCTCTCTACATCTAGCTCTCTGAGGGCGACGCTGGGCGCTCGAGG	1080
Db	1073	CAGCTGGGGGCGCTCTCTCTACTCTAGCTCTCTCTGAGGGCGACGCTGGGCGCTCGAGG	1132
QY	1081	CTGCTGAGAACCACTTTTCTGGGTTCCAGGACCTGTAGTCCAGGAGCTCCCGCAGGTTG	1140
Db	1133	CTGCTGAGAACCACTTTTCTGGGTTCCAGGACCTGTAGTCCAGGAGCTCCCGCAGGTTG	1192
QY	1141	CCCCGCGCTGGCCCCGCTACTGGCAAAATCGGGCCCCGTGTTCTGAGAGCTGTTGGGAAC	1200
Db	1193	CCCCGCGCTGGCCCCGCTACTGGCAAAATCGGGCCCCGTGTTCTGAGAGCTGTTGGGAAC	1252
QY	1201	CACGCGCAGTGCCTCTACGGGGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTC	1260

Db	1253	CACGGCAGTGGCCCTTACGAGGAGTGCTCTCAAGACGCACTGGCCGCTGACGCTGGCGCT	13112
QY	1261	ACCCGAGAGCCGGGTGTGTGTGCCCGGAGAAAGCCCCAGGGCTCTGTGGCCCCCGAG	1320
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Db	1373	GAGGAGGACACAGACCCCGTTCGCTGGTGCAGCTGCTCCGACAGCAACGAGAGCCCTGG	1432
QY	1381	CAGGTGTAACGGCTTGTGTGGGAGCTGCTGGGAGCGGCTGGGAGCGGCTGGGAGCG	1440
Db	1433	CAGGTGTAACGGCTTGTGTGGGAGCTGCTGGGAGCGGCTGGGAGCGGCTGGGAGCG	1492
QY	1441	TCGAGGCAACAGAACGCCGCTTCTCAGAAACACCAAGAAATTATCTCCCTGGGAG	1500
Db	1493	TCGAGGCAACAGAACGCCGCTTCTCAGAAACACCAAGAAATTATCTCCCTGGGAG	1552
QY	1501	CATGCGAAGCTCTCGCTGACAGAGGTGACGAGAAAGTGAACGTGGGAGCATGGCTTGG	1560
Db	1553	CATGCGAAGCTCTCGCTGACAGAGGTGACGAGAAAGTGAACGTGGGAGCATGGCTTGG	1612
QY	1561	CTGCGCAGAGAGCCAGAGGGTGTGCTGTGTTCGAGCCGACAGACACCGCTTGGAGAG	1620
Db	1613	CTGCGCAGAGAGCCAGAGGGTGTGCTGTGTTCGAGCCGACAGACACCGCTTGGAGAG	1672
QY	1621	ATCTCGGCAAGTTCTGTGCACTGGGTATGAGTGTACGACGTGGAGCTGTAGAGCT	1680
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QY	1681	TTCTTTTATGTACGAGAGACCAAGTTCAAAAAGAACAGGCTCTTTTCTACCGAAGT	1740
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QY	1741	GTCCTGAGCAAGTTTGCAAAAGCATTTGGAAATCAGACACTTGGAGAGGAGTCACTGG	1800
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QY	1801	GAGCTGTGGAAGACAGAGTCAAGCAGCATCGGAAAGCAGAGCCCGCTTGCTGACGTCC	1860
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Db	1913	AGACTCCGCTTCATCCCGAGGCTGACGAGGCGCGATTTGGAAATGAACTAGACGTTC	1972
QY	1921	GTGGGAGCCAGAACGTTCCGAGAGAAAGAGGCGCAGCGCTTCACCTCGAGGGTGAAG	1980
Db	1973	GTGGGAGCCAGAACGTTCCGAGAGAAAGAGGCGCAGCGCTTCACCTCGAGGGTGAAG	2032
QY	1981	GCACTGTTCAAGGTGTCAACATACAGAGGGGAGCGGCGCCCGGCTCTGGGGCGCTC	2040
Db	2033	GCACTGTTCAAGGTGTCAACATACAGAGGGGAGCGGCGCCCGGCTCTGGGGCGCTC	2092
QY	2041	GTGCTGGGAGCTGAGAGATATCAACAGGAGCTGGGAGCACTTGTGTGTGGTGGGAGC	2100
Db	2093	GTGCTGGGAGCTGAGAGATATCAACAGGAGCTGGGAGCACTTGTGTGTGGTGGGAGC	2152
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Db	2213	ATCCCGCCAGACAGGCTCAAGAGGTATGCGACGATCATCMAACCCAGAACACGTAC	2272
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Db	2273	TGCGTGCATGCTATGACCGTGGTTCAGAAAGGCGCCCATTTGGAGCAAGTCCGAGGCTTC	2332
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QY	2461	ATCAGGGGCAAGTCTCTAGTCCAGTGCATGCGAGGGATCCCGACAGGCTCCATCTCTCCACG	2520
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Dp	2693	GCGAAAACTTCTCTCAGAGACCTCTGTCCGAGGTCTCTTAGATATGCTGTGTGTGAC	2752
QY	2701	TTGGGGAAGACAGTGGTGAATTCCTCCGTGAAACAGAGGCTCGGGTGGCACGGCTTTT	2760
Dp	2753	TTGGGGAAGACAGTGGTGAATTCCTCCGTGAAACAGAGGCTCGGGTGGCACGGCTTTT	2812
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Dp	2813	GTTTCAAGATGCCGGGCCACGGCTTATTTCCCTGTGTGGGCTCTGCTGTGATACCCGAC	2872
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QY	3361	AAACCGGACATCGCCCTCAAGACTTCAAAACCATCTGTGACTGTATGGACACC	3411
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ACCESSION AR224455
VERSION AR224455.1 GI:23333293
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Gaeta, F.C.A.
TITLE Dendritic cell vaccine containing telomerase reverse transcriptase for the treatment of cancer
JOURNAL Patent: US 6440735-A 1 27-AUG-2002;
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Query Match 100.0%; Score 3411; DB 6; Length 4015;
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DB 473 CTGTGCGCGCGCTGCGAGCGCGCTTCCGCGCGCTGCGAGCGCGCTGCGAGCGCGCT 532
QY 481 GTGTGCGCGCGCTGCGAGCGCGCTTCCGCGCGCTGCGAGCGCGCTGCGAGCGCGCT 540
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 ORGANISM Unknown.
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 AUTHORS Geeth,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
 Hartley,C.B. and Andrews,W.H.
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OY	2701	TTGCGGAAAGACAGTGTGAACTTCCCTGTAGAAAGACGAGGCTGGGTGGACAGGCTTTT	2766
Db	2753	TTGCGGAAAGACAGTGTGAACTTCCCTGTAGAAAGACGAGGCTGGGTGGACAGGCTTTT	2812
OY	2761	GTTACAGATGCGCGGCCACAGGCTATATCCCTCTGTGTCGGGCTGTGCTGAAATACCAGAC	2822
Db	2813	GTTACAGATGCGCGGCCACAGGCTATATCCCTCTGTGTCGGGCTGTGCTGAAATACCAGAC	2872
OY	2821	CTGAGAGTGCAGAGGCACTACTCCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCAC	2888
Db	2873	CTGAGAGTGCAGAGGCACTACTCCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCAC	2932
OY	2881	TTCAACCGCGGCTTCAAGCTGGGAGGAAACATGCGTCGCAAACTTTGGGGTCTTGGGG	2944
Db	2933	TTCAACCGCGGCTTCAAGCTGGGAGGAAACATGCGTCGCAAACTTTGGGGTCTTGGGG	2992
OY	2941	CTGAAGTGCACAGCCTGTTTCTGGAATTGCAAGTGAACAGCTTCAGACGGTGTGCACC	3000
Db	2993	CTGAAGTGCACAGCCTGTTTCTGGAATTGCAAGTGAACAGCTTCAGACGGTGTGCACC	3052
OY	3001	AACATCTCAAGATCTCCTGTGTGAGGGGATACAGTTCACGCAATGTCTGTAGAGCTC	3066
Db	3053	AACATCTCAAGATCTCCTGTGTGAGGGGATACAGTTCACGCAATGTGTGTGAGAGCTC	3112
OY	3061	CCATTTCATCAGCAAGTTTGGAGAAACCCACATTTTCTGCGGGTCACTCTGACAG	3128
Db	3113	CCATTTCATCAGCAAGTTTGGAGAAACCCACATTTTCTGCGGGTCACTCTGACAG	3172
OY	3121	GGCTCCCTCTGTACTCCATCTGTAAAGCAAGAACGAGAGGATGTGCTGAGGGGCCAAG	3188
Db	3173	GGCTCCCTCTGTACTCCATCTGTAAAGCAAGAACGAGAGGATGTGCTGAGGGGCCAAG	3232
OY	3181	GGCGCGCGGCGCTCTGCGCTCCGAGGCCGTGCAAGTGAAGTGTGCGACCAAGACTTCG	3248
Db	3233	GGCGCGCGGCGCTCTGCGCTCCGAGGCCGTGCAAGTGAAGTGTGCGACCAAGACTTCG	3292
OY	3241	CTCAAGCTGACCTGACACCGTGTCACTACGCGCACACTCTGAGGGTCACTACAGGACAC	3300
Db	3293	CTCAAGCTGACCTGACACCGTGTCACTACGCGCACACTCTGAGGGTCACTACAGGACAC	3352
OY	3301	CAGACGCACTGATGTGGAAGTCCCGGAGACGACGTGACTGCCCTGAGAGCGCGACGC	3366
Db	3353	CAGACGCACTGATGTGGAAGTCCCGGAGACGACGTGACTGCCCTGAGAGCGCGACGC	3412
OY	3361	AACCGGCACTGCGCTCTCAGACTTCAAGACATCTGAGACTATGGCCACC	3411
Db	3413	AACCGGCACTGCGCTCTCAGACTTCAAGACATCTGAGACTATGGCCACC	3463

LOCUS	AR243328	4015 bp	mRNA	linear	PAT 20-DEC-2002
DEFINITION	AR243328 Sequence 1 from patent US 6475789.				
ACCESSION	AR243328				
VERSION	AR243328.1 GI:27290539				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 4015) Cech,T.R., Linger,J., Nakamura,T., Chapman,K.B., Morin,G.B., Hatley,C.B. and Andrews,W.H. Human telomerase catalytic subunit: diagnostic and therapeutic methods				
TITLE	Patent: US 6475789-A 1 05-NOV-2002;				
JOURNAL	Location/Qualifiers				
FEATURES	1..4015				
source	/organism="unknown" /mol_type="mRNA"				
ORIGIN					
Query Match	100.0%; Score 3411; DB 6; Length 4015;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 3411; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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QY	61	GAGATGCTGCCTGTCGACGATTCATGACGAGCGCTGAGGCGCCGAGGCTGCGCTGATG	120		
DB	113	GAGATGCTGCCTGTCGACGATTCATGACGAGCGCTGAGGCGCCGAGGCTGCGCTGATG	172		
QY	121	CAGCGCGGAGACCCGCGCGCTTCCGCGCGCTGATGACCAATGCTGATGCTGCTGCC	180		
DB	173	CAGCGCGGAGACCCGCGCGCTTCCGCGCGCTGATGACCAATGCTGATGCTGCTGCC	232		
QY	181	TGGAGACGAGCGGCG	240		
DB	233	TGGAGACGAGCGGCG	292		
QY	241	CTGATGCGCGCGAGTGTCTGACAGAGGTGTGTGAGCGCGAGCGAGAAAGTGTGCTGCTTC	300		
DB	293	CTGATGCGCGCGAGTGTCTGACAGAGGTGTGTGAGCGCGAGCGAGAAAGTGTGCTGCTTC	352		
QY	301	GGCTTCGGCGCTGTGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	360		
DB	353	GGCTTCGGCGCTGTGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	412		
QY	361	CGAGCTACCTGACCCCAACACGATGACCGACGCACTGCGGAGGAGCGGAGCGTGGAGCTG	420		
DB	413	CGAGCTACCTGACCCCAACACGATGACCGACGCACTGCGGAGGAGCGGAGCGTGGAGCTG	472		
QY	421	CTGATGCGCGCGCGTGTGACGAGCTGTGATCACTGCTGAGGACGCTGCGCGCTCTT	480		
DB	473	CTGATGCGCGCGCGTGTGACGAGCTGTGATCACTGCTGAGGACGCTGCGCGCTCTT	532		
QY	481	GTGCTGTGTGTCTCCAGCTGTGCTTACAGATGTGCGGAGCGCGCTGTACAGATCTGAGC	540		
DB	533	GTGCTGTGTGTCTCCAGCTGTGCTTACAGATGTGCGGAGCGCGCTGTACAGATCTGAGC	592		
QY	541	GCTGCACCTACGAGCG	600		
DB	593	GCTGCACCTACGAGCG	652		
QY	601	GACGAGGCTGTGAACCAATAGCTCAGAGGAGCGCGGAGTCCCTGTGAGCTTGACAGCCCG	660		
DB	653	GACGAGGCTGTGAACCAATAGCTCAGAGGAGCGCGGAGTCCCTGTGAGCTTGACAGCCCG	712		
QY	661	GGTGTGAGAGAGCG	720		
DB	713	GGTGTGAGAGAGCG	772		

QY 721 CTTGCGCTGCTCCCTGAGCCGAGCGAGCCGCTTGGGAGGGGCTCTGAGCCCG 780
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QY 781 GGCAGGAGCGGTGAGCGAGTGAACCGGTGTTCTGTGTGTGTGAACCTGTGCAAGCCCGC 840
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QY 841 GAAAGAGCGACCTCTTTTGAAGGGTGGCTCTGTGCAAGCGCGCACTCCCAATCCGTT 900
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QY 2101 CAGAGCCGCGCGCTGAGCTGTACTTGTCAAGGTGAGTGAAGCGGCGGCTGAGAGC 2160
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QY 2281 AAGAGCAAGTCTTACCTTGAAGAGAGCTTCAAGCGCTGATGAGAGCAAGTGTGGCTAC 2340
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QY 2641 GCGAGAACTTCTCAGAGAGCTTGTGTGAGAGTGTCTGTGAGTGTGCTGTGTGAG 2700
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LOCUS Sequence 3 from patent US 6331399.
DEFINITION AR263555
ACCESSION AR263555
VERSION AR263555.1 GI:28075300
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Montu, B. P., Gaarde, W. A. and Wanciewicz, E.
TITLE Antisense inhibition of c-erbB expression
JOURNAL Patent: US 6331399-A 3 18-DEC-2001;
FEATURES
Source Location/Qualifiers
1..4015
/organism="unknown"
/mol_type="genomic DNA"

Query Match 100.0%; Score 3411; DB 6; Length 4015;
Best Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GCGATGCGCGCGCTCCCGCTGCGAGCGTGCCTCTGCTGCGACGACCTACACG 60
Qy 53 GCGATGCGCGCGCTCCCGCTGCGAGCGTGCCTCTGCTGCGACGACCTACACG 112
Db 61 GAGCTGCTCGCTGCGCTGCGACGCTTCTGCGCGCGCTGAGGCGCCAGAGGCTGCGCTGAGT 120
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Db 121 CAGCGCGAGGACCCGCGCGCTTCCGCGCGCTGAGTGCCTGAGTGCCTGAGTGCCTGAGTGC 180
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Qy 421 CTGCTGCGCGCGGAGCGAGAGTGTCTGCTTCACTGCTGACAGCTGCGGCTTT 480
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Db 533 GTGCTGTGCTCTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCTGTACAGCTGCGC 592
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ACCESSION AR265996
VERSION AR265996.1 GI:29694842
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Montu, B.P., Gaarde, W.A., Freier, S.M. and Wanciewicz, E.
TITLE Antisense modulation of TERT expression
JOURNAL Patent: US 6492171-A 3 10-DEC-2002;
FEATURES
Location/Qualifiers
source 1..4015
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Query Match 100.0%; Score 3411; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db GCGATGCGCGCGCTCCCGCTGCGAGACCGTGCCTCCCTGCTGCGGACCACTACCGC 112
QY 61 GAGGTGCTGCGCTGCGGACCACTGCTGCGGCGCTGCGGCGCCCAAGGCGGCTGCG 120
Db 113 GAGGTGCTGCGCTGCGGACCACTGCTGCGGCGCTGCGGCGCCCAAGGCGGCTGCG 172
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QY 181 TGGACGACG 240
Db 233 TGGACGACG 292
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VERSION	AR93084.1				
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SOURCE	unknown.				
ORGANISM	unknown.				

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AUTHORS	Cech,T.R., Ungerer,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
TITLE	Hatley,C.B. and Andrews,W.H. Cells immortalized with telomerase reverse transcriptase for use in drug screening
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QY	121 CAGGCGCGGAGACCCGGCGGCTTTCCGGCGCTGTGTGGCCAGATGCTGTGTGTGTGCC 180
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REFERENCE
1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
TITLE
Damm, M. W., Phelps, R. C. and Brockmeyer, C.
Method for quantitatively analyzing tumor cells in a body fluid and
test kits suited therefor
JOURNAL
Patent: WO 9940221-A 10 12-AUG-1999;
DAMM MICHAEL W (DE); PHELPS ROBERT C (DE); BROCKMEYER CARSTEN (DE)
FEATURES
Location/Qualifiers
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ORIGIN

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LOCUS AX133979
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ACCESSION AX133979
VERSION AX133979.1 GI:14139919
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Chang S.Y. and Santini, C.D.
AUTHORS Quantitation of heart mRNA expression
TITLE Patent: EP 1108789-A 1 20-JUN-2001;
JOURNAL F. HOFMANN-LA ROCHE AG (CH)
FEATURES
source location/Qualifiers
1..4015
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ORIGIN
Query Match 100.0%; Score 3411; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 53 GCGATGCCGCGCGTCTCCCGCTGCGAGCGCTGCTGCTGCGAGAGAGAGAGAG 112
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Db 113 GAGGTGCTGCGAG 172
QY 121 CAGGCGGAG 180
Db 173 CAGGCGGAG 232
QY 181 TGAGAGCAG 240
Db 233 TGAGAGCAG 292
QY 241 CTGAG 300

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Dp	2573	CTGCTCTGCAGCCTGTGTCTGATCGGCGCGACATGAGAAACAAGCTTTGCGGGATTCGCGG	2632
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Dp	2633	GACGGGCTGTCTCTCCGCTTTGGTGAATTTCTTTGTGTGACACCTCACTCAACCAC	2692
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QY	2821	CTGAGAGTGTGACAGCGCATTACTCCAGCTATGCCCCGAGCTTCATATAGACCATCTCAC	2880
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QY	2941	CTGAAGTGTCAACAGCTGTCTTCTGAGTTTGAGGTGAACAGCTTCAGACGTTGTGACC	3000
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Dp	3053	AACATCTTCAAGATCTCTGT	3112
QY	3061	CCATTTCATCGCAAGTTTGGAGAAACCCACATTTTCTCGCGCGTATCTGACAGC	3120
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Dp	3173	GCGTCCCTCTGTCTCTCGATCCTGTAAAGGCCAAGAACGAGGAGTGTGCTGGGGGCCAAG	3232
QY	3181	GCGCGCGCGGCGCTCTGTGCGCTCTCGAGGCGGTGAGTGTGCTGTCCACAAGCATTCCTG	3240
Dp	3233	GCGCGCGCGGCGCTCTGTGCGCTCTCGAGGCGGTGAGTGTGCTGTCCACAAGCATTCCTG	3292
QY	3241	CTCAAGCTGATTCGACACCGTGTCAACCTTACCTGTGCACTCTCTGGGGTCACTCAGACGCC	3300
Dp	3293	CTCAAGCTGATTCGACACCGTGTCAACCTTACCTGTGCACTCTCTGGGGTCACTCAGACGCC	3352
QY	3301	CAGACGCACTGATGTGGAGACTCCCGGGACGACGCTGACTGTGCTGTGAGGCGCGACGCC	3360
Dp	3353	CAGACGCACTGATGTGGAGACTCCCGGGACGACGCTGACTGTGCTGTGAGGCGCGACGCC	3412
QY	3361	AAACCCGCACTGCGCTCTAGACTTTTAAGACCATCTGTGAATGTATGCGCACCC	3411
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DEFINITION	Sequence 1 from Patent WO0207949.		linear
ACCESSION	AX552695		
VERSION	AX552695.1	GI:25896697	
KEYWORDS			
SOURCE	Homo sapiens (human)		

ORGANISM	Homo sapiens
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1
AUTHORS	Deming,C., Clark,A.J. and Schiff,J.M.
TITLE	Animal tissue with carbohydrate antigens compatible for human transplantation
JOURNAL	Patent: WO 02074948-A 1 26-SEP-2002; Geron Corporation (US)
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ORIGIN	

Query Match	100.0%	Score 3411;	DB 6;	Length 4015;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 3411; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

[illegible]

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QY	1141	CCCCGCTTGCCCCCAGCGCTACTGGCAATGCGGCCCTGTGTTCTGTAGGCTGTGGAAAC	1200
Db	1193	CCCCGCTTGCCCCCAGCGCTACTGGCAATGCGGCCCTGTGTTCTGTAGGCTGTGGAAAC	1255
QY	1201	CACGCGCAGTGGCCCCCTACGAGGGGGTGGCTCCACAGGCACTTGCCGCTGGGAATCGGTC	1266
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Db	1793	GTCGTGGACCAAGTTTCAAAAGCATTTGGATTCAGACAGCACTTGAAAGGGGTGCACTGTGGG	1852
QY	1801	GAGCTGTGGAAGCAGAGGTGACGACAGATCGGAGAGCAGAGCCGCGCTGTGACGTCC	1866
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Db	2033	GCACTGTTCAAGGTGTCTAACTACAGAGGGGCGGGCGGCCCCGGCTCTCTGGGCGCTCT	2092
Qy	2041	GTGCTGGGCTGAGACGATATCCACAGGGCGCTGGGCGACCTTCGTGTCTCGTGGGCGGCG	2100
Db	2093	GTGCTGGGCTGAGACGATATCCACAGGGCGTGGGCGACCTTCGTGTCTCGTGGGCGGCG	2152
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Db	2213	ATCCCCCAGAGACAGGCTCAGCGAGAGGTATGCGCACGACATCAACAAACCAGAACCGAC	2272
Qy	2221	TGCGTGCCTGCGTATGCGGTGTCCGAGAGGCGGCCATGGGCAAGTCCGCAAGGCTTC	2280
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Qy	2281	AAGAGCCACGCTCTCTACCTTTACAGACCTCCAGCGCGTACATGCGCACGTTGTGGCTCAC	2340
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Qy	2581	GACGGGCTGCTCTCGCGTTTGTGGAGATTTCTCTGTGTGGAGAACCTCACCTCACCCAC	2640
Db	2633	GACGGGCTGCTCTCGCGTTTGTGGAGATTTCTCTGTGTGGAGAACCTCACCTCACCCAC	2692
Qy	2641	GCGAAAACTTCTCAGAGACCTGTGTCGAGGTGTCCCTGAGTATGCTGTGTGTGTAAAC	2700
Db	2693	GCGAAAACTTCTCAGAGACCTGTGTCGAGGTGTCCCTGAGTATGCTGTGTGTGTAAAC	2752
Qy	2701	TTTGGGAAAGACAGTGTGGAATCTTCCCTGTGTAAGAAAGAGGCGCTGGGTGGCACGGCTTTT	2760
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OY 3061 CCATTTCATGAGCAAGTTTGAGAGAACCCACATTTTCTGCGCGTCAATCTGACAG 3120
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Search completed: March 1, 2004, 14:22:25
Job time : 8575.51 secs

PT proliferation conditions especially cancer and ageing.

XX Claim 5; Fig 16; 387bp; English.

XX The present sequence encodes human telomerase reverse transcriptase
CC (hTERT), which is a ribonucleoprotein. The present invention also
CC describes the following methods: (A) determining whether a test compound
CC is a modulator of hTERT, by detecting the change in hTERT recombinant
CC protein or polynucleotide on administration of the compound; (B)
CC preparation of recombinant telomerase by contacting a protein preparation
CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
CC protein in a sample by binding a relevant probe to the sample and
CC detecting the complex formed or in the case of RNA detection, amplifying
CC the product and correlating the presence of complex or amplification
CC product with presence of hTERT in the sample; and (D) increasing the
CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
CC the use of an agent that causes an increase in cell vertebrate cell
CC proliferation to create a medicament that inhibits ageing. A protein
CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
CC the manufacture of medicaments for inhibiting the effect of ageing or
CC cancer. Inhibitors of telomerase activity can be used to treat conditions
CC that are associated with high telomerase activity. A protein preparation
CC of hTERT can also be used in the new methods

SQ Sequence 3955 BP; 648 A; 1353 C; 1251 G; 703 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 2; Length 3955;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 113 GAGGTGCTGCGCTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 172
QY 121 CAGGCGGAGGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 173 CAGGCGGAGGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 232
QY 181 TGGGACGCGAGCG 240
DB 223 TGGGACGCGAGCG 292
QY 241 CTGCTGCGCGCGAGCTGCGAGAGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 293 CTGCTGCGCGCGAGCTGCGAGAGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GAGCTTCCGCGCTGCGAGAGCG 360
DB 353 GAGCTTCCGCGCTGCGAGAGCG 412
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DB 473 CTGCTGCGCGCGAGCTGCGAGAGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 532
QY 481 GTGCT 540
DB 533 GTGCT 592
QY 541 GCTGCGCACTCAGGCG 600
DB 593 GCTGCGCACTCAGGCG 652
QY 601 GAAAGCGCGCTGAGAACATAGCTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 653 GAAAGCGCGCTGAGAACATAGCTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 712

QY 661 GGTGCGAGAGCG 720
DB 713 GGTGCGAGAGCG 772
QY 721 CTTGCGCGCTGCG 780
DB 773 CTTGCGCGCTGCG 832
QY 781 GCGAGAGCGCTGAGAGCG 840
DB 833 GCGAGAGCGCTGAGAGCG 892
QY 841 GAAAGAGCGCACTCTTGAAGAGTGCCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
DB 893 GAAAGAGCGCACTCTTGAAGAGTGCCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 952
QY 901 GGCCTGCGAGCG 960
DB 953 GGCCTGCGAGCG 1012
QY 961 CTTGCTGCGCGCGTGAAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
DB 1013 CTTGCTGCGCGCGTGAAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1072
QY 1021 CAGTGCAGCGCGCT 1080
DB 1073 CAGTGCAGCGCGCT 1132
QY 1081 CTGCTGAGAGCACTTTTCTGAGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB 1133 CTGCTGAGAGCACTTTTCTGAGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1192
QY 1141 CCGCGCTGCG 1200
DB 1193 CCGCGCTGCG 1252
QY 1201 CAGCGCGAGTCCCTTCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
DB 1253 CAGCGCGAGTCCCTTCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1312
QY 1261 ACCCGAGAGCGCGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
DB 1313 ACCCGAGAGCGCGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1372
QY 1321 GAGAGAGCAACAGAGCG 1380
DB 1373 GAGAGAGCAACAGAGCG 1432
QY 1381 CAGGTGTAAGGCTTGTGCG 1440
DB 1433 CAGGTGTAAGGCTTGTGCG 1492
QY 1441 TCCAGAGCAACAGAGCG 1500
DB 1493 TCCAGAGCAACAGAGCG 1552
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DB 1553 CATGCGAAGCTTCTGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1612
QY 1561 CTGCGCAGAGCGCGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1613 CTGCGCAGAGCGCGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1672
QY 1621 ATCTGCGCAAGTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1680
DB 1673 ATCTGCGCAAGTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1732
QY 1681 TTTCTTTATGTCAGAGAGCAAGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1740
DB 1733 TTTCTTTATGTCAGAGAGCAAGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1792

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 DB 1793 GTCTGAGCAAGTTGCAAGCATTTGATGACAGACATTTGAAGAGGTGACGTGCGG 1852
 QY 1801 GAGCTGTGGAAGAGGTGACAGCATTTGGAGAGCCAGGCCCTGCTGACGTGCGG 1860
 DB 1853 GAGCTGTGGAAGAGGTGACAGCATTTGGAGAGCCAGGCCCTGCTGACGTGCGG 1912
 QY 1861 AGACTGTGAGGTGACATTTGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 1920
 DB 1913 AGACTGTGAGGTGACATTTGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 1972
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 DB 1973 GTGAGAGCCAGAAAGTTTCCGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2032
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 DB 2033 GCACTGTGAGGTGACATTTGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2092
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 DB 2273 TGCTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2332
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 QY 2341 CTGAGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2400
 DB 2393 CTGAGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2452
 QY 2401 GAGGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2460
 DB 2453 GAGGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2512
 QY 2461 ATCAGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2520
 DB 2513 ATCAGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2572
 QY 2521 CTGCTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2580
 DB 2573 CTGCTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2632
 QY 2581 GAGGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2640
 DB 2633 GAGGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2692
 QY 2641 GCGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2700
 DB 2693 GCGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2752
 QY 2701 TTGAGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2760
 DB 2753 TTGAGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2812
 QY 2761 GTTCAAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2820
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 DB 2933 TTCAACCGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2992
 QY 2941 CTGAAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3000
 DB 2993 CTGAAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3052
 QY 3001 AACATCTAAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3060
 DB 3053 AACATCTAAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3112
 QY 3061 CCAATCTAAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3120
 DB 3113 CCAATCTAAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3172
 QY 3121 GCTTCCCTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3180
 DB 3173 GCTTCCCTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3232
 QY 3181 GAGGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3240
 DB 3233 GAGGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3292
 QY 3241 CTCAAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3300
 DB 3293 CTCAAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3352
 QY 3301 CAGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3360
 DB 3353 CAGAGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3412
 QY 3361 AACCGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3411
 DB 3413 AACCGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3463

RESULT 2
 AA200724
 ID AA200724 standard; DNA; 4015 BP.
 XX
 AC AA200724;
 DT 06-OCT-1999 (first entry)
 DE Human telomerase catalytic domain DNA.
 KW Telomerase; catalytic domain; human; quantitation; tumour cell; melanoma;
 KW body fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
 KW acute lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer;
 KW breast cancer; ss.
 OS Homo sapiens.
 PN DE19804372-A1.
 PD 05-AUG-1999.
 PF 04-FEB-1998; 98DE-01004372.
 PR 04-FEB-1998; 98DE-01004372.
 PA (DAHM/) DAHM M W.
 PI Dahn MW;
 DR WPI; 1999-431408/37.
 XX
 PT Quantifying tumor cells by amplifying mRNA encoding the catalytic subunit
 of telomerase.

XX Example; Fig 1A-B; 26p; German.

CC This invention describes a novel method for the quantitation of tumour
CC cells in a body fluid which comprises (1) enrichment or isolation of
CC tumour cells in the sample; (2) amplification of mRNA from these cells
CC that encodes the catalytic subunit of telomerase and (3) quantifying the
CC amount of amplified mRNA. The method is applied to tumour cells derived
CC from (micro)metastases, e.g. associated with a wide range of tumours such
CC as T-cell lymphoblastoma, chronic myeloid or acute lymphatic leukaemia,
CC melanoma, pulmonary carcinoma, cancer of colon or breast etc. This
CC sequence encodes a human telomerase protein catalytic domain

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 2; Length 4015;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCGATGCCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGTCGCGACCACTACCGC 60
DB 53 GCGATGCCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGTCGCGACCACTACCGC 112
QY 61 GAGGTGCTGCGCTGCGAGCTGCTGCGGCGCTGCGGCGCCAGAGGCTGCGGCTGCG 120
DB 113 GAGGTGCTGCGCTGCGAGCTGCTGCGGCGCTGCGGCGCCAGAGGCTGCGGCTGCG 172
QY 121 CAGCGCGGAGACCCGCGCGCTTTCGCGCGCTGAGTGCAGTGTGTGCTGCGCC 180
DB 173 CAGCGCGGAGACCCGCGCGCTTTCGCGCGCTGAGTGCAGTGTGTGCTGCGCC 232
QY 181 TGGAGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 233 TGGAGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 292
QY 241 CTGCTGCGCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 300
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QY 301 GCGTTCGCGCTGCTGAGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 353 GCGTTCGCGCTGCTGAGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGCAGTACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB 413 CGCAGTACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472
QY 421 CTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 473 CTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 532
QY 481 GTGCTGCGCGCTCCGAGTGCCTGCTACAGTGTGCGGCGCGCGCGCGCGCGCG 540
DB 533 GTGCTGCGCGCTCCGAGTGCCTGCTACAGTGTGCGGCGCGCGCGCGCGCGCG 592
QY 541 GCTGCGCACTAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
DB 593 GCTGCGCACTAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 652
QY 601 GAACGGGCTGGAACCTACCTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 653 GAACGGGCTGGAACCTACCTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GGTGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
DB 713 GGTGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 772
QY 721 GGTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
DB 773 GGTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 832
QY 781 GGCAGGAGCGCGTGAACCGAGTGAACCGTGTGCTGTGCTGTGCTGTGCTGTG 840

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DB 893 GAAAGAGCCACTCTTTTGAAGGTCGCTCTCTGCGACGCGCACTCCCACTCCGTC 952
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DB 953 GGCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1012
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DB 1013 CTTTGTCCCGGTCGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1072
QY 1021 CAGTGGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
DB 1073 CAGTGGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1132
QY 1081 CTGTCGAGAGCAATCTTTCTGAGGTCAGAGCCCTGAGTGCAGGAGACTCCCG 1140
DB 1133 CTGTCGAGAGCAATCTTTCTGAGGTCAGAGCCCTGAGTGCAGGAGACTCCCG 1192
QY 1141 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
DB 1193 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1252
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DB 1253 CAGCGCGAGTCCCTCTAGAGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1312
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DB 1313 ACCCAGAGAGCGGTCGTGTGTCGCGCGAGAGAGCGCGCGCGCGCGCGCG 1372
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DB 1373 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1432
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DB 1433 CAGGTGTCAGGCTTGTGTCGCGCGCTGTCGCGCGCTGTCGCGCGCTGTCG 1492
QY 1441 TCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
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QY 1561 CTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
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DB 1673 ATCTGCGCAAGTCTCTGCACTGCGTATGATGATGATGATGATGATGATGAT 1732
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DB 1733 TTCTTTTATGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1792
QY 1741 GTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1793 GTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1852
QY 1801 GAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB 1853 GAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1912
QY 1861 AGACTGCGCTTCAATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
DB 1913 AGACTGCGCTTCAATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1972

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QY 1921 GTGGAGCCAGACGTTCCGACAGAGAAAAGAGGCGGACGCTCACCCTCGAGGGTGAAG 1980
 DB 1973 GTGGAGCCAGAACGTTCCGACAGAGAAAAGAGGCGGACGCTCACCCTCGAGGGTGAAG 2032
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 DB 2033 GCACTGTTCAGGTGTCTAACTACAGAGGGGCGCGCGCCCGGCTCTCTGGGGGCTCT 2092
 QY 2041 GTGCTGGGCTGTGAGAGTATCCACAGAGGCTGGCGACCTTGTGCTGTGTGTGGGGCC 2100
 DB 2093 GTGCTGGGCTGTGAGAGTATCCACAGAGGCTGGCGACCTTGTGCTGTGTGTGGGGCC 2152
 QY 2101 CAGAACCCGCGCGCTGAGCTGTACTTTGTCAAAGTGAATGTGACGGGCGGTACAGACCC 2160
 DB 2153 CAGAACCCGCGCGCTGAGCTGTACTTTGTCAAAGTGAATGTGACGGGCGGTACAGACCC 2212
 QY 2161 ATCCCGCAGAGACAGGCTCAGCGAGGTCATCCGACAGATCATCAACCCAGAAACAGCTAC 2220
 DB 2213 ATCCCGCAGAGACAGGCTCAGCGAGGTCATCCGACAGATCATCAACCCAGAAACAGCTAC 2272
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 DB 2273 TGCCTGCGCTCGGTATGCCGTGTGTCCAGAAAGCCGCCATGGGCACTGTCGAGAGCTTC 2332
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 DB 2333 AAGAACCCAGCTCTTACCTTGAACAGACCTCCAGCCGTGATGCGACAGCTTGTGGCTCAC 2392
 QY 2341 CTGACAGAGACAGAGCCCGCTGAGAGGATGCCGTGTCATCGACAGAGCTCTCCCTGAAT 2400
 DB 2393 CTGACAGAGACAGAGCCCGCTGAGAGGATGCCGTGTCATCGACAGAGCTCTCCCTGAAT 2452
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 DB 2453 GAGGCCAGAGTGGCTCTTGTGACGCTCTTCTAAGCTTCATGTGCCACAGCCGCTGCGC 2512
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 DB 2573 CTGCTCTGACGCTGTGTGTGTACGCGACATGAGAAACAAGCTTTTGCGGGATTCGCGCG 2632
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 QY 2761 GTTCAGATGCGCGCCCAAGGCTTATCCCTGTGAGGCGCTGCTGCTGTAATCCCGGAC 2820
 DB 2813 GTTCAGATGCGCGCCCAAGGCTTATCCCTGTGAGGCGCTGCTGCTGTAATCCCGGAC 2872
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 DB 2873 CTGAGAGTGAAGAGGACTACTCAGACTATGCCCGGACCTTCATCAGAGCCAGTCTCAC 2932
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 DB 2993 CTGAAGTGTCAAGCCTGTCTTCTGATTTTGAGGTGAACAGCTCCAGACGATGTGAC 3052

QY 3001 AACATCTACAAAGTCTCTGCTGTGACAGGCTACAGGTTTACGCATGTGTGCTGACAGCTC 3060
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 DB 3173 GCCTCCCTGTGCTACTCCATCCCTGAAAGCAAGAAACGAGGATGTGCTGGGGGCGCAAG 3232
 QY 3181 GGGCGCGCGCGCCCTGTGCGCTCCAGAGCCGTGACAGTGTGCTGACCAAGCAATTCCTG 3240
 DB 3233 GGGCGCGCGCGCCCTGTGCGCTCCAGAGCCGTGACAGTGTGCTGACCAAGCAATTCCTG 3292
 QY 3241 CTGAAGTGTCAAGCCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
 DB 3293 CTGAAGTGTCAAGCCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3352
 QY 3301 CAGACGCACTGAGTGTGAGAGCTCCCGGGGAGAGAGCTGACCTGAGAGGCGGAGCC 3360
 DB 3353 CAGACGCACTGAGTGTGAGAGCTCCCGGGGAGAGAGCTGACCTGAGAGGCGGAGCC 3412
 QY 3361 AACCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3411
 DB 3413 AACCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3463

RESULT 3

AAZ20279

ID AAZ20279 standard; cDNA; 4015 BP.

AC AAZ20279;

DT 17-JAN-2000 (first entry)

XX Human telomerase reverse transcriptase (hTERT) cDNA.

XX Telomerase reverse transcriptase; human; hTERT; cell proliferation;

XX cancer; ss.

XX Homo sapiens.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 56..3454

FT tag= a

PN W0950386-A2.

PD 07-OCT-1999.

PF 31-MAR-1999; 99WO-US007097.

PR 31-MAR-1998; 98US-00052864.

PR 03-AUG-1998; 98US-00128354.

XX (GERO-) GERON CORP.

XX Morin GB;

XX MPI; 1999-610842/52.

DR P-PSDB; AAY32090.

XX New catalytic polypeptide and polynucleotide, useful for increasing

PT catalytic activity in a cell.

PS Disclosure; Fig 2; 24pp; English.

XX This is the nucleotide sequence of cDNA encoding human telomerase reverse

CC transcriptase (hTERT; see AAY32090). Human telomerase is a target for

CC diagnosing and treating diseases relating to cell proliferation and

CC senescence, such as cancer, or for increasing the proliferative capacity

CC of a cell. A claimed method for increasing the proliferative capacity of
CC a vertebrate cell, especially a human or other mammalian cell, involves
CC introducing into the cell a recombinant hprt polynucleotide encoding an
CC hprt variant in which residues 192-323, 192-271, 200-271, 222-
CC 240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A
CC claimed method for reducing telomerase activity in a cell involves
CC introducing a recombinant polynucleotide encoding an hprt variant having
CC a deletion of amino acids 192-450, 560-565, 637-660, 748-764 or
CC 1055-1071. The polynucleotides are obtained by mutagenesis of the hprt
CC coding sequence

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 2; Length 4015;

Best Local Similarity 100.0%; P-adj. No. 0;

Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGCAGCACTACCG 60
DB 53 GCGATGCGCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGCAGCACTACCG 112
QY 61 GAGGTGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 120
DB 113 GAGGTGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 172
QY 121 CAGCGCGCGCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGCAGCACTACCG 180
DB 173 CAGCGCGCGCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGCAGCACTACCG 232
QY 181 TGGGACGCAAGCG 240
DB 223 TGGGACGCAAGCG 292
QY 241 CTGGTGGCGCGAGTGTGCTGCAAGGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 300
DB 293 CTGGTGGCGCGAGTGTGCTGCAAGGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GGGCTTGGCGCTGCTGCAAGGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 353 GGGCTTGGCGCTGCTGCAAGGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGGAGCTACCTGCG 420
DB 413 CGGAGCTACCTGCG 472
QY 421 CTGCTGCG 480
DB 473 CTGCTGCG 532
QY 481 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 533 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
QY 541 GCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 593 GCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652
QY 601 GAAAGCGCGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTG 660
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DB 713 GGTGCGAGAGAGCG 772
QY 721 GGTGCGAGAGAGCG 780
DB 773 GGTGCGAGAGAGCG 832
QY 781 GCGAGAGAGCG 840
DB 833 GCGAGAGAGCG 892

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QY 1201 CAGCGAG 1260
DB 1253 CAGCGAG 1312
QY 1261 ACCCGAG 1320
DB 1313 ACCCGAG 1372
QY 1321 GAG 1380
DB 1373 GAG 1432
QY 1381 CAGGTGTAAG 1440
DB 1433 CAGGTGTAAG 1492
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DB 1493 TCCAG 1552
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QY 1561 CTGCGAG 1620
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DB 1673 ATCTGCGAG 1732
QY 1681 TTTCTTTATGTCAG 1740
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Db      2933  TTCAACCGCGCTTCAAGGCTGAGAGAGATGCTGTGCAAACTTTGGGCTCTGGCG 2992
Qy      2941  CTGAAGGTCAACAGCTCTTGTGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 3000
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Db      3353  CAGAGCGAGCTGATGTGAGAGTCTCCGAGGAGCAGAGCTGATGCTCTGAGGCGCGAGC 3412
Qy      3361  AACCGGCGAGCTGCTGAGCTTCAAGACCAATCTGATGATGAGCAACC 3411
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RESULT 4
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ID AAZ30154 standard; cDNA; 4015 BP.
XX
XX
AC AAZ30154;
XX
XX
DT 26-JAN-2000 (first entry)
XX
XX
DE cDNA encoding a human telomerase reverse transcriptase (TRT).
XX
XX
KW Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
XX dendritic cell; telomerase activity; cancer cell; proliferating cell;
XX immunological destruction; telomerase; cancer; proliferation disease; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT CDS 56..3454
XX FT /tag= a
XX FT /product= "telomerase reverse transcriptase"
XX
XX PN WO9950392-A1.
XX
XX PD 07-OCT-1999.
XX
XX PP 30-MAR-1999; 99MO-US006898.
XX
XX PR 31-MAR-1999; 98US-011206P.
XX
XX PA (GERO-) GERON CORP.
XX
XX PI Gaeta FCA;
XX
XX DR WPI; 1999-610845/52.
XX
XX DR P-PSDB; AAY43621.
XX
XX PT Elucidating an in vivo immune response for prevention and treatment of
XX cancer.
XX
XX PS Disclosure: Fig 2; 26pp; English.
XX
XX CC The present sequence encodes a human telomerase reverse transcriptase
XX (TRT) polypeptide. The protein is used in the method of the invention.
XX CC The specification describes a method for activating a T lymphocyte,
XX CC comprising contacting the T lymphocyte with a dendritic cell that
XX CC expresses a TRT peptide in the context of a MHC class I or MHC class II

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CC molecule. The protein causes induction of an in vivo immunological
CC response to telomerase activity. Cancer cells are characterized by
CC expression of endogenous TRF gene and the presence of detectable
CC telomerase activity. Therefore, by eliciting a specific immune response
CC to TRF or to TRF-expressing cells, it is possible to selectively target
CC proliferating cells for immunological destruction. The method is used for
CC eliciting an in vivo immune response to telomerase by activating a T
CC lymphocyte, and is useful for prevention and treatment of cancers and
CC other proliferation diseases/conditions

XX Sequence 4015 BP, 663 A, 1363 C, 1275 G, 714 T, 0 U, 0 Other;

Query Match 100.0%; Score 3411; DB 2; Length 4015;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 173 CAGCGCGCGGAGACCGCGCGCGCTTTCCGCGCGCTGCGCGCACTGCTGCTGCGCGCC 232
QY 181 TGGAGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
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XX      PF      15-DEC-2000; 2000EP-00127228.
XX      XX
XX      PR      16-DEC-1999; 99US-00465491.
XX      XX
XX      PA      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      PI      Chang SP, Santini CD;
XX      PR      WPI; 2001-376930/40.
XX      XX
XX      QT      Quantitating expression of mRNA encoding hTERT, the catalytic subunit of
XX      PT      telomerase, as an indicator of cancer, by amplifying RNA using primers
XX      PS      complementary to hTERT gene sequence and quantitating amplified products
XX      Claim 1; Page 5-7; 2pp; English.
XX      CC      The present sequence is that of the hTERT gene encoding the catalytic
XX      CC      subunit of the human telomerase, comprising 16 exons, which is useful in
XX      CC      a method for quantitating hTERT mRNA. The method is useful for detecting
XX      CC      the presence of beta-region (a 182 nucleotide region consisting of exons
XX      CC      7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis
XX      CC      of cancer. The method provides an accurate measure of telomerase activity
XX      CC      by selectively measuring mRNA that encodes an active hTERT protein
XX      Sequence 4015 BF; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
XX      100.0%; Score 3411; DB 4; Length 4015;

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	Best Local Similarity	100.0%	Pred. No. 0	Matches 3411	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Db	53	GCATGCGCGCGCTCCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGAGCACTACCG	112					
QY	61	GAGGTGCTGCGCTGCGCAAGTTCGTGTCGCGCGCTGAGGACCCAGAGGCTGCGCTG	120					
Db	113	GAGGTGCTGCGCTGCGCAAGTTCGTGTCGCGCGCTGAGGACCCAGAGGCTGCGCTG	172					
QY	121	CAGGCGCGGAGACCCGCGCTTTCGCGCGCTGTGAGCCCACTGCTGTGTGTGCTGCC	180					
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QY	181	TGGAGCAGCAGGCGCGCCCGCGCGCCCTCTCTCCGCAAGTGTCTTGCTTAAGAG	240					
Db	233	TGGAGCAGCAGGCGCGCCCGCGCGCCCTCTCTCCGCAAGTGTCTTGCTTAAGAG	292					
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Db	353	GAGTTCGCGCTGTGAGCAGGAGCCCGCGGAGCCCGCCAGAGCTTTCACCAACAGGTG	412					
QY	361	CGCAGCTACTGCTCCCAACAGGTGACCGAGCACTGCGGAGGAGCGGAGGCTG	420					
Db	413	CGCAGCTACTGCTCCCAACAGGTGACCGAGCACTGCGGAGGAGCGGAGGCTG	472					
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QY	481	GTGTGTGTGTGTCTCCCACTGCGCTTACAGGTGTGCGGCGCGCGTGTACAGCTGCG	540					
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QY	541	GCTGCACTAGAGCGCCCGCGCCCGCAACAGCTAGTGAACCCCGAAGCGTCTGAGATG	600					
Db	593	GCTGCACTAGAGCGCCCGCGCCCGCAACAGCTAGTGAACCCCGAAGCGTCTGAGATG	652					
QY	601	GAAAGGCGCTGTGAACCAATAGGTTCAGGAGAGCGCGGGTCCCTGTGGGCTGTGCAAGCCCG	660					
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Qy 1621 ATCTGCGAGAGTCTGCTGCTGAGAGCTGAGCTGAGAGTCTGCTGAGAGTCT 1680
Db 1673 ATCTGCGAGAGTCTGCTGCTGAGAGCTGAGCTGAGAGTCTGCTGAGAGTCT 1732
Qy 1681 TTTCTTTATGTCAACGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGT 1740
Db 1733 TTTCTTTATGTCAACGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGT 1792
Qy 1741 GTCTGAGAGAGTTGCAAGATTTGAGATTCAGACAGCATTTGAAGAGGGTTCAGCTGG 1800
Db 1793 GTCTGAGAGAGTTGCAAGATTTGAGATTCAGACAGCATTTGAAGAGGGTTCAGCTGG 1852
Qy 1801 GAGCTGTGAGAGAGGTCAGGAGCATGCGAGAGCGAGCGCCGCTGCTGAGCTGC 1860
Db 1853 GAGCTGTGAGAGAGGTCAGGAGCATGCGAGAGCGAGCGCCGCTGCTGAGCTGC 1912
Qy 1861 AGACTCGGCTTCATCCCAAGCTTCGAGCGCTGCGCGCGATTTGAAACATGAGTACGTC 1920
Db 1913 AGACTCGGCTTCATCCCAAGCTTCGAGCGCTGCGCGCGATTTGAAACATGAGTACGTC 1972
Qy 1921 GTGGAGAGCAGAAAGTTCCGAGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAG 1980
Db 1973 GTGGAGAGCAGAAAGTTCCGAGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAG 2032
Qy 1981 GCACTGTTCAAGCTGCTCACTAGAGAGCGCGCGCGCGCGCTCTTCTGAGCGCTCT 2040
Db 2033 GCACTGTTCAAGCTGCTCACTAGAGAGCGCGCGCGCGCGCGCTCTTCTGAGCGCTCT 2092
Qy 2041 GTGCTGAGAGCAGATATTCAGAGGAGCTGAGAGCATTTGAGTGTGAGGGGCGCTGAG 2100
Db 2093 GTGCTGAGAGCAGATATTCAGAGGAGCTGAGAGCATTTGAGTGTGAGGGGCGCTGAG 2152
Qy 2101 CAGAGAGCGCGCGCTGAGCTGATCTTTGTCAAGGTGATGTGAGCGGCGCTGAGAGAC 2160
Db 2153 CAGAGAGCGCGCGCTGAGCTGATCTTTGTCAAGGTGATGTGAGCGGCGCTGAGAGAC 2212
Qy 2161 ATCCCCAGAGACAGGCTCAAGAGGTCATGCGACAGATATCAAAACCCAGAGACAGTAC 2220
Db 2213 ATCCCCAGAGACAGGCTCAAGAGGTCATGCGACAGATATCAAAACCCAGAGACAGTAC 2272
Qy 2221 TGCCTGCTGATATGCGCTGCTGAGAGAGCGCGCCATGAGGACAGTCCGAGAGCTTC 2280
Db 2273 TGCCTGCTGATATGCGCTGCTGAGAGAGCGCGCCATGAGGACAGTCCGAGAGCTTC 2332
Qy 2281 AAGAGCAGTCTCTACCTTTGACAGACCTTCAGCGGTATATGAGCAGTTCGTGCTAC 2340
Db 2333 AAGAGCAGTCTCTACCTTTGACAGACCTTCAGCGGTATATGAGCAGTTCGTGCTAC 2392
Qy 2341 CTGAGAGAGACAGAGCCCGCTGAGAGGATGCGCTGCTACAGAGAGCTCTCCCTGAAT 2400
Db 2393 CTGAGAGAGACAGAGCCCGCTGAGAGGATGCGCTGCTACAGAGAGCTCTCCCTGAAT 2452
Qy 2401 GAGGCGAGAGTGGCTCTTCCAGCTCTTCTACGCTTATGTGACACAGCGCTGGCG 2460
Db 2453 GAGGCGAGAGTGGCTCTTCCAGCTCTTCTACGCTTATGTGACACAGCGCTGGCG 2512
Qy 2461 ATCAGAGGAGAGTCTTACAGTCCAGAGGAGATCCGAGAGGCTCCATCTCTCCAG 2520
Db 2513 ATCAGAGGAGAGTCTTACAGTCCAGAGGAGATCCGAGAGGCTCCATCTCTCCAG 2572
Qy 2521 CTGCTGAGAGCTGTGCTGAGAGCATGAGAGAACAGCTGTTGCGGGATTCGCGG 2580
Db 2573 CTGCTGAGAGCTGTGCTGAGAGCATGAGAGAACAGCTGTTGCGGGATTCGCGG 2632
Qy 2581 GACGAGCTGCTCTGCTGCTGAGAGATTTCTGTTGAGACACCTACCTGACCCAG 2640
Db 2633 GACGAGCTGCTCTGCTGCTGAGAGATTTCTGTTGAGACACCTACCTGACCCAG 2692
Qy 2641 GCGAAACCTTCTCTAGAGACCTGTGTCGAGAGTGTCTGAGTATGCTGCGGTGAG 2700
Db 2693 GCGAAACCTTCTCTAGAGACCTGTGTCGAGAGTGTCTGAGTATGCTGCGGTGAG 2752
Qy 2701 TTGCGGAGAGAGTGTGAGACTTCCCTGTAGAGAGAGGCGCTGAGGAGCGGCTTT 2760
Db 2753 TTGCGGAGAGAGTGTGAGACTTCCCTGTAGAGAGAGGCGCTGAGGAGCGGCTTT 2812
Qy 2761 GTTCAGAGTCCGCGCCAGCGCTTATCCCTGCTGAGCGGCTGCTGATACCGAGAC 2820
Db 2813 GTTCAGAGTCCGCGCCAGCGCTTATCCCTGCTGAGCGGCTGCTGATACCGAGAC 2872
Qy 2821 CTGAGAGTGCAGAGAGCATCTCCAGCTATGCGCGGAGCTTCATAGAGAGCGTTCAC 2880
Db 2873 CTGAGAGTGCAGAGAGCATCTCCAGCTATGCGCGGAGCTTCATAGAGAGCGTTCAC 2932
Qy 2881 TTCAACCGCGCTTCAAGCTGAGAGAACATGCTCCAACTCTTTGGGCTCTTGGCG 2940
Db 2933 TTCAACCGCGCTTCAAGCTGAGAGAACATGCTCCAACTCTTTGGGCTCTTGGCG 2992
Qy 2941 CTGAAGTGTACAGCTGTTTCTGATTTGACAGGTGAAACAGCTTCAAGCGTGTGAC 3000
Db 2993 CTGAAGTGTACAGCTGTTTCTGATTTGACAGGTGAAACAGCTTCAAGCGTGTGAC 3052
Qy 3001 AACATCTAAGATCTCTGCTGAGAGGTCAGAGTTCAGAGTGTGTCAGCTC 3060
Db 3053 AACATCTAAGATCTCTGCTGAGAGGTCAGAGTTCAGAGTGTGTCAGCTC 3112
Qy 3061 CCAATTCATAGCAAGTTTGAAGAACCCCAATTTTCTGCGGTATCTTGAACG 3120
Db 3113 CCAATTCATAGCAAGTTTGAAGAACCCCAATTTTCTGCGGTATCTTGAACG 3172
Qy 3121 GCTCTGCTGCTACCTCATCTGTAAGGCAAGAGATGCTGCTGGGGCCAG 3180
Db 3173 GCTCTGCTGCTACCTCATCTGTAAGGCAAGAGATGCTGCTGGGGCCAG 3232
Qy 3181 GAGCGCGCGCGCTCTGCTGCTGAGAGCGGTGAGTGTGTGACCAAGATTCCTG 3240
Db 3233 GAGCGCGCGCGCTCTGCTGCTGAGAGCGGTGAGTGTGTGACCAAGATTCCTG 3292

QY 3361 AACCCGCGACCTGCTCAGACTTCAAGACCATCTGAGTATGAGCACCC 3411
Db 3413 AACCCGCGACCTGCTCAGACTTCAAGACCATCTGAGTATGAGCACCC 3463

RESULT 7

ABA97534
ID ABA97534 standard; DNA; 4015 BP.

ABA97534;

05-APR-2002 (first entry)

Cancer cell discrimination method related human DNA.

Human; telomerase; enzyme; cancer cell discrimination; gene;

reverse transcriptase; ds.

Homo sapiens.

JP2001309791-A.

06-NOV-2001.

02-MAY-2000; 2000JP-00138250.

02-MAY-2000; 2000JP-00138250.

(KANE/) KANEUCHI H.

(KAMI/) KAMIMORI M.

WPI; 2002-134853/18.

Discrimination of a cancer cell in a sample tissue, comprises determining the expression level of a reverse transcriptase component of telomerase PT using a hybridization assay.

Claim 2; Page 9-10; 16pp; Japanese.

The present invention relates to a method for the discrimination of a cancer cell in a sample tissue, which involves determining the expression level of a reverse transcriptase component of telomerase in a cell constituting the sample tissue by an in situ hybridization of the mRNA of the enzyme, and judging a cell showing a higher expression level than that of the reverse transcriptase component of telomerase in a normal cell to be a cancer cell. The present sequence is a human DNA used in the exemplification of the invention

Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGCTGCGAGCGCTGCTGCTGCGAGCCATACCGC 60
Db 53 GCGATGCGCGCGCTCCCGCTGCGAGCGCTGCTGCTGCGAGCCATACCGC 112
QY 61 GAGGTGCTGCGCTGCGCACTTCTGCGCGCGCTGCGAGCGCTGCGAGTGTG 120
Db 113 GAGGTGCTGCGCTGCGCACTTCTGCGCGCGCTGCGAGCGCTGCGAGTGTG 172
QY 121 CAGCGCGGAGACCCGCGGCTTTCGCGCGCTGCTGCGAGCGCTGCGAGTGTG 180
Db 173 CAGCGCGGAGACCCGCGGCTTTCGCGCGCTGCTGCGAGCGCTGCGAGTGTG 232
QY 181 TGGAGACGACGCGCGCGCGCGCGCGCGCTGCTGCGAGCGCTGCGAGTGTG 240
Db 233 TGGAGACGACGCGCGCGCGCGCGCGCGCTGCTGCGAGCGCTGCGAGTGTG 292
QY 241 CTGTGCGCGGAGTGTGCTGCGAGCGCTGCTGCGAGCGCGCGCGAGTGTGCTTC 300

Db 293 CTGTGCGCGGAGTGTGCTGCGAGCGCTGCTGCGAGCGCGCGCGAGTGTGCTTC 352
QY 301 GCGTTCGCGCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTCAGTGTG 360
Db 353 GCGTTCGCGCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTCAGTGTG 412
QY 361 CGCAGCTACCTGCGCGCAACAGCGTGTGCGAGCGCTGCGAGCGCGCGCGTGTG 420
Db 413 CGCAGCTACCTGCGCGCAACAGCGTGTGCGAGCGCTGCGAGCGCGCGTGTG 472
QY 421 CTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTCAGTGTG 480
Db 473 CTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTCAGTGTG 532
QY 481 GTGCTGTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTCAGTGTG 540
Db 533 GTGCTGTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTCAGTGTG 592
QY 541 GCTGCGCTACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTC 600
Db 593 GCTGCGCTACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTC 652
QY 601 GAAAGCGCGCTGGAACCACTAGAGGTGAGAGAGCGCGCGCGCGCGCGCGCGCG 660
Db 653 GAAAGCGCGCTGGAACCACTAGAGGTGAGAGAGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GGTGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTC 720
Db 713 GGTGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTC 772
QY 721 GGTGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTC 780
Db 773 GGTGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCTTC 832
QY 781 GGCAGAGAGCGCGTGTGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 833 GGCAGAGAGCGCGTGTGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 892
QY 841 GAAAGAGCGACCTTTTGTGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 893 GAAAGAGCGACCTTTTGTGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952
QY 901 GGCAGAGAGCGCGTGTGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 953 GGCAGAGAGCGCGTGTGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1012
QY 961 CCTGTGCGCGCGCGTGTGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 1013 CCTGTGCGCGCGCGTGTGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1072
QY 1021 CAGTGTGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1080
Db 1073 CAGTGTGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1132
QY 1081 CTGTGTGAGACACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1140
Db 1133 CTGTGTGAGACACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1192
QY 1141 CCGCGCTGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
Db 1193 CCGCGCTGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1252
QY 1201 CAGCGAGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1260
Db 1253 CAGCGAGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1312
QY 1261 ACCCGAGAGCGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1320
Db 1313 ACCCGAGAGCGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1372
QY 1321 GAGGAGAGCAAGACCGCGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1380
Db 1373 GAGGAGAGCAAGACCGCGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1432

QY 1381 CAGGTGTATCGGCTTGTGCGGCGCTGCTGCGCCGGCTGTGTGCCCCAGGCGCTTGGGGC 1440
Db 1433 CAGGTGTATCGGCTTGTGCGGCGCTGCTGCGCCGGCTGTGTGCCCCAGGCGCTTGGGGC 1492
QY 1441 TCCAGGCAACAGAACGCCGCTTCTCAGGAAACACCAAGAGTTGATCTCCCTGGGGAG 1500
Db 1493 TCCAGGCAACAGAACGCCGCTTCTCAGGAAACACCAAGAGTTGATCTCCCTGGGGAG 1552
QY 1501 CATGCGAAGCTCTCGCTGAGAGAGTGAAGTGAAGATGAGCGGTGGGAGCTGGCTTGG 1560
Db 1553 CATGCGAAGCTCTCGCTGAGAGAGTGAAGTGAAGATGAGCGGTGGGAGCTGGCTTGG 1612
QY 1561 CTGCGCAGAGAGCCCGAGGGGTGGCTGTGTGTTCCGGCCCGAGAGCACCGTCTGCGAGAG 1620
Db 1613 CTGCGCAGAGAGCCCGAGGGGTGGCTGTGTGTTCCGGCCCGAGAGCACCGTCTGCGAGAG 1672
QY 1621 ATCTGCGCAAGTTCTGCTGCACTGCTGATGAGTGTGATGCTGCTGAGCTGCTAGGCT 1680
Db 1673 ATCTGCGCAAGTTCTGCTGCACTGCTGATGAGTGTGATGCTGCTGAGCTGCTAGGCT 1732
QY 1681 TTCTTTTATGTACGGAACCAAGCTTTCAAAAAGAACAGGCTCTTTTCTTACCGGAGAGT 1740
Db 1733 TTCTTTTATGTACGGAACCAAGCTTTCAAAAAGAACAGGCTCTTTTCTTACCGGAGAGT 1792
QY 1741 GTCTGAGAGAGTTGCAAGAGATTTGAGATCAGACAGCACTTGAAGAGGGTGCAGCTGG 1800
Db 1793 GTCTGAGAGAGTTGCAAGAGATTTGAGATCAGACAGCACTTGAAGAGGGTGCAGCTGG 1852
QY 1801 GAGCTGTGGAAGCAGAGAGTCAAGCAGATCGGAGAGCCCGGCTGCTGACCTCC 1860
Db 1853 GAGCTGTGGAAGCAGAGAGTCAAGCAGATCGGAGAGCCCGGCTGCTGACCTCC 1912
QY 1861 AGACTCGGCTTCACTCCCAAGCTGACGGGCTGCGGCGATTTGGAACATGAGACTAGTC 1920
Db 1913 AGACTCGGCTTCACTCCCAAGCTGACGGGCTGCGGCGATTTGGAACATGAGACTAGTC 1972
QY 1921 GTGGAGCCAGAAAGCTTCCGAGAGAAAGAGGCGCAGAGCTTCACTGAGGGTGAAG 1980
Db 1973 GTGGAGCCAGAAAGCTTCCGAGAGAAAGAGGCGCAGAGCTTCACTGAGGGTGAAG 2032
QY 1981 GCACCTTTCAAGCTGTCTCAACTACAGAGCGGGCGCGGCGCTTCTGGGGGCTCT 2040
Db 2033 GCACCTTTCAAGCTGTCTCAACTACAGAGCGGGCGCGGCGCTTCTGGGGGCTCT 2092
QY 2041 GTGCTGGGCTTGAAGATATCACAAGGGCTGCGGCACTTCTGCTGCTGCTGCGGGCC 2100
Db 2093 GTGCTGGGCTTGAAGATATCACAAGGGCTGCGGCACTTCTGCTGCTGCTGCGGGCC 2152
QY 2101 CAGAGACCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACAGACCC 2160
Db 2153 CAGAGACCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACAGACCC 2212
QY 2161 ATCCCGCAGAGCAGGCTCAGAGAGGTATCGCCAGCATCATCAAAACCCAGAAACAGTAC 2220
Db 2213 ATCCCGCAGAGCAGGCTCAGAGAGGTATCGCCAGCATCATCAAAACCCAGAAACAGTAC 2272
QY 2221 TGCGTGTGCTGTATGCTGCTGTGTCAGAGAGCGCGCCATGAGGCACTGTCGGAAGGCTTC 2280
Db 2273 TGCGTGTGCTGTATGCTGCTGTGTCAGAGAGCGCGCCATGAGGCACTGTCGGAAGGCTTC 2332
QY 2281 AAGAGCAGAGCTCTTACCTTGAAGAGCTTCAAGCGGTGACATGAGAGAGTTCGAGTCAAC 2340
Db 2333 AAGAGCAGAGCTCTTACCTTGAAGAGCTTCAAGCGGTGACATGAGAGAGTTCGAGTCAAC 2392
QY 2341 CTGAGAGAGAGCAGCCCGCTGAGAGAGTCCGCTGTCAATCAGAGAGAGCTTCTCCCTGAAT 2400
Db 2393 CTGAGAGAGAGCAGCCCGCTGAGAGAGTCCGCTGTCAATCAGAGAGAGCTTCTCCCTGAAT 2452
QY 2401 GAGGCGAGAGTGGCTCTTTCAGAGTCTTCTCAAGCTTCAATGAGAGAGAGAGCGCGCTGGCG 2460
Db 2453 GAGGCGAGAGTGGCTCTTTCAGAGTCTTCTCAAGCTTCAATGAGAGAGAGAGCGCGCTGGCG 2512

QY 2461 ATCAGAGGAGAGTCTTACCTTCAAGTGCAGAGGAGATCCCGCAGAGGCTCTCATCTCCACAG 2520
Db 2513 ATCAGAGGAGAGTCTTACCTTCAAGTGCAGAGGAGATCCCGCAGAGGCTCTCATCTCCACAG 2572
QY 2521 CTGCTCTGAGAGCTGTGTGCTACGCGCAGATGAGAGAACAGCTGTGTTGGGGGATTTGGCGG 2580
Db 2573 CTGCTCTGAGAGCTGTGTGCTACGCGCAGATGAGAGAACAGCTGTGTTGGGGGATTTGGCGG 2632
QY 2581 GACGGGCTGCTCTGCTGTGTGAGTGAATTTCTGTTGATGACCTGACCTCAACCCAG 2640
Db 2633 GACGGGCTGCTCTGCTGTGTGAGTGAATTTCTGTTGATGACCTGACCTCAACCCAG 2692
QY 2641 GCGAAAACCTTCTCTAGAGACCTGTGTCGAGAGTGTCTTGAATGATGCTGCGTGTGAAC 2700
Db 2693 GCGAAAACCTTCTCTAGAGACCTGTGTCGAGAGTGTCTTGAATGATGCTGCGTGTGAAC 2752
QY 2701 TTGCGGAGAGAGTGTGTAATTTCCCTGTGAGAGAGAGGCGCTGGGTGGCAGCGCTTTT 2760
Db 2753 TTGCGGAGAGAGTGTGTAATTTCCCTGTGAGAGAGAGGCGCTGGGTGGCAGCGCTTTT 2812
QY 2761 GTTCAGATGCGGCGCCAGCGCTATTTCCCTGTGAGAGAGAGGCGCTGTGATACCGGAGC 2820
Db 2813 GTTCAGATGCGGCGCCAGCGCTATTTCCCTGTGAGAGAGAGGCGCTGTGATACCGGAGC 2872
QY 2821 CTGAGAGTGCAGAGAGCTTCTCCAGCTATGCTGAGAGAGAGGCGCTGTGATACCGGAGC 2880
Db 2873 CTGAGAGTGCAGAGAGCTTCTCCAGCTATGCTGAGAGAGAGGCGCTGTGATACCGGAGC 2932
QY 2881 TTCAACCGCGGCTTCAAGCTGAGAGAAACATGCTGCGAACTCTTTGGGGTCTTGGCG 2940
Db 2933 TTCAACCGCGGCTTCAAGCTGAGAGAAACATGCTGCGAACTCTTTGGGGTCTTGGCG 2992
QY 2941 CTGAAGTGCAGAGCTGTTTGTGATTTGAGAGTGAACAGCTTCCAGAGGTGTGAC 3000
Db 2993 CTGAAGTGCAGAGCTGTTTGTGATTTGAGAGTGAACAGCTTCCAGAGGTGTGAC 3052
QY 3001 AACATCTCAAGATCTCTGCTGAGAGGATCAAGCTTCAAGAGTGTGCTGAGCTC 3060
Db 3053 AACATCTCAAGATCTCTGCTGAGAGGATCAAGCTTCAAGAGTGTGCTGAGCTC 3112
QY 3061 CCAATTCATCAGAGATTTGAGAAACCCCAATTTTCTGCGGTATCTTGAGACG 3120
Db 3113 CCAATTCATCAGAGATTTGAGAAACCCCAATTTTCTGCGGTATCTTGAGACG 3172
QY 3121 GCTCCCTCTGCTATCTCATCTGTAAGAGCAAGAGAGATGCTGGGGGCGCAG 3180
Db 3173 GCTCCCTCTGCTATCTCATCTGTAAGAGCAAGAGAGATGCTGGGGGCGCAG 3232
QY 3181 GCGCGCGCGCGCTCTGCGCTTCCAGAGCGGTGAGAGTGTGTCACCAAGATCTCTG 3240
Db 3233 GCGCGCGCGCGCTCTGCGCTTCCAGAGCGGTGAGAGTGTGTCACCAAGATCTCTG 3292
QY 3241 CTCAAGCTGATCTGCAACCGGTGACCTTACCTGAGTGCACCTGCTGGGTGCTAGAGACAGC 3300
Db 3293 CTCAAGCTGATCTGCAACCGGTGACCTTACCTGAGTGCACCTGCTGGGTGCTAGAGACAGC 3352
QY 3301 CAGAGCAGCTGAGTGCAGAGCTCCCGGAGCAGAGCTGATGCTGCTGAGAGCGCAGAGC 3360
Db 3353 CAGAGCAGCTGAGTGCAGAGCTCCCGGAGCAGAGCTGATGCTGCTGAGAGCGCAGAGC 3412
QY 3361 AACCGGAGCTGCGCTGAGATCTTCAAGACATCTTGAATGAGACAGCC 3411
Db 3413 AACCGGAGCTGCGCTGAGATCTTCAAGACATCTTGAATGAGACAGCC 3463

RESULT 8
ACCS8039
ID ACCS8039 standard; cdna; 4015 BP.
XX
ACCS8039;
XX
ACCS8039;
XX
DT 11-AUG-2003 (first entry)
XX

DE Human telomerase reverse transcriptase CDNA.
XX
XX Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
KW short interfering RNA; siRNA; cancer; tumour; cytosolic; contraceptive;
KW immunosuppressive; anti-infectivity; fungicide; antiparasitic;
XX anti-inflammatory; human; gene therapy; gene; ss.
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT CDS 56..3454
FT /*tag= a
FT /product= "TERT"
XX
XX MO2003035667-A2.
XX
XX 01-MAY-2003.
XX
XX 16-OCT-2002; 2002MO-US033065.
XX
XX 22-OCT-2001; 2001US-0345326P.
XX 20-FEB-2002; 2002US-0359196P.
XX 22-MAY-2002; 2002US-0383195P.
XX
XX (UVRP) UNIV ROCHESTER.
XX
XX
XX Rowley PT;
XX
XX WPI; 2003-403336/38.
XX
XX P-PSDB; ABR42384.
XX
XX Novel double-stranded short interfering RNA having sense and antisense
PT nucleic acids which are complementary to each other and to target nucleic
PT acid e.g., telomerase RNA or mRNA encoding telomerase reverse
XX transcriptase.
XX
XX Disclosure; Fig 3A-B; 37pp; English.
XX
XX The present sequence is that of human telomerase reverse transcriptase
CC (TERT) CDNA. The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in anti-inflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germ-line cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX
XX
XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other:
SO
Query Match 100.0%; Score 3411; DB 7; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCATGCGCGGCGCTCCCGCTGCGAGCGTGCCTGCTGCGAGCCACTACGCG 60
DB 53 GCGATGCGCGGCGCTCCCGCTGCGAGCGTGCCTGCTGCGAGCCACTACGCG 112
QY 61 GAGGTCTGCGCGCTGCGAGCTTCTGTCGCGCGCTTGGGCGCCAGGCGCTGGCTGTG 120
DB 113 GAGGTCTGCGCGCTGCGAGCTTCTGTCGCGCGCTTGGGCGCCAGGCGCTGGGTG 172
QY 121 CAGCGCGGAGACCGCGCGCTTCCGCGCGCTGTCGAGCCCACTGCTGTCGTCGCC 180
DB 173 CAGCGCGGAGACCGCGCGCTTCCGCGCGCTGTCGAGCCCACTGCTGTCGTCGCC 232
QY 181 TGGGAGCGACG 240
DB 233 TGGGAGCGACG 292

QY 241 CTGTGCGCGCGAGCTGCTGCAAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 300
DB 293 CTGTGCGCGCGAGCTGCTGCAAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GAGCTTGGCGCTGCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 353 GAGCTTGGCGCTGCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CCGAGCTTCTGCTGCGCAAGCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB 413 CCGAGCTTCTGCTGCGCAAGCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472
QY 421 CTGTGCGCGCGAGCTGCTGCAAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 480
DB 473 CTGTGCGCGCGAGCTGCTGCAAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 532
QY 481 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 533 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 592
QY 541 GCTGCACTGAGCG 600
DB 593 GCTGCACTGAGCG 652
QY 601 GAACGAGCGCTGGAACCACTAGGCTGAGGAGGCGCGCGCGCGCGCGCGCGCGCG 660
DB 653 GAACGAGCGCTGGAACCACTAGGCTGAGGAGGCGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GATGCGAGAGGCG 720
DB 713 GATGCGAGAGGCG 772
QY 721 GATGCGAGAGGCG 780
DB 773 GATGCGAGAGGCG 832
QY 781 GCGAGAGCGCTGGAACCACTAGGCTGAGGAGGCGCGCGCGCGCGCGCGCGCGCG 840
DB 833 GCGAGAGCGCTGGAACCACTAGGCTGAGGAGGCGCGCGCGCGCGCGCGCGCGCG 892
QY 841 GAAGAGCGCACTTCTTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 893 GAAGAGCGCACTTCTTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 952
QY 901 GCGCGCGAGAGCG 960
DB 953 GCGCGCGAGAGCG 1012
QY 961 CTTGTGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 1013 CTTGTGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1072
QY 1021 CAGCTGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
DB 1073 CAGCTGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1132
QY 1081 CTGTGAGAGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1140
DB 1133 CTGTGAGAGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1192
QY 1141 CCGCGCGCTGCGCGAGCGCTTCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
DB 1193 CCGCGCGCTGCGCGAGCGCTTCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1252
QY 1201 CAGCGCGAGCGCGCTTCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
DB 1253 CAGCGCGAGCGCGCTTCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1312
QY 1261 ACCCGAGAGCGCGCTTCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
DB 1313 ACCCGAGAGCGCGCTTCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1372

QY	1321	GAGGAGAGACAGACCCCCCGTGGCTCGTGGTGCAGCTGCTCCGACAGACAGACCCCTCGG	1380
Db	1373	GAGAGAGACAGACCCCCCGTGGCTCGTGGTGCAGCTGCTCCGACAGACAGACCCCTCGG	1432
QY	1381	CAGGTGTACGGGCTGTGTCGGGGCTGCCTGCAGCCCGGCTGGTATCCCCAGAGCCTCTGGGGC	1440
Db	1433	CAGGTGTACGGGCTGTGCGGGGCTGCCTGCAGCCCGGCTGGTATCCCCAGAGCCTCTGGGGC	1492
QY	1441	TCGAGGCACAGAGAACGCCCTTTCCTCAGGAAACCAAGAAATTATCTCCCTGGGAG	1500
Db	1493	TCGAGGCACAGAGAACGCCCTTTCCTCAGGAAACCAAGAAATTATCTCCCTGGGAG	1552
QY	1501	CATGCGAAGCTCTCGCTGCAGAGGTCGACGTGGAAATGAGCGTGCAGGACCTGGGCTTGG	1560
Db	1553	CATGCGAAGCTCTCGCTGCAGAGGTCGACGTGGAAATGAGCGTGCAGGACCTGGGCTTGG	1612
QY	1561	CTGCGCAGGAGCCCAAGGGTTGGCTGTGTTCCGAGCCGACAGACACGTCGTGAGAG	1620
Db	1613	CTGCGCAGGAGCCCAAGGGTTGGCTGTGTTCCGAGCCGACAGACACGTCGTGAGAG	1672
QY	1621	ATCCTGGCCCAAGTTCCTGCACATGGGTGAATGAGTGTATCGTGTGCAGCTCTCAGGTCT	1680
Db	1673	ATCCTGGCCCAAGTTCCTGCACATGGGTGAATGAGTGTATCGTGTGCAGCTCTCAGGTCT	1732
QY	1681	TTCTTTTATGTACGAGAGACACGTTTAAAAAGAACAGGCTCTTTTCTACCGAAGAT	1740
Db	1733	TTCTTTTATGTACGAGAGACACGTTTAAAAAGAACAGGCTCTTTTCTACCGAAGAT	1792
QY	1741	GTTCTGAGAGAAATTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCAGTCCGG	1800
Db	1793	GTTCTGAGAGAAATTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCAGTCCGG	1852
QY	1801	GAGCTGTGCGAAGCAGAGGTCAAGCAGCATCGGAAAGCAGAGCCGCGCTGCATAGTCC	1860
Db	1853	GAGCTGTGCGAAGCAGAGGTCAAGCAGCATCGGAAAGCAGAGCCGCGCTGCATAGTCC	1912
QY	1861	AGACTCCGCTTATATCCCAAGCTTGAACGGGCTGCAGCCGATTTGGAACATGACCTACGTC	1920
Db	1913	AGACTCCGCTTATATCCCAAGCTTGAACGGGCTGCAGCCGATTTGGAACATGACCTACGTC	1972
QY	1921	GTTGGAGGCAGAACGTTCCGACAGAAAGAGGGCCAGAGGCTCTCAACTGAGGGTTAAG	1980
Db	1973	GTTGGAGGCAGAACGTTCCGACAGAAAGAGGGCCAGAGGCTCTCAACTGAGGGTTAAG	2032
QY	1981	GCACTGTTCAAGGTGCTCAACTACAGAGCGAGCGAGCCCGGCTCTTGGAGGCTCT	2040
Db	2033	GCACTGTTCAAGGTGCTCAACTACAGAGCGAGCGAGCCCGGCTCTTGGAGGCTCT	2092
QY	2041	GTTGCTGGGCTGGAGAGATATCCAAGGGCTCTGGGAGCACTTGTGTGCTGTGTCGGGCT	2100
Db	2093	GTTGCTGGGCTGGAGAGATATCCAAGGGCTCTGGGAGCACTTGTGTGCTGTGTCGGGCT	2152
QY	2101	CAGGACCCGCGGCTGAGCTGTACTTTGTCAAGGTGATGAGCGGCGGCTACGACAC	2160
Db	2153	CAGGACCCGCGGCTGAGCTGTACTTTGTCAAGGTGATGAGCGGCGGCTACGACAC	2212
QY	2161	ATCCCCCAAGACAGGCTACAGAGGTATGCGCAGCATCATCAAAACCCCAAGACAGTAC	2220
Db	2213	ATCCCCCAAGACAGGCTACAGAGGTATGCGCAGCATCATCAAAACCCCAAGACAGTAC	2272
QY	2221	TGCGTGCCTGGTATGACGCTGATCAGAGAGGCCCATGAGGACGTCGCGCAAGGCTTTC	2280
Db	2273	TGCGTGCCTGGTATGACGCTGATCAGAGAGGCCCATGAGGACGTCGCGCAAGGCTTTC	2332
QY	2281	AAGAGCCACGTTCTTACCTTGAACAGACTTCAAGCCGTACATGCGACAGTTCTGATGTAC	2340
Db	2333	AAGAGCCACGTTCTTACCTTGAACAGACTTCAAGCCGTACATGCGACAGTTCTGATGTAC	2392
QY	2341	CTGACAGAGACACACCCGCTGAGAGGATGCGGTGTATGAGACAGGCTCTCCCTGAAT	2400
Db	2393	CTGACAGAGACACACCCGCTGAGAGGATGCGGTGTATGAGACAGGCTCTCCCTGAAT	2452
QY	2401	GAGGCGAGCACTGAGCTCTTTCAGAGTTCCTTACGCTTACATGTCACACACAGCCGCTGGCC	2460

[illegible]

Db 1313 ACCCAGAGCGGGTCTGTGCCCCGGAGAGGCCCAAGGGCTGTGTGGGGCCCCGAG 1372
Qy 1321 GAGAGGACACAGACCCCGCTGCTGTGTGAGCTGTCCGCGACAGACAGCCCTGG 1380
Db 1373 GAGAGGACACAGACCCCGCTGCTGTGTGAGCTGTCCGCGACAGACAGCCCTGG 1432
Qy 1381 CAGGTGTACGGCTTGTGTGCGGGCTGTGTGCGGGGGTGTGTGCGGGGGCTGTGGGG 1440
Db 1433 CAGGTGTACGGCTTGTGTGCGGGCTGTGTGCGGGGGTGTGTGCGGGGGCTGTGGGG 1492
Qy 1441 TCAGAGCAACAGACCGCGCTTCTCAGAGAACCAAGAAATTCATCTCTGGGGAG 1500
Db 1493 TCAGAGCAACAGACCGCGCTTCTCAGAGAACCAAGAAATTCATCTCTGGGGAG 1552
Qy 1501 CATGCGAAGCTCTGTGTGAGAGAGCTGTGTGAGAGAGTGTGAGCTGTGGGGAGCTGGGG 1560
Db 1553 CATGCGAAGCTCTGTGTGAGAGAGCTGTGTGAGAGAGTGTGAGCTGTGGGGAGCTGGGG 1612
Qy 1561 CTGCGAGAGAGCCAGAGGGGTGTGTGTGCTGTGTGCGCGCAGAGACACCTGTGCGTGAAG 1620
Db 1613 CTGCGAGAGAGCCAGAGGGGTGTGTGTGCTGTGTGCGCGCAGAGACACCTGTGCGTGAAG 1672
Qy 1621 ATCTGTGCGAAGTCTGTGTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
Db 1673 ATCTGTGCGAAGTCTGTGTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1732
Qy 1681 TTCTTTTATGTCAAGAGAGACACCTTCAAAAGAACAGGCTCTTTTCTACCGGAGAGT 1740
Db 1733 TTCTTTTATGTCAAGAGAGACACCTTCAAAAGAACAGGCTCTTTTCTACCGGAGAGT 1792
Qy 1741 GTCTGTGAGCAAGTGTGCAAGAGATTTGAATCAGACGACTTTGAAAGAGGTGTGAGCTGG 1800
Db 1793 GTCTGTGAGCAAGTGTGCAAGAGATTTGAATCAGACGACTTTGAAAGAGGTGTGAGCTGG 1852
Qy 1801 GAGGTGTGAGAGAGAGGTGTGAGAGAGATTCGAGAGACAGAGCCCGCTGTGAGAGTGTG 1860
Db 1853 GAGGTGTGAGAGAGAGGTGTGAGAGAGATTCGAGAGACAGAGCCCGCTGTGAGAGTGTG 1912
Qy 1861 AGACTGTGCTTCAATCCCAAGCTGTGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
Db 1913 AGACTGTGCTTCAATCCCAAGCTGTGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1972
Qy 1921 GTGAGAGAGAGAGTGTGTGAG 1980
Db 1973 GTGAGAGAGAGAGTGTGTGAG 2032
Qy 1981 GCAGTGTGTGAGAGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Db 2033 GCAGTGTGTGAGAGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2092
Qy 2041 GTGTGTGAG 2100
Db 2093 GTGTGTGAG 2152
Qy 2101 CAG 2160
Db 2153 CAG 2212
Qy 2161 ATCTGTGAG 2220
Db 2213 ATCTGTGAG 2272
Qy 2221 TGCTGTGAG 2280
Db 2273 TGCTGTGAG 2332
Qy 2281 AAG 2340
Db 2333 AAG 2392
Qy 2341 CTGAG 2400
Db 2393 CTGAG 2452

Qy 2401 GAGGCGAG 2460
Db 2453 GAGGCGAG 2512
Qy 2461 ATCAG 2520
Db 2513 ATCAG 2572
Qy 2521 CTGCTGTGAG 2580
Db 2573 CTGCTGTGAG 2632
Qy 2581 GAGGCGAG 2640
Db 2633 GAGGCGAG 2692
Qy 2641 GCGAAACCTTCTCAG 2700
Db 2693 GCGAAACCTTCTCAG 2752
Qy 2701 TTGCGAG 2760
Db 2753 TTGCGAG 2812
Qy 2761 GTTCAAGATGCGAG 2820
Db 2813 GTTCAAGATGCGAG 2872
Qy 2821 CTGAG 2880
Db 2873 CTGAG 2932
Qy 2881 TTCAACCGGAG 2940
Db 2933 TTCAACCGGAG 2992
Qy 2941 CTGAG 3000
Db 2993 CTGAG 3052
Qy 3001 AACATCTAAG 3060
Db 3053 AACATCTAAG 3112
Qy 3061 CCATTTCAAG 3120
Db 3113 CCATTTCAAG 3172
Qy 3121 GCTTCTCTGT 3180
Db 3173 GCTTCTCTGT 3232
Qy 3181 GCG 3240
Db 3233 GCG 3292
Qy 3241 CTCAAG 3300
Db 3293 CTCAAG 3352
Qy 3301 CAG 3360
Db 3353 CAG 3412
Qy 3361 AACCGGAG 3411
Db 3413 AACCGGAG 3463

RESULT 10
AB222474
ID AB222474 standard; cdna; 4015 bp.

XX AB222474;
XX
XX 25-MAR-2003 (first entry)
XX
XX Human telomerase reverse transcriptase encoding cDNA SEQ ID NO:1.
XX
XX Human; telomerase reverse transcriptase; enzyme: hTERT; chromosome 5;
XX vulnery; antilicer; epithelial cell migration promoter; wound;
XX epithelisation; skin wound; lesion; burn; surgical incision; ulcer;
XX epithelial cell; keratinocyte; epidermal; mucosal; gene; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 56..3454
XX FT /tag=a
XX FT /product="human telomerase reverse transcriptase"
XX
XX WO200291999-A2.
XX
XX 21-NOV-2002.
XX
XX 09-MAY-2002; 2002MO-US014867.
XX
XX 09-MAY-2001; 2001US-0289903P.
XX
XX (GERO-) GERON CORP.
XX
XX Jiang X, Chai C, Harley CB;
XX MPI. 2003-120591/11.
XX P-FSDS; ABB5676.
XX
XX Composition for treating wounds and enhancing epithelization of a skin
XX surface, comprises vector encoding telomerase reverse transcriptase or
XX telomerized epithelial cells on a microparticle or a matrix.
XX
XX Disclosure; Page 31-32; 68pp; English.
XX
XX The present invention describes a pharmaceutical composition (I)
XX comprising a vector encoding telomerase reverse transcriptase (TERT) in
XX an excipient or device, or comprises telomerized epithelial cells on a
XX microparticle or a matrix suitable for topical administration or
XX administration to a wound site. (I) has vulnery and antilicer
XX activities and can be used to promote epithelial cell migration. (I) is
XX useful for treating a wound and enhancing epithelization of a skin
XX surface. The wound is especially skin wound including acute lesion such
XX as traumatic lesion, burn, or surgical incision, chronic lesion such as
XX chronic venous ulcer, diabetic ulcer or compression ulcer and the wound
XX is further monitored for closure. The telomerase activity or TERT
XX expression is increased in epithelial cells at the site of treatment and
XX also in fibroblasts or endothelial cells at the site of treatment. The
XX epithelial cells are especially keratinocytes. A polynucleotide encoding
XX TERT is useful for the preparation of a medicament for treatment of a
XX wound or an epithelial surface in a human or animal. An epithelial cell
XX with increased telomerase activity or increased expression of TERT is
XX useful for preparation of a medicament for the treatment of a wound in a
XX human or animal. (I) is also useful for treating wounds of other
XX epidermal surfaces including mucosal surfaces such as bronchus, mouth,
XX nose, oesophagus, stomach or intestine. The present sequence encodes
XX human TERT (hTERT), which is given in the exemplification of the present
XX invention. hTERT is located to chromosome 5
XX
XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 3411; DB 7; Length 4015;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 GAGTGTCTGCGCTGCGCAAGTTCGTGCGCGCCCTGCGGCCCCAGAGGCTGCGGCTGATG 120
DB 113 GAGTGTCTGCGCTGCGCAAGTTCGTGCGCGCCCTGCGGCCCCAGAGGCTGCGGCTGATG 172
QY 121 CAGCGCGGAGGACCGCGGCTTTCCGCGCGCTGCGGCGCCAGTGTGCTGCGGCTGCGG 180
DB 173 CAGCGCGGAGGACCGCGGCTTTCCGCGCGCTGCGGCGCCAGTGTGCTGCGGCTGCGG 232
QY 181 TGGAGCGACG 240
DB 233 TGGAGCGACG 292
QY 241 CTGTGTGCGCGCGCTGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 293 CTGTGTGCGCGCGCTGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GCGTTCGCGCTGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 353 GCGTTCGCGCTGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CCGAGCTACTGCGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB 413 CCGAGCTACTGCGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472
QY 421 CTGTGTGCGCGCGCTGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 473 CTGTGTGCGCGCGCTGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 532
QY 481 GTCGTGTGCGCGCTGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
DB 533 GTCGTGTGCGCGCTGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 592
QY 541 GCTGCACTCAGGCG 600
DB 593 GCTGCACTCAGGCG 652
QY 601 GACGCGCGCTGGAACATGAGTTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 653 GACGCGCGCTGGAACATGAGTTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GGTGCGAGGAGGCG 720
DB 713 GGTGCGAGGAGGCG 772
QY 721 CGTGCGCTGCGCTGAGCG 780
DB 773 CGTGCGCTGCGCTGAGCG 832
QY 781 GCGAGAGCGCGTGAACGAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
DB 833 GCGAGAGCGCGTGAACGAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 892
QY 841 GAGAGAGCGCGCTTGAAGGCG 900
DB 893 GAGAGAGCGCGCTTGAAGGCG 952
QY 901 GCG 960
DB 953 GCG 1012
QY 961 CTTGTGCGCGCGTGAACGAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
DB 1013 CTTGTGCGCGCGTGAACGAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1072
QY 1021 CAGCTGCGCGCGCTGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
DB 1073 CAGCTGCGCGCGCTGCGCAAGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1132
QY 1081 CTGTGTGAGACCATCTTCTGAGGTTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB 1133 CTGTGTGAGACCATCTTCTGAGGTTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1192

1141 CCCCCTGCCCCAGCGTACTGCGAAATGCGGCCCTCTTTCTGAGCTGCTTGGGAC 1200
Db CCCCCCTGCCCCAGCGTACTGCGAAATGCGGCCCTCTTTCTGAGCTGCTTGGGAC 1252
1201 CACGCGCAGTGCCTTACGCGGTGCTCTCAAGACGACCTGCGCGTACGCGAGCGGTC 1260
Db CACGCGCAGTGCCTTACGCGGTGCTCTCAAGACGACCTGCGCGTACGCGAGCGGTC 1312
1261 ACCCGACAGCGCGGTGCTGTCGCCCGGAGAAAGCCCGAGCTTGTGTGCGGCCGAG 1320
Db ACCCGACAGCGCGGTGCTGTCGCCCGGAGAAAGCCCGAGCTTGTGTGCGGCCGAG 1372
1331 ACCCGACAGCGCGGTGCTGTCGCCCGGAGAAAGCCCGAGCTTGTGTGCGGCCGAG 1380
1332 GAGGAGACACAGACCCCGTGCCTGTCAGTGCCTGCGCGACGACACAGCGCCCTGG 1432
1373 GAGGAGACACAGACCCCGTGCCTGTCAGTGCCTGCGCGACGACACAGCGCCCTGG 1440
1381 CAGGTGTAAGGCTTGTGTCGCGGCTGCTGCGCGCGGCTGTCGCGCGCTTGGGCG 1492
1433 CAGGTGTAAGGCTTGTGTCGCGGCTGCTGCGCGCGGCTGTCGCGCGCTTGGGCG 1500
1441 TCCAGGACACAGACCCCGTGCCTGTCAGTGCCTGCGCGACGACACAGCGCCCTGG 1552
1493 TCCAGGACACAGACCCCGTGCCTGTCAGTGCCTGCGCGACGACACAGCGCCCTGG 1560
1501 CATGCGCAGCTCTGCTGCGCGAGCTGACGTCGAGATGAGCTGCGCGGACCTGCGCTGG 1612
1553 CATGCGCAGCTCTGCTGCGCGAGCTGACGTCGAGATGAGCTGCGCGGACCTGCGCTGG 1620
1561 CTGCGCGAGAGACCCCGGCTGTCGTCGTCGCGCGCGGACGACGCTGTCGTCGAGAG 1672
1613 CTGCGCGAGAGACCCCGGCTGTCGTCGTCGCGCGCGGACGACGCTGTCGTCGAGAG 1680
1621 ATCTGCGCAGATCTGCTGCGAGCTGATGATGATGATGATGATGATGATGATGATGAT 1732
1673 ATCTGCGCAGATCTGCTGCGAGCTGATGATGATGATGATGATGATGATGATGATGAT 1740
1681 TTCTTTTATGTCAGGAGACCAAGTTTCAAAAGAAAGAGCTCTTTTCTAACCGAAGAT 1792
1733 TTCTTTTATGTCAGGAGACCAAGTTTCAAAAGAAAGAGCTCTTTTCTAACCGAAGAT 1800
1741 GTCTGAGACAGTGTGCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1852
1793 GTCTGAGACAGTGTGCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1860
1801 GAGCTGTGAGACAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1912
1853 GAGCTGTGAGACAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
1861 AGACTCCGCTTCACTCCCAAGCTGACGCGCTGCGCGCGGCTGCTGCTGCTGCTGCTGCT 1972
1913 AGACTCCGCTTCACTCCCAAGCTGACGCGCTGCGCGCGGCTGCTGCTGCTGCTGCTGCT 1980
1921 GTGAGAGACAGAGCTTTCGAGAGAAAGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2032
1973 GTGAGAGACAGAGCTTTCGAGAGAAAGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
1981 GCACTGTTCAAGGCTGCTCACTAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCT 2092
2033 GCACTGTTCAAGGCTGCTCACTAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCT 2100
2041 GTGCTGAGGCTGACGATATCACAGGAGCTGCGGACCTTCTGCTGCTGCTGCTGCTGCTGCT 2152
2093 GTGCTGAGGCTGACGATATCACAGGAGCTGCGGACCTTCTGCTGCTGCTGCTGCTGCTGCT 2160
2101 CAGAGACCGCGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2212
2153 CAGAGACCGCGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
2161 ATCCCGACAGACAGGCTTACAGAGGCTGATGCGCGACATCAAAAGCCCGAAGACGATAC 2272
2213 ATCCCGACAGACAGGCTTACAGAGGCTGATGCGCGACATCAAAAGCCCGAAGACGATAC 2280
2221 TGCGTGGCTGGATGCGCGTGTGCGAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCTTCC 2280

2273 TGCGTGGCTGGATGCGCGTGTGCGAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCTTCC 2332
2281 AAGAGACAGCTGCTTACCTTGAACAGACCTCCAGCGGCTCATGCGACAGTGTGCTGAC 2340
2333 AAGAGACAGCTGCTTACCTTGAACAGACCTCCAGCGGCTCATGCGACAGTGTGCTGAC 2392
2341 CTGACAGAGACAGCGCGCTGAGAGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
2393 CTGACAGAGACAGCGCGCTGAGAGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2452
2401 GAGGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
2453 GAGGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2512
2461 ATCAGGAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
2513 ATCAGGAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2572
2521 CTGCT 2580
2573 CTGCT 2632
2581 GACGAGCT 2640
2633 GACGAGCT 2692
2641 GCGAAACCTTCTTACAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
2693 GCGAAACCTTCTTACAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2752
2701 TTGCGGAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
2753 TTGCGGAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2812
2761 GTTCAGATGCT 2820
2813 GTTCAGATGCT 2872
2821 CTGAGAGTGCAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
2873 CTGAGAGTGCAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2932
2881 TTCAAACCGGCTTCAAGGCTGAGAGAAATGCTGCGCAACTCTTTGGGCTCTTGGCG 2940
2933 TTCAAACCGGCTTCAAGGCTGAGAGAAATGCTGCGCAACTCTTTGGGCTCTTGGCG 2992
2941 CTGAGAGTGCAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
2993 CTGAGAGTGCAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3052
3001 AACATCTACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
3053 AACATCTACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3112
3061 CCAATTTACAGCAAGTTTGAAGAAAGCCCAATTTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 3120
3113 CCAATTTACAGCAAGTTTGAAGAAAGCCCAATTTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 3172
3121 GCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
3173 GCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3232
3181 GCT 3240
3233 GCT 3292
3241 CTCAAGCT 3300
3293 CTCAAGCT 3352
3301 CAGAGCAGCTGAGTGCAGAACTCCCGGAGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360

Db 3353 CAGAGCAGCTAGTCCGGAAGCTCCCGGAGACGAGCTGAGTCCCTGAGGCCGACGCC 3412
QY 3351 AACCCGCGACTGCTCCCTCAGACTTCAAGACCATCTCTGAGCTGATGCCACCC 3411
Db 3413 AACCCGCGACTGCTCCCTCAGACTTCAAGACCATCTCTGAGCTGATGCCACCC 3463

RESULT 11
ACC44482
ID ACC44482 standard; DNA; 4015 BP.
XX
AC ACC44482;
XX
DT 29-AUG-2003 (first entry)
XX
DE Human telomerase reverse transcriptase gene.
XX
KW Gene; ds; human; telomerase reverse transcriptase; adipogenic capacity;
KM primary preadipocyte cell; adipogenesis; obesity; adipocytokine;
XX anorectic; adiponectin; insulin.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 56..3454
FT CDS /*tag= a
FT /product= "telomerase reverse transcriptase"
XX
PN MO2003031640-A2.
XX
PD 17-APR-2003.
XX
PF 07-OCT-2002; 2002WO-US031635.
XX
PR 06-OCT-2001; 2001US-0327650P.
PR 06-OCT-2001; 2001US-0327651P.
XX
PA (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI Kirkland J, Tchoukua T;
XX
DR WPI; 2003-421278/39.
DR P-PSDB; ABR58045.
XX
PT New primary preadipocyte strain expressing telomerase reverse
PT transcriptase, useful in research applications, screening assays,
PT clinical applications, and in the administration of therapeutic agents,
PT particularly for obesity.
XX
PS Disclosure; Page 11-13; 53pp; English.
XX
CC The invention relates to the generation of primary preadipocyte cell
CC strains that express telomerase reverse transcriptase (TERT- the
CC catalytic subunit of telomerase), and maintain and/or enhance replicative
CC potential and maintain adipogenic capacity of the cell. This sequence
CC represents the gene encoding the TERT protein. The cell strain can be
CC used in research to study all aspect of adipogenesis, especially in
CC relation to researching treatments for e.g. obesity. The cell can also be
CC used to identify adipogenesis modulators for use as therapeutic agents
CC such as hormones, growth factors, cytokines, enzymes, cholesterol binding
CC proteins, cholesterol removing proteins or their combinations.
CC Alternatively, the therapeutic agent may be an adipocytokine, preferably
CC adiponectin, or insulin
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 7; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGCTCCGAGCGCTGCTCCCTGTCGCGACCACTACCGC 60
Db 53 GCGATGCGCGCGCTCCCGCTCCGAGCGCTGCTCCCTGTCGCGACCACTACCGC 112

QY 61 GAGTGTCTGCGCGTGGCCACGTTGCTGCGGCGCTTGAGGCCCAAGCGCTGCGTGTG 120
Db 113 GAGTGTCTGCGCGTGGCCACGTTGCTGCGGCGCTTGAGGCCCAAGCGCTGCGTGTG 172
QY 121 CAGCGCGGAGACCGCGCGGCTTTCCGCGCGCTGAGGCGCGAGCTGAGTGTGCGC 180
Db 173 CAGCGCGGAGACCGCGCGGCTTTCCGCGCGCTGAGGCGCGAGCTGAGTGTGCGC 232
QY 181 TGGAGCGACG 240
Db 233 TGGAGCGACG 292
QY 241 CTGAGTGGCGCGAGCTGTCAGAGCTGTCAGAGCGCGCGCGCGCGCGCGCGCGCTC 300
Db 293 CTGAGTGGCGCGAGCTGTCAGAGCTGTCAGAGCGCGCGCGCGCGCGCGCGCGCTC 352
QY 301 GCGTTCGCGCTGTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 360
Db 353 GCGTTCGCGCTGTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 412
QY 361 CGCAGCTACCTGCG 420
Db 413 CGCAGCTACCTGCG 472
QY 421 CTGCTGCTTT 480
Db 473 CTGCTGCTTT 532
QY 481 GTGCTGTGTGTCTCCAGCTGCTGCTTACAGAGTGTGCGCGCGCGCGCGCTGTAC 540
Db 533 GTGCTGTGTGTCTCCAGCTGCTGCTTACAGAGTGTGCGCGCGCGCGCGCTGTAC 592
QY 541 GCTGCACTCAGCG 600
Db 593 GCTGCACTCAGCG 652
QY 601 GAAAGGCGCTGGAACCATAGCGTCAAGAGGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 653 GAAAGGCGCTGGAACCATAGCGTCAAGAGGCGCGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GGTGAGAGAGAGCG 720
Db 713 GGTGAGAGAGAGCG 772
QY 721 CGTGGCGCTGCTTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 773 CGTGGCGCTGCTTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 832
QY 781 GCGAGAGAGCGTGAACGAGTGAACGAGTTCGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 833 GCGAGAGAGCGTGAACGAGTGAACGAGTTCGTGTGTGTGTGTGTGTGTGTGTGTGT 892
QY 841 GAAAGAGCACTTTTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 893 GAAAGAGCACTTTTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 952
QY 901 GCGCGCGAGACAGCG 960
Db 953 GCGCGCGAGACAGCG 1012
QY 961 CTTTGTCCCGGTGTGACCGCGAGACCAAGCACTTCTCTTACTCTGAGCGACAGAG 1020
Db 1013 CTTTGTCCCGGTGTGACCGCGAGACCAAGCACTTCTCTTACTCTGAGCGACAGAG 1072
QY 1021 CAGCTGCGCGCGCTCTCTTACTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 1073 CAGCTGCGCGCGCTCTCTTACTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1132
QY 1081 CTGCTGAGAGCACTTTTGTGAGTTCAGGCGCTGTGATGTCAGAGGACTCCCGAGGTTG 1140
Db 1133 CTGCTGAGAGCACTTTTGTGAGTTCAGGCGCTGTGATGTCAGAGGACTCCCGAGGTTG 1192

QY 1141 CCCCCCTGCCCCAGCGCTACTGCAAAATGCGGCCCTGTTCTGAGACTGTTGGAGAC 1200
Db 1193 CCCCCCTGCCCCAGCGCTACTGCAAAATGCGGCCCTGTTCTGAGACTGTTGGAGAC 1232
QY 1201 CACGCGAGTGCCTCTACGCGGGTGTCTCTCAAGACATGCGCTGCGAGTGCAGTC 1260
Db 1253 CACGCGAGTGCCTCTACGCGGGTGTCTCTCAAGACATGCGCTGCGAGTGCAGTC 1312
QY 1261 ACCCGACGACCGGCTGTCTGTGCGCGGAGAGCCCGAGGGTCTGTGCGCGCCCGAG 1320
Db 1313 ACCCGACGACCGGCTGTGTGTCCGAGAGAGCCCGAGGGTCTGTGCGCGCCCGAG 1372
QY 1321 GAGAGAGACAGACCCCGCTGCTGTGTGACGCTCTCCGACAGACAGAGCCCTGAG 1380
Db 1373 GAGAGAGACAGACCCCGCTGCTGTGTGACGCTCTCCGACAGACAGAGCCCTGAG 1432
QY 1381 CAGGTGTAGAGTGTGTGTGCGGGCTGCTGCGCGCGCTGTGTGCGCGCTGTGCGGC 1440
Db 1433 CAGGTGTAGAGTGTGTGTGCGGGCTGCTGCGCGCGCTGTGTGCGCGCTGTGCGGC 1492
QY 1441 TCCAGGCAACAAGAACGCGCTTCTCAGAGAACACAGAAAGTTATCTCCCTGGAGAG 1500
Db 1493 TCCAGGCAACAAGAACGCGCTTCTCAGAGAACACAGAAAGTTATCTCCCTGGAGAG 1552
QY 1501 CATGCCAGCTCTCGCTGAGAGAGCTGACGTGGAAGATGAGCGTGGAGCTGCGCTTG 1560
Db 1553 CATGCCAGCTCTCGCTGAGAGAGCTGACGTGGAAGATGAGCGTGGAGCTGCGCTTG 1612
QY 1561 CTGCGAGAGAGCCAGAGGGTGTGCTGTGTTCGCGCGAGACACGCTGTGCGTGAAGAG 1620
Db 1613 CTGCGAGAGAGCCAGAGGGTGTGCTGTGTTCGCGCGAGACACGCTGTGCGTGAAGAG 1672
QY 1621 ATCTGCGCAAGTCTCTGCACTGCTGATGAGTGTGATCTGTGCACTGCTCAAGCT 1680
Db 1673 ATCTGCGCAAGTCTCTGCACTGCTGATGAGTGTGATCTGTGCACTGCTCAAGCT 1732
QY 1681 TTCTTTTATGTACGAGAGACACGTTTCAAAAGAACAGGCTTTTCTTACCGAAGAGT 1740
Db 1733 TTCTTTTATGTACGAGAGACACGTTTCAAAAGAACAGGCTTTTCTTACCGAAGAGT 1792
QY 1741 GTCTGAGCAAGTTGCAAAAGATTGAAATCAGACAGCACTTGAAAGGGTCACTGCGG 1800
Db 1793 GTCTGAGCAAGTTGCAAAAGATTGAAATCAGACAGCACTTGAAAGGGTCACTGCGG 1852
QY 1801 GAGCTGTGGAAGACAGAGTCAAGAGATGAGGAGACAGAGCCCGCTGCTGACGCTC 1860
Db 1853 GAGCTGTGGAAGACAGAGTCAAGAGATGAGGAGACAGAGCCCGCTGCTGACGCTC 1912
QY 1861 AGACTCCGCTTCATCCCAAGCTGACGCGCTGCGCGCGATTGTAACATGAGCTGCTC 1920
Db 1913 AGACTCCGCTTCATCCCAAGCTGACGCGCTGCGCGCGATTGTAACATGAGCTGCTC 1972
QY 1921 GTGGAGAGCAAAAGTTCCTCGAGAGAAAGAGGCGCGAGCTCTCACTCGAGGGTGAAG 1980
Db 1973 GTGGAGAGCAAAAGTTCCTCGAGAGAAAGAGGCGCGAGCTCTCACTCGAGGGTGAAG 2032
QY 1981 GCACTGTTCAAGGCTCAACTACAGAGGCGCGCGCGCCCGGCTCTGAGGCGCTCT 2040
Db 2033 GCACTGTTCAAGGCTCAACTACAGAGGCGCGCGCGCCCGGCTCTGAGGCGCTCT 2092
QY 2041 GTGCTGGGCTGAGAGATATCAAGAGGCTGCGCGACCTTGTGTGCTGTGTGGGCGC 2100
Db 2093 GTGCTGGGCTGAGAGATATCAAGAGGCTGCGCGACCTTGTGTGCTGTGTGGGCGC 2152
QY 2101 CAGAGCCGCGCGCTGAGCTGTAATTTGTCAAGGTGATGACGCGCGCTACAGAC 2160
Db 2153 CAGAGCCGCGCGCTGAGCTGTAATTTGTCAAGGTGATGACGCGCGCTACAGAC 2212
QY 2161 ATCCCGGAGACAGGCTCAAGAGGCTATGCGCAGCATCATCAAAACCCAGAACAGTAC 2220
Db 2213 ATCCCGGAGACAGGCTCAAGAGGCTATGCGCAGCATCATCAAAACCCAGAACAGTAC 2272
QY 2221 TGCGTGCCTGATGATGCGGTGTCAGAAAGCCGCCCATGGGACGTCGCCAAGAGCTTC 2280
Db 2273 TGCGTGCCTGATGATGCGGTGTCAGAAAGCCGCCCATGGGACGTCGCCAAGAGCTTC 2332
QY 2281 AAGAGCCAGCTCTCTACCTTGAAGACAGCTCAAGCCGTACATGCGAGTCTGTGCTCAC 2340
Db 2233 AAGAGCCAGCTCTCTACCTTGAAGACAGCTCAAGCCGTACATGCGAGTCTGTGCTCAC 2392
QY 2241 CTGAGAGAGACAGCCCGCTGAGAGGATGCGGTGTATGAGAGAGCTCTCTGTAAT 2400
Db 2293 CTGAGAGAGACAGCCCGCTGAGAGGATGCGGTGTATGAGAGAGCTCTCTGTAAT 2452
QY 2401 GAGGCGAGAGTGGCTCTTCTGAGAGCTTCTGAGCTTCTGATGAGGACAGCGCGCGCG 2460
Db 2453 GAGGCGAGAGTGGCTCTTCTGAGAGCTTCTGAGCTTCTGATGAGGACAGCGCGCGCG 2512
QY 2461 ATCAGGGGCAAGTCTTACGTCAGTGCAGAGGAGATCCGAGGGCTCATCTCTTCACG 2520
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QY 2521 CTGCTGAGAGCTGTGCTACAGGCGCATGAGAGAACAGCTGTTGCGGGATTGCGCGG 2580
Db 2573 CTGCTGAGAGCTGTGCTACAGGCGCATGAGAGAACAGCTGTTGCGGGATTGCGCGG 2632
QY 2581 GACGGGCTGCTCTGCGTTTGTGTGATGATTTCTTGTGTGACACCTCAGCTCACCCAC 2640
Db 2633 GACGGGCTGCTCTGCGTTTGTGTGATGATTTCTTGTGTGACACCTCAGCTCACCCAC 2692
QY 2641 GCGAAGAACCTTCTCAGAGACCCGTGTCAGAGGTCCTGAGATGAGCTGCGGTGTGAC 2700
Db 2693 GCGAAGAACCTTCTCAGAGACCCGTGTCAGAGGTCCTGAGATGAGCTGCGGTGTGAC 2752
QY 2701 TTGCGAAGACAGTGTGAACTTCCCTGTAGAAGACAGAGCCCTGCGGTGCAAGCTTT 2760
Db 2753 TTGCGAAGACAGTGTGAACTTCCCTGTAGAAGACAGAGCCCTGCGGTGCAAGCTTT 2812
QY 2761 GTTCAGATGCGGCGCCACCGGCTATTCCTGCTGTGCGGCTGCTGTGATACCGGAGAC 2820
Db 2813 GTTCAGATGCGGCGCCACCGGCTATTCCTGCTGTGCGGCTGCTGTGATACCGGAGAC 2872
QY 2821 CTGAGAGTCAAGACCACTTCACTCAGTATGCGCGGACCTTCATCAGACAGCTCACCC 2880
Db 2873 CTGAGAGTCAAGACCACTTCACTCAGTATGCGCGGACCTTCATCAGACAGCTCACCC 2932
QY 2881 TTCAACCGGCTTCAAGGCTGAGAGAACATGCGTCCGAACTCTTGGGGTCTTGGCG 2940
Db 2933 TTCAACCGGCTTCAAGGCTGAGAGAACATGCGTCCGAACTCTTGGGGTCTTGGCG 2992
QY 2941 CTGAGAGTCAAGACCTGTTTCTGAGATTGCAAGTGAACAGGCTCAGAGGCTGACCC 3000
Db 2993 CTGAGAGTCAAGACCTGTTTCTGAGATTGCAAGTGAACAGGCTCAGAGGCTGACCC 3052
QY 3001 AACATTTACAGATCTCTGCTGAGAGGCTACAGGCTTACAGCATGTGTGTGACGCTC 3060
Db 3053 AACATTTACAGATCTCTGCTGAGAGGCTACAGGCTTACAGCATGTGTGTGACGCTC 3112
QY 3061 CCAATTTACAGAGTGTGAAGAACCCCAATTTTCTGCGGTGATCTCTGACAGC 3120
Db 3113 CCAATTTACAGAGTGTGAAGAACCCCAATTTTCTGCGGTGATCTCTGACAGC 3172
QY 3121 GCTCTCTCTGTACTCATCTCTGAAAGCAAGAACGAGAGTGTGCTGGGGCCAG 3180
Db 3173 GCTCTCTCTGTACTCATCTCTGAAAGCAAGAACGAGAGTGTGCTGGGGCCAG 3232
QY 3181 GCGGCGCGCGGCTCTGCGCTCCGAGAGCGGTCAGTGGCTGTGACCAAGATTTCTG 3240
Db 3233 GCGGCGCGCGGCTCTGCGCTCCGAGAGCGGTCAGTGGCTGTGACCAAGATTTCTG 3292
QY 3241 CTCAAGCTGACTGACACCGGTGTCACTTACGTGCACTCTTGGGGTCACTGAGACAGCC 3300
Db 3293 CTCAAGCTGACTGACACCGGTGTCACTTACGTGCACTCTTGGGGTCACTGAGACAGCC 3352
QY 3301 CAGAGCAGCTGAGTCCGAGAGCTCCCGGGAGACAGCTGACGCTGAGGCGCGAGCC 3360

Db 3353 CAGACGACGTGATCGGAGAGCTCCCGGAGACGAGCTGACTGCTCCGTCGAGGCGGACGCC 3412
Qy 3361 AACCGGACATGCGCTCTGAGCTTCAAGACCATCTCTGAGCTGATGCCACCC 3411
Db 3413 AACCGGACATGCGCTCTGAGCTTCAAGACCATCTGAGCTGATGCCACCC 3463

RESULT 12
ABZ18391
ID ABZ18391 standard: CDNA, 4015 BP.
XX
XX ABZ18391;
AC
XX 23-JAN-2003 (first entry)
XX
XX
DE Group III cDNA cancer related clone SEQ ID NO:817.
KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
KW immune response; virology; immunology; microbiology; molecular biology;
KW recombinant DNA technology; gene; ss.
OS Homo sapiens.
XX
XX MO200278516-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US010421.
XX
XX 30-MAR-2001; 2001US-0280255P.
XX PR 28-AUG-2001; 2001US-0315563P.
XX PR 09-JAN-2002; 2002US-0347313P.
XX
XX (CORI-) CORIYA CORP.
XX
XX Wang T, Wang S, Bangur CS, Gaiger A;
XX WPI, 2003-058387/05.
XX
XX
XX New immunogenic polynucleotides or polypeptides useful for diagnosing,
XX preventing and treating cancer expressing CT or CP mRNA antigens, and in
XX virology, immunology, microbiology, molecular biology and recombinant DNA
XX techniques.
XX
XX Claim 1; SEQ ID NO 817; 207bp; English.
XX
XX ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
XX ABP5446 to ABP5447 represent protein (II) sequences, from the present
XX invention. (I) and (II) have cytostatic activity and can be used in gene
XX therapy and vaccines. (I), (II), antibodies and compositions from the
XX present invention are useful for diagnosing, preventing and treating
XX cancer, which expresses CT or CP mRNA antigens. They are useful for
XX stimulating immune response. They can also be useful in virology,
XX immunology, microbiology, molecular biology and recombinant DNA
XX techniques. N.B. The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WPIO at [ftp.wipo.int/pub/published_pcl_sequences](http://wipo.int/pub/published_pcl_sequences)
XX
XX Sequence 4015 BP; 664 A; 1363 C; 1275 G; 713 T; 0 U; 0 Other;
XX

Query Match 100.0%; Score 3411; DB 7; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGATGCGCGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGACGACTACCG 60
Db 53 GCGATGCGCGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGACGACTACCG 112
Qy 61 GAGGTGCTGCGCGCTGCGACGCTGCTGCGCGCGCTGCGCGCGCGCGCGCGCGG 120
Db 113 GAGGTGCTGCGCGCTGCGACGCTGCTGCGCGCGCTGCGCGCGCGCGCGCGG 172
Qy 121 CAGCGCGGAGACCGCGCGCGCTTTCGCGCGCTGCTGCGCGCGCGCGCGCGG 180

Db 173 CAGCGCGGAGACCGCGCGCGCTTTCGCGCGCTGCTGCGCGCGCGCGCGCGG 232
Qy 181 TGGAGCGACG 240
Db 233 TGGAGCGACG 292
Qy 241 CTGCTGCG 300
Db 293 CTGCTGCG 352
Qy 301 GCGCTGCG 360
Db 353 GCGCTGCG 412
Qy 361 GCGACTACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 413 GCGACTACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472
Qy 421 CTGCTGCG 480
Db 473 CTGCTGCG 532
Qy 481 GTGCTGCG 540
Db 533 GTGCTGCG 592
Qy 541 GCTGCACTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db 593 GCTGCACTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 652
Qy 601 GAAAGCG 660
Db 653 GAAAGCG 712
Qy 661 GGTGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db 713 GGTGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 772
Qy 721 GGTGCG 780
Db 773 GGTGCG 832
Qy 781 GCGAGAGCG 840
Db 833 GCGAGAGCG 892
Qy 841 GAAAGAGCG 900
Db 893 GAAAGAGCG 952
Qy 901 GCG 960
Db 953 GCG 1012
Qy 961 CTTTGTCCCG 1020
Db 1013 CTTTGTCCCG 1072
Qy 1021 CAGCTGCG 1080
Db 1073 CAGCTGCG 1132
Qy 1081 CTGCTGAGAGCG 1140
Db 1133 CTGCTGAGAGCG 1192
Qy 1141 CCG 1200
Db 1193 CCG 1252
Qy 1201 CAGCGAGTGCCTCCCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260

Db 1253 CACGCGAGTGCCCTTACGCGGAGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTC 1312
QY 1261 ACCCAGAGCGGCTGCTGCTGAGCCGGAGAAAGCCCGAGGGCTCTGAGGCGGCCCCGAG 1320
Db 1313 ACCCGAGAGCGGCTGCTGCTGAGCCGGAGAAAGCCCGAGGGCTCTGAGGCGGCCCCGAG 1372
QY 1321 GAGGAGGACACAGACCCCGCTGCTGCTGAGCTGCTGCTGAGGACACAGACCCCGCTG 1380
Db 1373 GAGGAGGACACAGACCCCGCTGCTGCTGAGCTGCTGCTGAGGACACAGACCCCGCTG 1432
QY 1381 CAGGTGACGCTGCTGCTGAGGAGGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 1440
Db 1433 CAGGTGACGCTGCTGCTGAGGAGGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 1492
QY 1441 TCCAGGACACAGACCCCGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 1500
Db 1493 TCCAGGACACAGACCCCGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 1552
QY 1501 CATGCCAAGCTCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 1560
Db 1553 CATGCCAAGCTCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 1612
QY 1561 CTGCGAGGAGGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 1620
Db 1613 CTGCGAGGAGGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 1672
QY 1621 ATCTGCGCAAGTCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 1680
Db 1673 ATCTGCGCAAGTCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 1732
QY 1681 TTCTTTATGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 1740
Db 1733 TTCTTTATGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 1792
QY 1741 GTCTGAGGACAGTGTGCAAGAGTGTGAAATGACAGCACTTGAAGAGGCTGAGCTGCG 1800
Db 1793 GTCTGAGGACAGTGTGCAAGAGTGTGAAATGACAGCACTTGAAGAGGCTGAGCTGCG 1852
QY 1801 GAGCTGCGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 1860
Db 1853 GAGCTGCGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 1912
QY 1861 AGACTGCGCTTCACTCCCAAGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 1920
Db 1913 AGACTGCGCTTCACTCCCAAGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 1972
QY 1921 GTGCGAGGACAGTGTGCAAGAGTGTGAAATGACAGCACTTGAAGAGGCTGAGCTGCG 1980
Db 1973 GTGCGAGGACAGTGTGCAAGAGTGTGAAATGACAGCACTTGAAGAGGCTGAGCTGCG 2032
QY 1981 GCACTGTTTCAAGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2040
Db 2033 GCACTGTTTCAAGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2092
QY 2041 GTGCTGAGGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2100
Db 2093 GTGCTGAGGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2152
QY 2101 CAGGACCCGCGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2160
Db 2153 CAGGACCCGCGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2212
QY 2161 ATCTGCGAGGACAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2220
Db 2213 ATCTGCGAGGACAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2272
QY 2221 TGGCTGAGGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2280
Db 2273 TGGCTGAGGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2332
QY 2281 AAGAGGACAGTCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2340
Db 2333 AAGAGGACAGTCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2392

QY 2341 CTGCGAGGACAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2400
Db 2393 CTGCGAGGACAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2452
QY 2401 GAGGCGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2460
Db 2453 GAGGCGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2512
QY 2461 ATCAGGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2520
Db 2513 ATCAGGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2572
QY 2521 CTGCTCTGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2580
Db 2573 CTGCTCTGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2632
QY 2581 GAGGCGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2640
Db 2633 GAGGCGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2692
QY 2641 GCGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 2700
Db 2693 GCGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 2752
QY 2701 TTGCGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 2760
Db 2753 TTGCGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 2812
QY 2761 GTTGAAGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 2820
Db 2813 GTTGAAGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 2872
QY 2821 CTGAGGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 2880
Db 2873 CTGAGGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGG 2932
QY 2881 TTCAAAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2940
Db 2933 TTCAAAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 2992
QY 2941 CTGAAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3000
Db 2993 CTGAAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3052
QY 3001 AACATCTTCAAGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3060
Db 3053 AACATCTTCAAGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3112
QY 3061 CCATTTCATGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3120
Db 3113 CCATTTCATGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3172
QY 3121 GCTTCTGCTGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3180
Db 3173 GCTTCTGCTGCTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3232
QY 3181 GGGCGCGCGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3240
Db 3233 GGGCGCGCGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3292
QY 3241 CTCAAGCTGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3300
Db 3293 CTCAAGCTGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3352
QY 3301 CAGAGGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3360
Db 3353 CAGAGGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3412
QY 3361 AACCGGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3411
Db 3413 AACCGGAGGAGTGTGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGGCTGCTGAGGAGG 3463

RESULT 13
AAV72117
ID AAV72117 standard; CDNA; 4042 BP.
XX
XX AAV72117;
AC
XX
XX 24-MAY-1999 (first entry)
DE Human catalytic telomerase sub-unit CDNA.
XX
XX Human; catalytic telomerase subunit; therapy; diagnosis; htc; assay;
XX modulator; treatment; inhibitor; cellular disorder; death; defect; cancer;
XX ageing; antisense; neoplastic cell; telomerase-related condition;
XX tumour cell; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 63..3461
XX FT /*tag= a
XX FT /product= "catalytic telomerase subunit"
XX
XX MO9859040-A2.
XX
XX 30-DEC-1998.
XX
XX 09-JUN-1998; 98MO-EP003468.
XX
XX 20-JUN-1997; 97DE-01026329.
XX 26-MAR-1998; 98DE-01013274.
XX 14-APR-1998; 98DE-01016496.
XX
XX (FARB) BAYER AG.
XX
XX Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;
XX
XX WPI: 1999-081276/07.
XX P-PSDB; AAW90251.
XX
XX New catalytically active subunit of human telomerase - used in the
XX modulation of telomerase activity, particularly for treating cancer and
XX ageing.
XX
XX
XX Claim 4; Fig 1; 76pp; German.
XX
XX This sequence encodes a novel human catalytic telomerase sub-unit (htc).
XX The encoded protein can be used in screening assays to identify
XX modulators of telomerase and to treat or inhibit cellular disorders,
XX death, defects and/or other pathological processes involving telomerase,
XX particularly cancer and ageing (also suitable for this are agents that
XX stimulate, inhibit or mimic the activity of the subunit). Antisense
XX nucleic acids inhibit telomerase action (by binding to specific mRNA),
XX particularly in neoplastic cells and may be expressed in vivo. Antibodies
XX and fragments of the protein, used as probes or primers, are used to
XX diagnose telomerase-related conditions (especially neoplasia) by (i)
XX detecting abnormal levels of the subunit protein in body fluids or
XX tissues or (ii) by measuring the amount of the encoding nucleic acid.
XX Expression of the nucleic acid encoding the subunit mRNA is confined to
XX tumour cells, in contrast to the ubiquitous expression of the telomerase
XX RNA subunit
XX
XX Sequence 4042 BP; 684 A; 1364 C; 1277 G; 717 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 3411; DB 2; Length 4042;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGATGCGCGCGCTCCCGCTGCGCGAGCCGTCGCTCCCTGCTGCGAGCCACTACCGC 60
DB 60 GCGATGCGCGCGCTCCCGCTGCGCGAGCCGTCGCTCCCTGCTGCGAGCCACTACCGC 119
QY 61 GAGGTGCTGCGCGCTGCGCGAGCTTCGTCGCGGCGCTGCGGCGCCCAAGGGCTGCGCGTGTG 120

DB 120 GAGGTGCTGCGCGCTGCGCGAGCTTCGTCGCGGCGCTGCGGCGCCCAAGGGCTGCGCGTGTG 179
QY 121 CAGCGCGGCGAGACCCGCGCGGCTTTCCGCGCGCTGCGGCGCCAGTGTGCTGTGCGTGGCC 180
DB 180 CAGCGCGGCGAGACCCGCGCGGCTTTCCGCGCGCTGCGGCGCCAGTGTGCTGTGCGTGGCC 239
QY 181 TGGAGCGACG 240
DB 240 TGGAGCGACG 299
QY 241 CTGCGCGCGCGAGTCTGTCAGAGGCTGTGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 300 CTGCGCGCGCGAGTCTGTCAGAGGCTGTGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 359
QY 301 GCGTTGCGCGCTGTCGAGCGGCG 360
DB 360 GCGTTGCGCGCTGTCGAGCGGCG 419
QY 361 GCGAGCTACTGCG 420
DB 420 GCGAGCTACTGCG 479
QY 421 CTGCTGCGCGCGCTGTCGAGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 480 CTGCTGCGCGCGCTGTCGAGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
QY 481 GTGCTGTGTGTGCTTCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 540 GTGCTGTGTGTGCTTCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599
QY 541 GCTGCGCTACTGAGCG 600
DB 600 GCTGCGCTACTGAGCG 659
QY 601 GAAAGGCGCTGGAACCATATGCTGCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 660 GAAAGGCGCTGGAACCATATGCTGCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
QY 661 GGTGCGAGAGAGCG 720
DB 720 GGTGCGAGAGAGCG 779
QY 721 GGTGCGCGCTGCGCTGAGCG 780
DB 780 GGTGCGCGCTGCGCTGAGCG 839
QY 781 GCGAGAGCGCTGAGACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 840 GCGAGAGCGCTGAGACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
QY 841 GAAAGAGCCACTCTTTGAGAGGTGCGCTGCTGCGACGCGCGCACTCCCACTCCGCTG 900
DB 900 GAAAGAGCCACTCTTTGAGAGGTGCGCTGCTGCGACGCGCGCACTCCCACTCCGCTG 959
QY 901 GCGCGCGAGACGACG 960
DB 960 GCGCGCGAGACGACG 1019
QY 961 CTTGTGCTGCGCGGTGTAAGCGCGAGACCAAGCACTTCTCTACTCTCTGAGCGGACAGAG 1020
DB 1020 CTTGTGCTGCGCGGTGTAAGCGCGAGACCAAGCACTTCTCTACTCTCTGAGCGGACAGAG 1079
QY 1021 CAGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1080 CAGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1139
QY 1081 CTGCTGAGACCATCTTTCTGAGGTTCCAGGCGCTGAGTGCAGAGGACTCCCGCGAGGTTG 1140
DB 1140 CTGCTGAGACCATCTTTCTGAGGTTCCAGGCGCTGAGTGCAGAGGACTCCCGCGAGGTTG 1199
QY 1141 CCGCGCGTGGCGCGCGCTACTGCGCAATGAGCGCGCGCTGTTCTTCTGAGCTGCTTGGAGAC 1200

[illegible]

QY	2281	AAGAGCGAAGTCTTCAACCTTGACAAGCTCCAGACCGTACATGACGACATGTGGTCAAC	2344
Db	2340	AAGAGCCAGTCTTCACTTGAACAGACTCCAGACCGTACATGACGACATGTGGTCAAC	2399
QY	2341	CTGCAAGAGACCAAGCCCGCTGAGGGATGCCGTCTCATGACGACAGCTTCTCCCTGAAT	2400
Db	2400	CTGCAAGAGACCAAGCCCGCTGAGGGATGCCGTCTCATGACGACAGCTTCTCCCTGAAT	2455
QY	2401	GAGGCACACAGTGGGCTCTTGACAAGTCTTCTCAAGCTTCAATGTGCACCAAGCCGTGGAC	2466
Db	2460	GAGGCACACAGTGGGCTCTTGACAAGTCTTCTCAAGCTTCAATGTGCACCAAGCCGTGGAC	2515
QY	2461	ATCAGGGGCAAGTCTTAAGTCCAGTGCACAGGGGATCCCGACGGGCTCCATCTCTCCACG	2522
Db	2520	ATCAGGGGCAAGTCTTAAGTCCAGTGCACAGGGGATCCCGACGGGCTCCATCTCTCCACG	2579
QY	2521	CTGCTCTGCAGCTGTGCTACGGGACATGAGAGAACAGCTGTTGCGGGGATTCCGCGG	2580
Db	2580	CTGCTCTGCAGCTGTGCTACGGGACATGAGAGAACAGCTGTTGCGGGGATTCCGCGG	2639
QY	2581	GACGGGCTGCTCTCCGCTTTGGTGGATGATTTCTTGTGTGGACACTCACCTCACCCAC	2640
Db	2640	GACGGGCTGCTCTCCGCTTTGGTGGATGATTTCTTGTGTGGACACTCACCTCACCCAC	2699
QY	2641	GCGAAGACCTTCTCAGAGACCCGTGATCCGAGGTGCTCCCTGAGTATGGCTGCGTGTGAAC	2700
Db	2700	GCGAAGACCTTCTCAGAGACCCGTGATCCGAGGTGCTCCCTGAGTATGGCTGCGTGTGAAC	2759
QY	2701	TTGCGGAGAGACAGTGTGAATTTCCCTGTGTAAGAACAGAGGCCCTGGGGTGGACGGCTTTT	2760
Db	2760	TTGCGGAGAGACAGTGTGAATTTCCCTGTGTAAGAACAGAGGCCCTGGGGTGGACGGCTTTT	2819
QY	2761	GTTCAAGATGCCGGGCCACAGGCTTATTCGCCCTGAGCGGCTCGCTGAGTAAACCCGAGAC	2820
Db	2820	GTTCAAGATGCCGGGCCACAGGCTTATTCGCCCTGAGCGGCTCGCTGAGTAAACCCGAGAC	2879
QY	2821	CTGAGAGGTGCAGAGAGACTCAAGCTATAGCCCGGACCTCCATCAAGACCAAGTCTCAC	2880
Db	2880	CTGAGAGGTGCAGAGAGACTCAAGCTATAGCCCGGACCTCCATCAAGACCAAGTCTCAC	2939
QY	2881	TTCAACCGGGCTTCAAGCTGGAGGAGAACATGCGTGCACAACTTTTGGGGTCTTGCGG	2940
Db	2940	TTCAACCGGGCTTCAAGCTGGAGGAGAACATGCGTGCACAACTTTTGGGGTCTTGCGG	2999
QY	2941	CTGAAGTGTCAAGACCTGTTTCTGAGTTTGAAGGTGAACAGCCCTCCAGACGGTGTGACCC	3000
Db	3000	CTGAAGTGTCAAGACCTGTTTCTGAGTTTGAAGGTGAACAGCCCTCCAGACGGTGTGACCC	3059
QY	3001	AACATCTTCAAGATCTCTCTGCTGACAGCGTACAGCTTTTCAAGCATGTGTCTCAAGTCTC	3060
Db	3060	AACATCTTCAAGATCTCTCTGCTGACAGCGTACAGCTTTTCAAGCATGTGTCTCAAGTCTC	3119
QY	3061	CCATTTTCAATCAGCAAGTTTGGAGAAACCCACATTTTTCGAGCGCTCAATCTGACAGC	3120
Db	3120	CCATTTTCAATCAGCAAGTTTGGAGAAACCCACATTTTTCGAGCGCTCAATCTGACAGC	3179
QY	3121	GGCTTCCTCTGCTACTCAATCTTGAAGCCAGAACCGAAGGATGTGCTGGGGGCCAAG	3180
Db	3180	GGCTTCCTCTGCTACTCAATCTTGAAGCCAGAACCGAAGGATGTGCTGGGGGCCAAG	3239
QY	3181	GGCGCCGCGCGCCCTCTGCGCCTCCGAGAGCGGTGACATGTGTGCACCAAGCACTTCTCTG	3240
Db	3240	GGCGCCGCGCGCCCTCTGCGCCTCCGAGAGCGGTGACATGTGTGCACCAAGCACTTCTCTG	3299
QY	3241	CTCAAGCTGACTGCAGACCGGTGTCACTTAAGTGCATCTCTGGGGTCACTCAAGACAGCC	3300
Db	3300	CTCAAGCTGACTGCAGACCGGTGTCACTTAAGTGCATCTCTGGGGTCACTCAAGACAGCC	3359
QY	3301	CAGACGCAAGTGAATCGGAAGCTTCCCGGGACGACGCTGACTGCCCTGAGAGGCGCGACGCC	3360
Db	3360	CAGACGCAAGTGAATCGGAAGCTTCCCGGGACGACGCTGACTGCCCTGAGAGGCGCGACGCC	3419

QY 3361 AACCCGGACACTGCCCTCAGACTTCAGACCATCTGAGTATGACCAACC 3411
Db 3420 AACCCGGACACTGCCCTCAGACTTCAGACCATCTGAGTATGACCAACC 3470

RESULT 14

ABL53711
ID ABL53711 standard; cDNA; 4070 BP.

XX ABL53711;

DT 17-JUN-2002 (first entry)

DE Human telomerase catalytic subunit hTERT cDNA.

KM hTERT; telomerase; reverse transcriptase; immortalization; human;

XX vaccine; enzyme; gene; ss.

OS Homo sapiens.

XX MO200216555-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001MO-GB003726.

PR 17-AUG-2000; 2000GB-00020246.

PR 17-AUG-2000; 2000US-0225734P.

PA (UYMA-) UNIV WALES COLLEGE OF MEDICINE.

PI Jones CJ, Kipling DG, Wilkinson G, Mcsharry B, Skinner JW;

DR WPI; 2002-315462/35.

PT Novel hTERT-immortalized cell line (human telomerase reverse
transcriptase) useful for human vaccine production and preparation of
antigen, such as a virus or virus-derived agent.

PS Example 1; Fig 1; 64pp; English.

XX The present sequence is that of hTERT cDNA in plasmid pGRN121. hTERT is
the catalytic subunit of human telomerase. Claimed immortalized cell
lines for use in vaccine production are adapted to express hTERT.
CC Suitable cell lines comprise human diploid fibroblasts, e.g. MRC-5 or
CC WI38 cells, transfected with hTERT cDNA or infected by a retrovirus
CC carrying hTERT cDNA, and are capable of supporting antigen production. A
CC method for preparing such cell lines using recombinant techniques is
CC provided. The cell lines are also used as a diagnostic test for the
CC presence of a virus, such as human cytomegalovirus, and to determine the
CC efficacy of antiviral agents by testing the capability of a modified
CC virus containing a reporter gene to infect the cells. The cell lines have
CC the ability, which can be impaired in cell lines immortalized by other
CC methods, of being able to support viral replication. The cells remain
CC morphologically suitable for viral/vaccine cultivation

XX Sequence 4070 BP; 670 A; 1383 C; 1296 G; 721 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 6; Length 4070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGATGCGCGGCGCTCCCGCGGAGCGCTGCGCTCTCTCTCGGACCACTACCGC 60
Db 73 GCGATGCGCGGCGCTCCCGCGGAGCGCTGCGCTCTCTCTCGGACCACTACCGC 132
QY 61 GAGGTGCTGCGCTGCGCACTTCTGCGCGCTGCGGACCCAGAGGCTGCGGCTGAGT 120
Db 133 GAGGTGCTGCGCTGCGCACTTCTGCGCGCTGCGGACCCAGAGGCTGCGGCTGAGT 192
QY 121 CAGCGGCGGAGACCCGCGGCTTTCCGCGGCTGAGTGGCCCAAGTGGCTGTGGTGGCC 180
Db 193 CAGCGGCGGAGACCCGCGGCTTTCCGCGGCTGAGTGGCCCAAGTGGCTGTGGTGGCC 252

QY 181 TGGAGCGACG 240
Db 253 TGGAGCGACG 312
QY 241 CTGTGTGCGCGCGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGCGAGAGAGTGTCTG 300
Db 313 CTGTGTGCGCGCGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGCGAGAGAGTGTCTG 372
QY 301 GCGTTTGGGCTGTGAGACGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 373 GCGTTTGGGCTGTGAGACGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 432
QY 361 CGCAGCTACCTTGCCCAACACAGGTGACCGACGCACTGCGGAGGAGCGGAGCGGAGCTG 420
Db 433 CGCAGCTACCTTGCCCAACACAGGTGACCGACGCACTGCGGAGGAGCGGAGCGGAGCTG 492
QY 421 CTGCTGCGCGCGCGGTGGGCGACGACGTGTGTGTCTCACTGCTGAGCGCTGCGGCTCTT 480
Db 493 CTGCTGCGCGCGCGGTGGGCGACGACGTGTGTGTCTCACTGCTGAGCGCTGCGGCTCTT 552
QY 481 GTGCTGTGTGCTCCAGCTGCGCTTACAGATGTGCGGCGCGCGCGCGCTGTACAGCTGCG 540
Db 553 GTGCTGTGTGCTCCAGCTGCGCTTACAGATGTGCGGCGCGCGCGCGCTGTGTACAGCTG 612
QY 541 GCTGCCACTGAGCG 600
Db 613 GCTGCCACTGAGCG 672
QY 601 GAACGGGCTGGAACCACTATGCTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 673 GAACGGGCTGGAACCACTATGCTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 732
QY 661 GGTGCGAGAGCG 720
Db 733 GGTGCGAGAGCG 792
QY 721 CGTGGCG 780
Db 793 CGTGGCG 852
QY 781 GCGAGAGCGCGTGAACCGAGTGAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 853 GCGAGAGCGCGTGAACCGAGTGAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 912
QY 841 GAGAGAGCGCGCTTTTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 913 GAGAGAGCGCGCTTTTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 972
QY 901 GCGCGCGAGACACAGCG 960
Db 973 GCGCGCGAGACACAGCG 1032
QY 961 CTTTGTTCCTCCGCTGTGACCGCGAGCACTTCTTCACTCCCTCAGCGCAAGAGAG 1020
Db 1033 CTTTGTTCCTCCGCTGTGACCGCGAGCACTTCTTCACTCCCTCAGCGCAAGAGAG 1092
QY 1021 CAGCTGCGCGCGCTTCTCTCACTCACTGAGGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 1093 CAGCTGCGCGCGCTTCTCTCACTCACTGAGGCGCGCGCGCGCGCGCGCGCGCGCG 1152
QY 1081 CTGTGTGAGACCACTTTTCTGAGTTCCAGGCGCTGTGATGCGAGGACTCCCGCAGGTTG 1140
Db 1153 CTGTGTGAGACCACTTTTCTGAGTTCCAGGCGCTGTGATGCGAGGACTCCCGCAGGTTG 1212
QY 1141 CCGCGCGTGGCGCGAGGCTATGCAATGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
Db 1213 CCGCGCGTGGCGCGAGGCTATGCAATGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1272
QY 1201 CAGCGGAGTGGCGCGCTTACGAGGCTGTCTGAAAGCGCACTGCGCGCGCGCGCGCG 1260
Db 1273 CAGCGGAGTGGCGCGCTTACGAGGCTGTCTGAAAGCGCACTGCGCGCGCGCGCGCG 1332

[illegible]

Db	2413	CTGCAGGAGCACAGCCCGCTGAGGGATCCGTCGTCATCGACAGAGCTCTCCCTCGTAAT	2472
Qy	2401	GAGCGCAGAGTGGGCTCTTGCAAGTCTCTTCAAGCTTCATGTGCACACAGCCGTGGC	2466
Db	2473	GAGGCCAAGAGTGGCTCTTGCAAGCTCTCTTACGCTTCATGTGCACACAGCCGTGGC	2533
Qy	2461	ATCAGGGGCAAGTCTCTAGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACG	2520
Db	2533	ATCAGGGGCAAGTCTCTAGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACG	2592
Qy	2521	CTGCTCTGACGCTGTGCTACGGCGCAGTGTGAGAACAAAGCTGTTTGCGGGGATTCGCGGG	2580
Db	2593	CTGCTCTGACGCTGTGCTACGGCGCAGTGTGAGAACAAAGCTGTTTGCGGGGATTCGCGGG	2652
Qy	2581	GACGGGCTGCTCTGCGCTTGGTGGATGATTTCTGTGTGACACCTCACTCACCCAC	2640
Db	2653	GACGGGCTGCTCTGCGCTTGGTGGATGATTTCTGTGTGACACCTCACTCACCCAC	2712
Qy	2641	GCGAAACCTTCTCTAGGACCTCGTCCGAGAGTCTCTAGTATGCTGTGCTGTGAAC	2700
Db	2713	GCGAAACCTTCTCTAGGACCTCGTCCGAGAGTCTCTAGTATGCTGTGCTGTGAAC	2772
Qy	2701	TTGCGGAAAGACAGTGTGATCTTCCTCTTAAGAACAGAGGCTTGGGGGACAGGCTTTT	2760
Db	2773	TTGCGGAAAGACAGTGTGATCTTCCTCTTAAGAACAGAGGCTTGGGGGACAGGCTTTT	2832
Qy	2761	GTTTCAGATGCCGGCCACAGGCTTATTCCTGTGTGGGCTGTGCTGTGAATCCGGAC	2820
Db	2833	GTTTCAGATGCCGGCCACAGGCTTATTCCTGTGTGGGCTGTGCTGTGAATCCGGAC	2892
Qy	2821	CTGAGAGTGCAGAGGACCTACCTCCAGCTATGCCGGAACCTCCATCAGAGCAGTCTACC	2880
Db	2893	CTGAGAGTGCAGAGGACCTACCTCCAGCTATGCCGGAACCTCCATCAGAGCAGTCTACC	2952
Qy	2881	TTCAACCGCGGCTTCAAGGCTTGGAGAACATGCGTGCACAACTTTTGGGGTCTTGGC	2940
Db	2953	TTCAACCGCGGCTTCAAGGCTTGGAGAACATGCGTGCACAACTTTTGGGGTCTTGGC	3012
Qy	2941	CTGAAGTGCACAGGCTGTTCTTGAGATTTGGAGGTGAACAGCCTCCAGAGGCTGTGACC	3000
Db	3013	CTGAAGTGCACAGGCTGTTCTTGAGATTTGGAGGTGAACAGCCTCCAGAGGCTGTGACC	3072
Qy	3001	AACATCTTCAAGATCTCTGCTGCTGACAGCGTACAGGTTTTCACGATGTGTCTGACGTC	3060
Db	3073	AACATCTTCAAGATCTCTGCTGCTGACAGCGTACAGGTTTTCACGATGTGTCTGACGTC	3132
Qy	3061	CCATTTTCATCAGAGATTTTGGAAACACCCACATTTTCTCGGCGCTCATCTGTACACG	3120
Db	3133	CCATTTTCATCAGAGATTTTGGAAACACCCACATTTTCTCGGCGCTCATCTGTACACG	3192
Qy	3121	GCTTCCTCTGTACTCATCTCTGAAGCCACAGAACCAAGGATGTGCTGGGGGCGCAAG	3180
Db	3193	GCTTCCTCTGTACTCATCTCTGAAGCCACAGAACCAAGGATGTGCTGGGGGCGCAAG	3252
Qy	3181	GCGCGCGCGGCTCTTGCCCTCCGAGGCGGTGACGTGCTGTGCCACCAAGCATTCCTG	3240
Db	3253	GCGCGCGCGGCTCTTGCCCTCCGAGGCGGTGACGTGCTGTGCCACCAAGCATTCCTG	3312
Qy	3241	CTCAAGCTGATCTGACACCGGTACCTTACGTGCACCTCTGGGGGTCACTCAGAACAGCC	3300
Db	3313	CTCAAGCTGATCTGACACCGGTACCTTACGTGCACCTCTGGGGGTCACTCAGAACAGCC	3372
Qy	3301	CAGACGACGCTGAGTCCGAAAGCTCCCGGGGACGACGCTGACCTCTGAGAGGCGGACCC	3360
Db	3373	CAGACGACGCTGAGTCCGAAAGCTCCCGGGGACGACGCTGACCTCTGAGAGGCGGACCC	3432
Qy	3361	AACCCGGACCTGCCCTCAGACTTCAAGACCATCTGTGACCTGATGGGCCACCC	3411
Db	3433	AACCCGGACCTGCCCTCAGACTTCAAGACCATCTGTGACCTGATGGGCCACCC	3483

AAV27876
ID AAV27876 standard; cDNA; 3798 BP.
AC AAV27876;
XX 25-MAR-2003 (revised)
DT 12-OCT-1998 (first entry)
XX Human telomerase protein 2 (TP2) full-length cDNA.
DE TP2; human; telomerase protein 2; cancer; AIDS; ageing; therapy; ss.
XX Homo sapiens.
OS Key Location/Qualifiers
FH 2.3466
FT CDS /*tag= a
XX
XX MO9821343-A1.
XX
XX 22-MAY-1998.
XX
XX 13-NOV-1997; 97WO-US021248.
XX
XX 15-NOV-1996; 96US-00751189.
XX 11-JUN-1997; 97US-00873039.
XX 16-OCT-1997; 97US-00951733.
XX
XX (AMGE-) AMGEN INC.
XX (AMGE-) AMGEN CANADA INC.
XX
XX Harrington LA, Robinson MO;
XX
XX WPI; 1998-297946/26.
XX P-PSDB; AAV27876.
XX
XX New nucleic acid encoding human telomerase protein-2 - used for
PT regulating telomerase activity, e.g. for treating cancer or acquired
PT immune deficiency syndrome.
XX
XX Claim 1c; Fig 8; 150pp; English.
XX
XX This full-length cDNA clone codes for a human telomerase protein 2 (TP2,
XX see AAV61350), a novel protein of the telomerase complex. The sequence
XX was deduced from overlapping partial clones #32 (see AAV27872) and TP2-15
XX (see AAV27875), which were obtained from a human colon tumour cell line
XX LIM1863 cDNA. Expressing TP2 genes in a cell is used to increase
XX telomerase activity and thus proliferation for treatment of e.g. HIV
XX infection, AIDS and ageing disorders, while expressing an inactive mutant
XX of TP2 (or molecule antisense to the gene) is used to decrease telomerase
XX activity, e.g. for treatment of cancer. TP2 polypeptides can also be used
XX to screen for agents that inhibit TP2 activity or its binding to TRF1
XX (see AAV61347) or telomerase RNA, potentially useful therapeutically,
XX also to raise specific antibodies useful in immunoassays and
XX diagnostic probes for detecting/quantifying TP2 DNA. Also contemplated
XX are transgenic animals in which the TP2 gene has been inactivated or is
XX overexpressed. TP2 polypeptides are administered i.v., s.c. or orally, or
XX they are delivered from engineered cells or gene therapy vectors.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 3798 BP; 613 A; 1311 C; 1212 G; 662 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 3409.4; DB 2; Length 3798;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 GCGATGCGGCGGCTCCCGCTGCGAGCGGTGCGCTCCCTGTCGGCGCCACTACCGC 60
XX 65 GCGATGCGGCGGCTCCCGCTGCGAGCGGTGCGCTCCCTGTCGGCGCCACTACCGC 124
XX 61 GAGGTGTCGCGGTGCGCACTGTCGGCGGCTGCGGAGCCCGAGGCTGCGGCTGTG 120

125 GAGGTGTCGCGGTGCGCACTTGTGTGGGCGCTTGAGGAGCCCGAGGCTGAGCGCTGTG 184
QY 121 CAGCGCGGAGAACCCGCGCGCTTTTCCGCGCGCTGTGTGGCCAGTGTGTGTGTGCTGCC 180
DB 185 CAGCGCGGAGAACCCGCGCGCTTTTCCGCGCGCTGTGTGGCCAGTGTGTGTGTGCTGCC 244
QY 181 TGAGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 245 TGAGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 304
QY 241 CTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
DB 305 CTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 364
QY 301 GCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
DB 365 GCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 424
QY 361 CGCAGCTACCTGTCCCAACACGCGTACCGGACCTGTGCGGAGAGCGGAGCGTGTGAGCGT 420
DB 425 CGCAGCTACCTGTCCCAACACGCGTACCGGACCTGTGCGGAGAGCGGAGCGTGTGAGCGT 484
QY 421 CTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB 485 CTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 544
QY 481 GT 540
DB 545 GT 604
QY 541 GCTGT 600
DB 605 GCTGT 664
QY 601 GAACGCGGCTGTGAACCATATAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 665 GAACGCGGCTGTGAACCATATAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 724
QY 661 GT 720
DB 725 GT 784
QY 721 GGT 780
DB 785 GGT 844
QY 781 GGT 840
DB 845 GGT 904
QY 841 GAAG 900
DB 905 GAAG 964
QY 901 GGT 960
DB 965 GGT 1024
QY 961 GGT 1020
DB 1025 GGT 1084
QY 1021 CAGGT 1080
DB 1085 CAGGT 1144
QY 1081 CTGT 1140
DB 1145 CTGT 1204
QY 1141 CCGCGCGT 1200
DB 1205 CCGCGCGT 1264

QY	1201	CACGCGCAATGGCCCCCAGAGGGGTGGCTCCCTCAAGACGCACTGGCCGCTGTAGCTTGGGCT	126
Db	1265	CAGCGCAATGGCCCCCAGAGGGGTGGCTCCCTCAAGACGCACTGGCCGCTGTAGCTTGGGCT	1324
QY	1261	ACCCCAAGCAGCCGATGTCTGTGTCCCGGAGAAAGCCCAAGAGCTCTGTGAAGCCCCCAAG	1320
Db	1325	ACCCCAAGCAGCCGATGTCTGTGTCCCGGAGAAAGCCCAAGAGCTCTGTGAAGCCCCCAAG	1384
QY	1321	GAGGAGGACACAGACCCCGGTGGCTGGTGAAGCTGTCCGACACACAGACGCCCTTGG	1380
Db	1385	GAGGAGGACACAGACCCCGGTGGCTGGTGAAGCTGTCCGACACACAGACGCCCTTGG	1444
QY	1381	CAGGTGTACAGCTTGGTGGGAGCTGGCTTGGCCGAGCTGTGGCCCAAGGCTCTGGAGG	1440
Db	1445	CAGGTGTACAGCTTGGTGGGAGCTGGCTTGGCCGAGCTGTGGCCCAAGGCTCTGGAGG	1504
QY	1441	TCCAGGACCAAGAAAGCCGCTTCCCTCAAGAAACACCAAGAAATATCTCCCTGGGAG	1500
Db	1505	TCCAGGACCAAGAAAGCCGCTTCCCTCAAGAAACACCAAGAAATATCTCCCTGGGAG	1564
QY	1501	CATGCCAAGCTCTCGCTGACAGAGCTGACGTGAAGATGAGCGTGGAGACTTGGCTTGG	1560
Db	1565	CATGCCAAGCTCTCGCTGACAGAGCTGACGTGAAGATGAGCGTGGAGACTTGGCTTGG	1624
QY	1561	CTGCGCAGGAGGCCCAAGGGGTTTGGCTGTTCGCGCCGACAGACACCGTCTCGTGAAGAG	1620
Db	1625	CTGCGCAGGAGGCCCAAGGGGTTTGGCTGTTCGCGCCGACAGACACCGTCTCGTGAAGAG	1684
QY	1621	ATCTGGCCAAATTCCTGACATGAGTGTATGAGTGTGTATCGTGTGAGACTCTAGGCT	1680
Db	1685	ATCTGGCCAAATTCCTGACATGAGTGTATGAGTGTGTATCGTGTGAGACTCTAGGCT	1744
QY	1681	TTCCTTTATGTACAGGAGACACCGTTTCAAAAAGACAGAGCTTTTCTTACCGGAAGAT	1740
Db	1745	TTCCTTTATGTACAGGAGACACCGTTTCAAAAAGACAGAGCTTTTCTTACCGGAAGAT	1804
QY	1741	GTCTGAGACAAATTGCAAAAGCATTTGAAATCAGACGACTTGAAGAGGGTGCAGCTGG	1800
Db	1805	GTCTGAGACAAATTGCAAAAGCATTTGAAATCAGACGACTTGAAGAGGGTGCAGCTGG	1864
QY	1801	GAGCTGTGGGAAGCAGAGGTACAGCGAGATGGGAAAGCAGAGCCGCTGTGTAGAGTCC	1860
Db	1865	GAGCTGTGGGAAGCAGAGGTACAGCGAGATGGGAAAGCAGAGCCGCTGTGTAGAGTCC	1924
QY	1861	AGACTCGGCTTCATCCCAAGGCTTGACGAGGCTGGCCGCGATTGTGAACATGACCTACGTC	1920
Db	1925	AGACTCGGCTTCATCCCAAGGCTTGACGAGGCTGGCCGCGATTGTGAACATGACCTACGTC	1984
QY	1921	GTGGGAGCAGAAAGCTTCGCGAGAAAGAGAGGCGCGACCTGACAGGCTGAAAG	1980
Db	1985	GTGGGAGCAGAAAGCTTCGCGAGAAAGAGAGGCGCGACCTGACAGGCTGAAAG	2044
QY	1981	GCACTGTTCAAGGTGTCAACTACGAGCGGAGCCCGGAGCTTCTTGGGCGCTCT	2040
Db	2045	GCACTGTTCAAGGTGTCAACTACGAGCGGAGCCCGGAGCTTCTTGGGCGCTCT	2104
QY	2041	GTGCTGGGCTGTGAAGATATCAGAGGCTGTGGGAGACCTTTCGTGTGCGGTGTGGGCGC	2100
Db	2105	GTGCTGGGCTGTGAAGATATCAGAGGCTGTGGGAGACCTTTCGTGTGCGGTGTGGGCGC	2164
QY	2101	CAGAACCCGCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACAGGAGCGCTAGACAC	2160
Db	2165	CAGAACCCGCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACAGGAGCGCTAGACAC	2224
QY	2161	ATCCCCCAGACAGGCTCAGCGAGGTCACTCGCAGCATCATCAAACCCAGAAACAGTAC	2220
Db	2225	ATCCCCCAGACAGGCTCAGCGAGGTCACTCGCAGCATCATCAAACCCAGAAACAGTAC	2284
QY	2221	TGCGTGTGCGGTATGCGGTGTGTCCAGAGGCGCCCATGGGACAGTGTCCGAGAGGCTTTC	2280
Db	2285	TGCGTGTGCGGTATGCGGTGTGTCCAGAGGCGCCCATGGGACAGTGTCCGAGAGGCTTTC	2344

QY	2281	AAGAGCCACGCTCTACCTTGAACAAGCCTCCAGCCGTCATGACGACAGTTGGTGGCTCAC	23140
Db	2345	AAGAGCCACGCTCTACCTTGAACAAGCCTCCAGCCGTCATGACGACAGTTGGTGGCTCAC	24040
QY	2341	CTGCAGAGAACCAAGCCCGCTAGAGGATGCGTGTCTCATGAGCAAGACTCTCCCTGAAT	24000
Db	2405	CTGCAGAGAGAACCAAGCCCGCTAGAGGATGCGTGTCTCATGAGAGAGACTCTCCCTGAAT	24640
QY	2401	GAGGCACACAGTGGGCTCTTGAGAGTCTTCTTAGAGCTTATATGACCAACAGCCGTGGC	24600
Db	2465	GAGGCACACAGTGGGCTCTTGAGAGTCTTCTTAGAGCTTATATGACCAACAGCCGTGGC	25240
QY	2461	ATCAGGGGCGAAGTCTTACGTCCAGTGCAGGGGATCCCGCAGGGCTCATCTCTCCACG	25200
Db	2525	ATCAGGGGCGAAGTCTTACGTCCAGTGCAGGGGATCCCGCAGGGCTCATCTCTCCACG	25840
QY	2521	CTGCTCTCAGACCTGTGTGTCAGGGACATGAGAAACAAGCTGTTGGGGGATTCGGCCGG	25800
Db	2585	CTGCTCTCAGACCTGTGTGTCAGGGACATGAGAAACAAGCTGTTGGGGGATTCGGCCGG	26440
QY	2581	GACGGGACCTGCTCCCTGCTTGGTGGATGATTTCTTGTGGTACACTCACCTCACCCAC	26400
Db	2645	GACGGGACCTGCTCCCTGCTTGGTGGATGATTTCTTGTGGTACACTCACCTCACCCAC	27040
QY	2641	GCGAAAACCTTCTCAGGACCCCTGATCCAGAGTGTCCCTGAGTATGCTGTGCTGTGAAC	27000
Db	2705	GCGAAAACCTTCTCAGGACCCCTGATCCAGAGTGTCCCTGAGTATGCTGTGCTGTGAAC	27640
QY	2701	TTGGGGAAGACAGATGTGTGAATTTCCCTGTGAGAGACAGAGCCCTGGGTGGACGGCTTTT	27600
Db	2765	TTGGGGAAGACAGATGTGTGAATTTCCCTGTGAGAGACAGAGCCCTGGGTGGACGGCTTTT	28240
QY	2761	GTTCAGATGCGGCGCCACGGGCTATTCCCTGTGAGCGGCTGTGCTGTGAATACCGGAC	28200
Db	2825	GTTCAGATGCGGCGCCACGGGCTATTCCCTGTGAGCGGCTGTGCTGTGAATACCGGAC	28840
QY	2821	CTGAGAGGTGACAGACGACTACTCCAGCTATGCCCCGACCTTCATCAGAGCCAGTCTAAC	28800
Db	2885	CTGAGAGGTGACAGACGACTACTCCAGCTATGCCCCGACCTTCATCAGAGCCAGTCTAAC	29440
QY	2881	TTCAACGCGGCTTCAAGGCTGGAGGACATGCTGTGCACAACTCTTGGGGGTCTTGGCG	29400
Db	2945	TTCAACGCGGCTTCAAGGCTGGAGGACATGCTGTGCACAACTCTTGGGGGTCTTGGCG	30040
QY	2941	CTGAAAGTGCACAGCCTGTTTCTGGATTTTGGAGGTGAACAGCCTTCCAGAGGTGTGCAC	30000
Db	3005	CTGAAAGTGCACAGCCTGTTTCTGGATTTTGGAGGTGAACAGCCTTCCAGAGGTGTGCAC	30640
QY	3001	AACATCTACAAGATCTCTCTGCTGACAGGCTTACAGGTTTACGCATGTGTGCTGACGCTC	30600
Db	3065	AACATCTACAAGATCTCTCTGCTGACAGGCTTACAGGTTTACGCATGTGTGCTGACGCTC	31240
QY	3061	CCATTTATCAGCAAGTTTGGAAAGAACCCACATTTTCTGTGGCGTCACTCTGACACG	31200
Db	3125	CCATTTATCAGCAAGTTTGGAAAGAACCCACATTTTCTGTGGCGTCACTCTGACACG	31840
QY	3121	GCTCCCTCTGTACTTCATCTGTAAGCCAAAGACAGAGGATGTGCTGGGGGCCAAG	31800
Db	3185	GCTCCCTCTGTACTTCATCTGTAAGCCAAAGACAGAGGATGTGCTGGGGGCCAAG	32440
QY	3181	GGCGCGCGCGCCCTCTGCGCCTCCAGAGCCGCTGACATGGCTGTGGCCACAAAGATTCCTG	32400
Db	3245	GGCGCGCGCGCCCTCTGCGCCTCCAGAGCCGCTGACATGGCTGTGGCCACAAAGATTCCTG	33040
QY	3241	CTCAAGCTGACTGCACACGCTGTCACTTACGTGCACTCTCTGGAGTCACTCAGACAGCC	33000
Db	3305	CTCAAGCTGACTGCACACGCTGTCACTTACGTGCACTCTCTGGAGTCACTCAGACAGCC	33640
QY	3301	CAGACGAGCTGAGTGGGAAAGCTCCCGGGGACGACGCTACATGCGCTCTGAGCGCGAGCC	33600
Db	3365	CAGACGAGCTGAGTGGGAAAGCTCCCGGGGACGACGCTACATGCGCTCTGAGCGCGAGCC	34240
QY	3361	AACCGGCACTGCGCTTCAACTTCAAGACCACTTGAAGTATGGCCACCC	3411

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Page 32

Db 3425 AACCGGCACTGCCCTCAGACTTCAGACATCCTGAGACTGATGCGCACCC 3475

Search completed: February 29, 2004, 21:00:14
Job time : 813.167 secs

QY 901 GGCCTGACGACCAAGCGGAGCCCGCATCAATGCGGCGGACCAAGCTCCCTGGGACAG 960
DB 901 GGCCTGACGACCAAGCGGAGCCCGCATCAATGCGGCGGACCAAGCTCCCTGGGACAG 960
QY 961 CTTTGTCCCGGAGTGTAGCGGAGCAAGCACTTCTCTCACTCTCAAGGAGCAAGAG 1020
DB 961 CTTTGTCCCGGAGTGTAGCGGAGCAAGCACTTCTCTCACTCTCAAGGAGCAAGAG 1020
QY 1021 CAGCTGCGGAGCCCTCTCTCTCACTCTCTCAAGGAGCCAGCTGAGCTGAGCTGAGG 1080
DB 1021 CAGCTGCGGAGCCCTCTCTCTCACTCTCTCAAGGAGCCAGCTGAGCTGAGCTGAGG 1080
QY 1081 CTCTGTGAGAGCAATCTTCTGTGGGTTCCAGGAGCCCTGAGTGCAGGAGACTCCCGGAGGTTG 1140
DB 1081 CTCTGTGAGAGCAATCTTCTGTGGGTTCCAGGAGCCCTGAGTGCAGGAGACTCCCGGAGGTTG 1140
QY 1141 CCCCCTGCCCCAGCGCTACTGTGCAATGCGGAGCCCTGTTTCTGAGCTGCTTGGAGAC 1200
DB 1141 CCCCCTGCCCCAGCGCTACTGTGCAATGCGGAGCCCTGTTTCTGAGCTGCTTGGAGAC 1200
QY 1201 CAGCGGAGCTGCCCCCTTAAGGAGGCTCTCTCAAGAGCACTGCGGCTGCGAGCTGCGGTC 1260
DB 1201 CAGCGGAGCTGCCCCCTTAAGGAGGCTCTCTCAAGAGCACTGCGGCTGCGAGCTGCGGTC 1260
QY 1261 ACCCGAGAGCGGAGTCTGTGCGCGGAGAGAGCCCGAGGAGCTGTGTGGGAGCCCGGAG 1320
DB 1261 ACCCGAGAGCGGAGTCTGTGCGCGGAGAGAGCCCGAGGAGCTGTGTGGGAGCCCGGAG 1320
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DB 1321 GAGGAGAGCAAGACCCCTGCTGCTGTGAGCACTGCTGCGGAGCAAGCAAGCCCTG 1380
QY 1381 CAGGAGTACGAGCTTGTGTGGGAGCCGCTGCGGAGGAGCTGTGTGGGAGCCCGGAG 1440
DB 1381 CAGGAGTACGAGCTTGTGTGGGAGCCGCTGCGGAGGAGCTGTGTGGGAGCCCGGAG 1440
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DB 1441 TCCAGGAGCAAGACCGGCTTCTCTCAAGAGCAAGCAAGGTTCTCTCTGAGGAG 1500
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DB 1501 CAGCGGAGCTCTGCTGAGAGAGCTGAGTGAATGAGAGCTGAGGAGCTGAGCTG 1560
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DB 1561 CTGCGAGAGAGCCAGGAGTGTGCTGTGTTCCGCGCAGAGAGCACTGCTGAGTGAAG 1620
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DB 1621 ATCTGTGAGAGTCTCTGAGCTGAGTGAATGAGTGTGCTGTGAGCTGCTGAGTGT 1680
QY 1681 TTCTTTTATGTCAAGAGAGCAAGCTTTCAAAAGAGAGCTTTTCTTCAAGAGAGT 1740
DB 1681 TTCTTTTATGTCAAGAGAGCAAGCTTTCAAAAGAGAGCTTTTCTTCAAGAGAGT 1740
QY 1741 GTCTGAGAGCAAGTGTGCAAGAGTGTGAGTGAATGAGAGCACTTTGAAGAGGAGTGG 1800
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QY 1801 GAGCTGTGAGAGCAAGTGTGAGAGCACTGAGGAGAGCCAGGAGCCGCTGAGTGAAGTGC 1860
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QY 1861 AGACTTCCGCTTCACTCCCAAGCTGAGAGGAGTGTGAGTGAATGAGAGCACTGAGTGAAG 1920
DB 1861 AGACTTCCGCTTCACTCCCAAGCTGAGAGGAGTGTGAGTGAATGAGAGCACTGAGTGAAG 1920
QY 1921 GTGAGAGCAAGAGCTTCCGAGAGAGAGAGGAGGAGTGTGAGTGAATGAGAGCACTGAGTGAAG 1980
DB 1921 GTGAGAGCAAGAGCTTCCGAGAGAGAGAGGAGGAGTGTGAGTGAATGAGAGCACTGAGTGAAG 1980

QY 1981 GCACTGTTCAGGAGTGTCTCACTTACAGAGCGGAGCGGAGCCCGGAGCTCTCTGAGGAGCTCT 2040
DB 1981 GCACTGTTCAGGAGTGTCTCACTTACAGAGCGGAGCGGAGCCCGGAGCTCTCTGAGGAGCTCT 2040
QY 2041 GTGCTGAGGAGTGTGAGAGTGTTCACAGAGGAGCTGAGGAGCACTTGTGTGTGTGTGTGTGTGT 2100
DB 2041 GTGCTGAGGAGTGTGAGAGTGTTCACAGAGGAGCTGAGGAGCACTTGTGTGTGTGTGTGTGTGT 2100
QY 2101 CAGGAGCCGAGGAGTGTGAGT 2160
DB 2101 CAGGAGCCGAGGAGTGTGAGT 2160
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DB 2281 AAGAGCAAGT 2340
QY 2341 CTGAGAGAGAGAGAGGAGGAGT 2400
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QY 2401 GAGGAGAGAGAGAGGAGGAGT 2460
DB 2401 GAGGAGAGAGAGAGGAGGAGT 2460
QY 2461 ATCAGAGAGAGAGT 2520
DB 2461 ATCAGAGAGAGAGT 2520
QY 2521 CTGCTGTGAGAGT 2580
DB 2521 CTGCTGTGAGAGT 2580
QY 2581 GAGGAGAGAGT 2640
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QY 2641 GCGAGAGAGT 2700
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QY 2701 TTGCGAGAGAGAGT 2760
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QY 2761 GTTCAAGAGAGAGT 2820
DB 2761 GTTCAAGAGAGAGT 2820
QY 2821 CTGAGAGAGAGAGT 2880
DB 2821 CTGAGAGAGAGAGT 2880
QY 2881 TTCAAGAGAGAGAGT 2940
DB 2881 TTCAAGAGAGAGAGT 2940
QY 2941 CTGAGAGAGAGAGT 3000
DB 2941 CTGAGAGAGAGAGT 3000
QY 3001 AAGATCTAAGAGAGT 3060
DB 3001 AAGATCTAAGAGAGT 3060
QY 3061 CCAATTCATGAGAGAGT 3120

Db 3061 CCATTTCATGACGAGATTGGAGAGACCCCAATTTTCTCGCGCTCATCTTGACAG 3120
Qy 3121 GCTTCCTCTGCTACTCATCTCTGAAAGCCAGAGACGAGATGTGCTGGGGGCAAG 3180
Db 3121 GCTTCCTCTGCTACTCATCTCTGAAAGCCAGAGACGAGATGTGCTGGGGGCAAG 3180
Qy 3181 GGGCCGCGCGGCTCTGCGCTCGAGCGCTGAGTGGCTGAGCCACCAAGATTCG 3240
Db 3181 GGGCCGCGCGGCTCTGCGCTCGAGCGCTGAGTGGCTGAGCCACCAAGATTCG 3240
Qy 3241 CTCAAGTGAAGTCAAGACCGGTGTCACCTACGTGCACTCTGAGGTCACAGAGCAGCC 3300
Db 3241 CTCAAGTGAAGTCAAGACCGGTGTCACCTACGTGCACTCTGAGGTCACAGAGCAGCC 3300
Qy 3301 CAGACGAGCTGAGTGGAGAGCTCCGGGGAGAGAGCTGAGCTGCGCTGAGAGCGCGAGCC 3360
Db 3301 CAGACGAGCTGAGTGGAGAGCTCCGGGGAGAGAGCTGAGCTGCGCTGAGAGCGCGAGCC 3360
Qy 3361 AACCCGCACTGCGCTCAGACTTCAGAGACCATCTGAGTGAATGACACCC 3411
Db 3361 AACCCGCACTGCGCTCAGACTTCAGAGACCATCTGAGTGAATGACACCC 3411

RESULT 2

US-08-951-733-19
Sequence 19, Application US/08951733

GENERAL INFORMATION:

APPLICANT: Harrington, Lea A.

APPLICANT: Robinson, Murray O.

TITLE OF INVENTION: NOVEL GENES ENCODING TELOMERASE PROTEINS

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: One Amgen Center Drive

CITY: Thousand Oaks

STATE: CA

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/951,733

FILING DATE: 16-OCT-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/873,039

FILING DATE: 11-JUN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/751,189

FILING DATE: 15-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Oleski, Nancy A.

REGISTRATION NUMBER: 34,688

REFERENCE/DOCKET NUMBER: A-433B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (805) 447-6504

TELEFAX: (805) 499-8011

INFORMATION FOR SEQ. ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 3798 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-951-733-19

Query Match 100.0%; Score 3411; DB 13; Length 3798;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGATGCGGCGGCTCCCGCTGCGGAGCCGCTGCGCTCCCTGCTGCGGAGCTACACGC 60
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Qy 61 GAGGTGCTGCGGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCG 120
Db 125 GAGGTGCTGCGGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCG 184
Qy 121 CAGCGGAGGAGCCCGGCGCTTTTCCGCGCGCTGCTGCGGAGCTGCTGCTGCTGAGAG 180
Db 185 CAGCGGAGGAGCCCGGCGCTTTTCCGCGCGCTGCTGCGGAGCTGCTGCTGCTGAGAG 244
Qy 181 TGGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 245 TGGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 304
Qy 241 CTGTGTGCGGCGGAGTGTGCGAGAGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGG 300
Db 305 CTGTGTGCGGCGGAGTGTGCGAGAGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGG 364
Qy 301 GGTTCGCGCTGCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db 365 GGTTCGCGCTGCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 424
Qy 361 CGCAGCTACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 425 CGCAGCTACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 484
Qy 421 CTGCTGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
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Qy 481 GTGCTGTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
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Db 605 GCTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 664
Qy 601 GAAAGGCGCTGGAACCACTAGCGTCAAGGAGCGGCGGCGGCGGCGGCGGCGG 660
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Qy 661 GTGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 725 GTGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 784
Qy 721 CGTGTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 785 CGTGTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 844
Qy 781 GGCAGAGCGGCTGGAACCACTAGCGTCAAGGAGCGGCGGCGGCGGCGGCGG 840
Db 845 GGCAGAGCGGCTGGAACCACTAGCGTCAAGGAGCGGCGGCGGCGGCGGCGG 904
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Db 905 GAAAGGCGGCTGGAACCACTAGCGTCAAGGAGCGGCGGCGGCGGCGGCGG 964
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Qy 961 CTTGTGCGGCTGGAACCACTAGCGTCAAGGAGCGGCGGCGGCGGCGGCGG 1020
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Qy 1021 CAGCTGCGGCGGCTGCTTCTTACTAGCTGCTGAGGCGGCGGCGGCGGCGG 1080
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1081 CTCTGAGACCATCTTTCTGGGTTCCAGGCTCGATGCGAGGACTCCCGAGGTTG 1140
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1141 CCGGCGCTGCGCGAGGCTACTGCGAATGCGGCGCTGTTCTGAGCTGCTTGGAAAC 1200
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1201 CAGCGGAGTGCCTTACGCGGCTGCTCTGAGAGGAGTCCCGCTGCGAGTGCCTG 1260
Db CAGCGGAGTGCCTTACGCGGCTGCTCTGAGAGGAGTCCCGCTGCGAGTGCCTG 1324
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1321 GAGAGGAGCAGAGACCCCGCTGCTGCTGAGCTGCTGCGAGCAGCAGACCCCTG 1380
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1381 CAGGTGTAACGCTTCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
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1501 CATGCGAGCTCTGCTGCGAGAGCTGAGCTGAGAGTGAAGCTGCGGAGCTGCTG 1560
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1741 GTCTGAGCAAGTGTGCAAGATGAGATGAGCAGCAGCTTGAAGAGGCTGAGCTG 1800
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2221 TGCCTGCTGCTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Db TGCCTGCTGCTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2344
2281 AAGAGCAGAGCTTACCTTGAAGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAG 2340
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2341 CTGAGAGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2400
Db CTGAGAGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2464
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Db GAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2524
2461 ATCAGGAGCAGAGCTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
Db ATCAGGAGCAGAGCTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2584
2521 CTGCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Db CTGCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2644
2581 GACGAGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Db GACGAGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2704
2641 GCGAGAGCTTCTGAGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
Db GCGAGAGCTTCTGAGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2764
2701 TTGCGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760
Db TTGCGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2824
2761 GTTCAAGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820
Db GTTCAAGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2884
2821 CTGAGAGGAGCAGAGCTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2880
Db CTGAGAGGAGCAGAGCTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2944
2881 TTCAACGAGGCTTCAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2940
Db TTCAACGAGGCTTCAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3004
2941 CTGAAGTGTCAAGCTGCTTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAG 3000
Db CTGAAGTGTCAAGCTGCTTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAG 3064
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Db AACATCTAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3124
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3181 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240
Db GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3304
3241 CTGAAGCTGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3300

Db 3305 CTCAAGCTGACTGACACCGGTGTCACCTAGTGCACCTCTGGGGTTCATCTAGAGACAGCC 3364
Qy 3301 CAGACGCACTGAGTGGAGAGCTCCCGGGGACGACGCTGACTGCTGAGGCGCCGACGC 3360
Db 3365 CAGACGCACTGAGTGGAGAGCTCCCGGGGACGACGCTGACTGCTGAGGCGCCGACGC 3424
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RESULT 3
PCT-US01-15774-3
Sequence 3, Application PC/TUS0115774
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Brett P. Monia
APPLICANT: William Gaarde
APPLICANT: Susan M. Freiler
APPLICANT: Edward V. Manciewicz
TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
FILE REFERENCE: ISPH-0568
CURRENT APPLICATION NUMBER: PCT/US01/15774
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/572,423
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 3
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56) ... (3454)
PCT-US01-15774-3

Query Match 100.0%; Score 3411; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGATGCGCGGCTCCCGCTGCGGACCGTGCCTCTGTCGACGACCTACCGC 60
Db 53 GCGATGCGCGGCTCCCGCTGCGGACCGTGCCTCTGTCGACGACCTACCGC 112
Qy 61 GAGGTGCTGCGCTGCGGACGCTGTCGCGGCGCTGCGGCGCCAGAGGCTGCGGCTG 120
Db 113 GAGGTGCTGCGCTGCGGACGCTGTCGCGGCGCTGCGGCGCCAGAGGCTGCGGCTG 172
Qy 121 CAGGCGGAGGACCGCGGCTTTCGCGGCGCTGAGGCGCCAGTGTGTCGTCGCC 180
Db 173 CAGGCGGAGGACCGCGGCTTTCGCGGCGCTGAGGCGCCAGTGTGTCGTCGCC 232
Qy 181 TGGAGGACGAGCG 240
Db 233 TGGAGGACGAGCG 292
Qy 241 CTGATGCGCGGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 300
Db 293 CTGATGCGCGGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 352
Qy 301 GGGTTCGCGGCTGCGAGCGGGGCGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 353 GGGTTCGCGGCTGCGAGCGGGGCGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCG 412
Qy 361 CGCAGCTACTGCGCAACAGAGTACGACGCACTGCGGAGGAGCGGCGGCTGCGGCTG 420
Db 413 CGCAGCTACTGCGCAACAGAGTACGACGCACTGCGGAGGAGCGGCGGCTGCGGCTG 472
Qy 421 CTGATGCGCGGAGTGTGCGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 473 CTGATGCGCGGAGTGTGCGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 532
Qy 481 GTGCTGATGCTCCAGCTGCGCTTACAGGTGTGCGGCGCGCGCTGTACAGAGTCCG 540

Db 533 GTGCTGATGCTCCAGCTGCGCTTACAGGTGTGCGGCGCGCGCTGTACAGCTCGGC 592
Qy 541 GCTGCACTCAGGCG 600
Db 593 GCTGCACTCAGGCG 652
Qy 601 GAAAGGCGCTGGAACCATAGGTGACAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 653 GAAAGGCGCTGGAACCATAGGTGACAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 712
Qy 661 GATGCGAGAGGCG 720
Db 713 GATGCGAGAGGCG 772
Qy 721 CTGATGCGCTGCGCTTGAAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 773 CTGATGCGCTGCGCTTGAAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 832
Qy 781 GCGAGAGCGCTGAGACCGAGTGAACCTGTGTTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 833 GCGAGAGCGCTGAGACCGAGTGAACCTGTGTTGTGTGTGTGTGTGTGTGTGTGTGT 892
Qy 841 GAAAGAGCACCTCTTTGAGAGGCTGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 893 GAAAGAGCACCTCTTTGAGAGGCTGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCG 952
Qy 901 GCGCGCGAGCACGAGCG 960
Db 953 GCGCGCGAGCACGAGCG 1012
Qy 961 CTTGTGCTCCCGGAGTACGCGGAGACCAAGCACTTCTTACTCTTCACTCTGAGGAG 1020
Db 1013 CTTGTGCTCCCGGAGTACGCGGAGACCAAGCACTTCTTACTCTTCACTCTGAGGAG 1072
Qy 1021 CAGGCGGAGGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1080
Db 1073 CAGGCGGAGGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1132
Qy 1081 CTGTGAGAGACCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1140
Db 1133 CTGTGAGAGACCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1192
Qy 1141 CCG 1200
Db 1193 CCG 1252
Qy 1201 CAGCGAGTGCCTCCCTTACGAGGCTCTCTTCAAGAGCGACCTGCGCGAGCTCGGTC 1260
Db 1253 CAGCGAGTGCCTCCCTTACGAGGCTCTCTTCAAGAGCGACCTGCGCGAGCTCGGTC 1312
Qy 1261 ACCCGAGAGCGCGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
Db 1313 ACCCGAGAGCGCGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1372
Qy 1321 GAGAGGAGCACAGACCCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db 1373 GAGAGGAGCACAGACCCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1432
Qy 1381 CAGGTGTACCGCTTCTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1440
Db 1433 CAGGTGTACCGCTTCTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1492
Qy 1441 TCCAGGAGCAACGAGCGCTTCTTCAAGAAACCAAGAGTTCATCTCTGCGGAG 1500
Db 1493 TCCAGGAGCAACGAGCGCTTCTTCAAGAAACCAAGAGTTCATCTCTGCGGAG 1552
Qy 1501 CATGCCAAGCTCTGCTGCGAGGAGCTGACGTTGAAATGAGCGTGGCGGAGCTGCGCT 1560
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 Db 1913 AGACTCCGCTTCAATCCCAAGCTGACGAGGCTGCGGCGAATTGTGAACATGACATGCTC 1972
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 Db 2333 AAGAGCAAGTCTTCACTTGAAGACCTTCAAGCGGCTTCAAGAGAGTGTGCTGAC 2392
 QY 2341 CTGAGAGAGACAGAGCGGCTGAGAGGATGCGGTGATGAGAGAGGCTTCCCTGAT 2400
 Db 2393 CTGAGAGAGACAGAGCGGCTGAGAGGATGCGGTGATGAGAGAGGCTTCCCTGAT 2452
 QY 2401 GAGGCGAGAGGCTTCTTCAAGAGTGTCTTCAAGCTTCAAGTGTGACAGCGGCTGCG 2460
 Db 2453 GAGGCGAGAGGCTTCTTCAAGAGTGTCTTCAAGCTTCAAGTGTGACAGCGGCTGCG 2512
 QY 2461 ATAGAGGAGCAAGTCTTCAAGTGTGAGGAGATGCGGAGGATGCGGAGGCTTCTTCAAG 2520
 Db 2513 ATAGAGGAGCAAGTCTTCAAGTGTGAGGAGATGCGGAGGAGTCTTCTTCAAG 2572
 QY 2521 CTGCTGAGAGCTTGTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGAT 2580
 Db 2573 CTGCTGAGAGCTTGTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGAT 2632
 QY 2581 GAGGAGGCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGAT 2640
 Db 2633 GAGGAGGCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGAT 2692
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 Db 2693 GCGAAACCTTCTCAAGAGACCTGATCGAGAGTGTGCTGAGATGCTGCTGAGTGAAC 2752

QY 2701 TTGCGAAGACAGTGTGAACTTCCCTGTAGAAAGACAGAGCCCTGGGTGACAGGCTTTT 2760
 Db 2753 TTGCGAAGACAGTGTGAACTTCCCTGTAGAAAGACAGAGCCCTGGGTGACAGGCTTTT 2812
 QY 2761 GTTCAAGTCCGCGCCCAAGGCTTATCCCTGTGTGAGGCTGTGCTGTGATACCGGAGC 2820
 Db 2813 GTTCAAGTCCGCGCCCAAGGCTTATCCCTGTGTGAGGCTGTGCTGTGATACCGGAGC 2872
 QY 2821 CTGAGAGTGCAGAGGCACTACTCCAGTATGCGCGGAGCTTCCATCAGAGCAGTCTCAC 2880
 Db 2873 CTGAGAGTGCAGAGGCACTACTCCAGTATGCGCGGAGCTTCCATCAGAGCAGTCTCAC 2932
 QY 2881 TTCAACCGGCGCTTCAAGGCTGAGAGAAATGCGTCCGAACTTTTGGGGTCTTTCGCG 2940
 Db 2933 TTCAACCGGCGCTTCAAGGCTGAGAGAAATGCGTCCGAACTTTTGGGGTCTTTCGCG 2992
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 Db 2993 CTGAAGTGCAGAGGCTTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3052
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 Db 3053 AACATCTACAGATCTCTCTGCTGAGGCGTACAGGTTTCAAGCATGTGTCTGAGCTC 3112
 QY 3061 CAATTTCATCAGCAAGTTTGAAGAAACCCCAATTTTCTGCGGCGTATCTGACAGC 3120
 Db 3113 CAATTTCATCAGCAAGTTTGAAGAAACCCCAATTTTCTGCGGCGTATCTGACAGC 3172
 QY 3121 GCTTCTCTGCTACTCTCATCTTGAAGCAAGAACCAAGAGGATGTGCTGAGGCGCAAG 3180
 Db 3173 GCTTCTCTGCTACTCTCATCTTGAAGCAAGAACCAAGAGGATGTGCTGAGGCGCAAG 3232
 QY 3181 GAGCGCGCGCGGCGCTCTGCGGCTTCCGAGGCGGCTGAGTGTGCTGACAGCACTTCTG 3240
 Db 3233 GAGCGCGCGCGGCGCTCTGCGGCTTCCGAGGCGGCTGAGTGTGCTGACAGCACTTCTG 3292
 QY 3241 CTCAAGTGTGACAGCAGGCTGACCTTCAAGTGTGACCTTCTGAGGAGTCACTGAGAGCAGCC 3300
 Db 3293 CTCAAGTGTGACAGCAGGCTGACCTTCAAGTGTGACCTTCTGAGGAGTCACTGAGAGCAGCC 3352
 QY 3301 CAGAGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3360
 Db 3353 CAGAGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3412
 QY 3361 AACCGGCACTGCGCTGAGCTTCAAGACATCTCTGAGCTGATGAGCAGCC 3411
 Db 3413 AACCGGCACTGCGCTGAGCTTCAAGACATCTCTGAGCTGATGAGCAGCC 3463

RESULT 4
 PCT-US02-10421-817
 ; Sequence 817, Application PC/TUS0210421
 ; GENERAL INFORMATION:
 ; APPLICANT: Corixa Corporation
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Wang, Siding
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Gaiger, Alexander
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.565PC
 ; CURRENT APPLICATION NUMBER: PCT/US02/10421
 ; CURRENT FILING DATE: 2002-03-26
 ; NUMBER OF SEQ ID NOS: 2959
 ; SEQ ID NO 817
 ; LENGTH: 4015
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; PCT-US02-10421-817

Query Match 100.0%; Score 3411; DB 1; Length 4015;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGCTGCGCGAGCGCGCTCCCTGCTGCGAGCCACTACCGC 60
Db 53 GCGATGCGCGCGCTCCCGCTGCGCGAGCGCGCTCCCTGCTGCGAGCCACTACCGC 112
QY 61 GAGGTGCTGCGCTGCGCGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 120
Db 113 GAGGTGCTGCGCTGCGCGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 172
QY 121 CAGGCGCGGAGCGCGCGCTTCCGCGCGCTGCGCGCGCGCTGCGCGCGCTGCGCG 180
Db 173 CAGGCGCGGAGCGCGCGCTTCCGCGCGCTGCGCGCGCGCTGCGCGCGCTGCGCG 232
QY 181 TGGAGCGAGCG 240
Db 233 TGGAGCGAGCG 292
QY 241 CTGGTGGCGCGAGCGCGAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 293 CTGGTGGCGCGAGCGCGAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GCGTTGCGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 353 GCGTTGCGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGGAGCTACTGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAG 420
Db 413 CGGAGCTACTGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAG 472
QY 421 CTGCTGCGCGCGCTGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAG 480
Db 473 CTGCTGCGCGCGCTGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAG 532
QY 481 GTGCTGCTGCTGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCG 540
Db 533 GTGCTGCTGCTGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCG 592
QY 541 GCTGCGACTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db 593 GCTGCGACTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 652
QY 601 GAAAGCGCGCTGGAACATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCG 660
Db 653 GAAAGCGCGCTGGAACATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GGTGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db 713 GGTGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 772
QY 721 CGTGCGCTGCGCGCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
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QY 781 GCGAGGAGCGGTGGAACGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 833 GCGAGGAGCGGTGGAACGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 892
QY 841 GAAAGAGCACTCTTTGAGAGGTGCGCTCTGCGAGCGCGCGCGCGCGCGCG 900
Db 893 GAAAGAGCACTCTTTGAGAGGTGCGCTCTGCGAGCGCGCGCGCGCGCGCG 952
QY 901 GCGCGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Db 953 GCGCGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1012
QY 961 CTTTGTCCCGGTGAGCGCGAGCAAGCACTTCTCTACTCTCTAGCGAGCAAGAG 1020
Db 1013 CTTTGTCCCGGTGAGCGCGAGCAAGCACTTCTCTACTCTCTAGCGAGCAAGAG 1072
QY 1021 CAGCTGCGCGCGCTCTCTCTACTCTCTAGCGCGCGAGCGCGCGCGCGCGCG 1080
Db 1073 CAGCTGCGCGCGCTCTCTCTACTCTCTAGCGCGCGAGCGCGCGCGCGCGCG 1132

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Db 1193 CCGCGCTGCGCGCGCTACTAGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCG 1252
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Db 1253 CAGCGCGAGTGCCTTACGCGGTGCTCTCAAGAGCACTGCGCGCGCGCGCGCG 1312
QY 1261 ACCCGAGCGCGGTGCTGCTGCGCGCGAGAAACCCCGAGGCTCTGCGCGCGCGCGAG 1320
Db 1313 ACCCGAGCGCGGTGCTGCTGCGCGCGAGAAACCCCGAGGCTCTGCGCGCGCGCGAG 1372
QY 1321 GAGAGGAGCAAGACCCCGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 1373 GAGAGGAGCAAGACCCCGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1432
QY 1381 CAGGTGACGAGCTTCTGCGCGAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 1440
Db 1433 CAGGTGACGAGCTTCTGCGCGAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 1492
QY 1441 TCCAGGCAACAGAACCGCGCTTCTCAGGAAACAGAGAGTTCACTCTCTGCGAGAG 1500
Db 1493 TCCAGGCAACAGAACCGCGCTTCTCAGGAAACAGAGAGTTCACTCTCTGCGAGAG 1552
QY 1501 CATGCGAGCTCTGCGCTGCGAGAGCTGAGCGTGAAGTGAAGTGAAGTGAAGTGA 1560
Db 1553 CATGCGAGCTCTGCGCTGCGAGAGCTGAGCGTGAAGTGAAGTGAAGTGAAGTGA 1612
QY 1561 CTGCGCGAGAGCGCGAGGCTTGTGCTTCCGCGCGCGAGAGCACTGCTGCTGAGAG 1620
Db 1613 CTGCGCGAGAGCGCGAGGCTTGTGCTTCCGCGCGCGAGAGCACTGCTGCTGAGAG 1672
QY 1621 ATCTGCGCAAGTTCTCTGCACTGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1680
Db 1673 ATCTGCGCAAGTTCTCTGCACTGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1732
QY 1681 TTCTTTTATGTACGAGAGCAACGTTTCAAAAAGAGGCTCTTTTCTTACCGAGAGT 1740
Db 1733 TTCTTTTATGTACGAGAGCAACGTTTCAAAAAGAGGCTCTTTTCTTACCGAGAGT 1792
QY 1741 GTCTGAGCAAGTTGCAAAAGCTTGAATCAGACAGCACTTGAAGAGGCTGAGCGCG 1800
Db 1793 GTCTGAGCAAGTTGCAAAAGCTTGAATCAGACAGCACTTGAAGAGGCTGAGCGCG 1852
QY 1801 GAGCTGCGAGAGCAAGGTCAGGAGCAATCGGAGAGCGAGGCGCGCTGCTGAGCGTCC 1860
Db 1853 GAGCTGCGAGAGCAAGGTCAGGAGCAATCGGAGAGCGAGGCGCGCTGCTGAGCGTCC 1912
QY 1861 AGACTCGCTTATCTCCCAAGGCTGAGCGGCTGCGCGCGCAATGTGAACATGAGCTAGTC 1920
Db 1913 AGACTCGCTTATCTCCCAAGGCTGAGCGGCTGCGCGCGCAATGTGAACATGAGCTAGTC 1972
QY 1921 GTGAGAGCAAGAGCTTCCGAGAGAAAGAGGCGCGAGCTCTCACTCGAGAGGTGAAG 1980
Db 1973 GTGAGAGCAAGAGCTTCCGAGAGAAAGAGGCGCGAGCTCTCACTCGAGAGGTGAAG 2032
QY 1981 GCACTGTTACGCGGTGCTCAATCAGAGCGCGCGCGCGCGCGCGCGCGCGCG 2040
Db 2033 GCACTGTTACGCGGTGCTCAATCAGAGCGCGCGCGCGCGCGCGCGCGCGCG 2092
QY 2041 GTGCTGCGCTGAGAGATATCCAAGAGGCTGCGCGAGCACTTCTGCTGCTGCTGCGCGCG 2100
Db 2093 GTGCTGCGCTGAGAGATATCCAAGAGGCTGCGCGAGCACTTCTGCTGCTGCTGCGCGCG 2152
QY 2101 CAGGACCGCGCGCTGAGCTGATCTTTGTCAAGAGTGAAGTGAAGCGGCGCGCTGAGCAAC 2160
Db 2153 CAGGACCGCGCGCTGAGCTGATCTTTGTCAAGAGTGAAGTGAAGCGGCGCGCTGAGCAAC 2212

QY	461	GGTGGCTGGTGGCTCCCAAGCTGGCCCTTACCAAGAGTGTGTGGGCGCCGCTGTATCAAGCTCGG	540
Db	553	GGTCTGGTGGCTCCCAAGCTGGCCCTTACCAAGAGTGTGTGGGCGCCGCTGTATCAAGCTCGG	592
QY	541	GCTGCACTCAGGCGCCGCGCCCGCACACAGCTAGTGAACCCCGAAGAGCTGTGGATGC	600
Db	553	GCTGCACTCAGGCGCCGCGCCCGCACACAGCTAGTGAACCCCGAAGAGTGTGGATGC	652
QY	601	GAAAGAGGCTGGAACCATAGCGTCAAGGAGAGCGCGGGGTCTCCCTGAGGCTGTGCAACCCG	660
Db	653	GAAAGAGGCTGGAACCATAGCGTCAAGGAGAGCGCGGGGTCTCCCTGAGGCTGTGCAACCCG	712
QY	661	GCTGCAAGAGGCGCGGGGAGAGTGCACAGCCGAACTTGTCCGTTGCCCAAGAGCCCAAG	720
Db	713	GCTGCAAGAGGCGCGGGGAGAGTGCACAGCCGAACTTGTCCGTTGCCCAAGAGCCCAAG	772
QY	721	CGTGGCGCTGGCCCTTGAAGCGGAGAGGAGACGCCGTGTGGGCAAGGGTCTCGGGCCCAACCG	780
Db	773	CGTGGCGCTGGCCCTTGAAGCGGAGAGGAGACGCCGTGTGGGCAAGGGTCTCGGGCCCAACCG	832
QY	781	GCGAGAGCGCTGGAACCGAGTGAACCGTGTCTGTGTGTGTCACTTCCAGAACCCCG	840
Db	833	GCGAGAGCGCTGGAACCGAGTGAACCGTGTGTCTGTGTGTGTCACTTCCAGAACCCCG	892
QY	841	GAAGAAGCACTCTTTGGAGGGTGGGCTGTGGCAGCGGCACTTCCACCACTCCGATG	900
Db	893	GAAGAAGCACTCTTTGGAGGGTGGGCTGTGGCAGCGGCACTTCCACCACTCCGATG	952
QY	901	GCGCGCCAGCACACAGCGGCGGCCCTTCATCACAATGCGGAGCCACCAAGTCTCTGGAGACG	960
Db	953	GCGCGCCAGCACACAGCGGCGGCCCTTCATCACAATGCGGAGCCACCAAGTCTCTGGAGACG	1012
QY	961	CGTTGTCCCGGGTATGCGCGAGACCAAGCACTCTCTACTCTTCAAGGGAGCAAGAG	1020
Db	1013	CGTTGTCCCGGGTATGCGCGAGACCAAGCACTCTCTACTCTTCAAGGGAGCAAGAG	1072
QY	1021	CAGCTGGGAGCTCTCTTCTTACTGCAAGCTCTGAGAGCCCAAGCTTGAAGCGCTTGAAG	1080
Db	1073	CAGCTGGGAGCTCTCTTCTTACTGCAAGCTCTGAGAGCCCAAGCTTGAAGCGCTTGAAG	1132
QY	1081	CTCGTGAAGACCATTTCTGGGGTTCAGAGCCCTGAGATGCCAGGGACCTCCCGAGAGTG	1140
Db	1133	CTCGTGAAGACCATTTCTGGGGTTCAGAGCCCTGAGATGCCAGGGACCTCCCGAGAGTG	1192
QY	1141	CCCGGCTGGCCCGACAGGCTACTGGCAATGCGGCCCTGTCTTGTGAAGCTGTGGAGAC	1200
Db	1193	CCCGGCTGGCCCGACAGGCTACTGGCAATGCGGCCCTGTCTTGTGAAGCTGTGGAGAC	1252
QY	1201	CACGCGAGTGGCCCTTACGGGGGTGCTCTCAAGAGCACTGCGCGCTGCGAGCTGGCGTG	1260
Db	1253	CACGCGAGTGGCCCTTACGGGGGTGCTCTCAAGAGCACTGCGCGCTGCGAGCTGGCGTG	1312
QY	1261	AACCCAGCAGCCGCTGTCTGTGCCCGAGAAAGCCCAAGGCTGTGTGAGCCCTCCGAG	1320
Db	1313	AACCCAGCAGCCGCTGTGTGCCCGAGAAAGCCCAAGGCTGTGTGAGCCCTCCGAG	1372
QY	1321	GAGAGAGACAGAACCCCGTGCCTGTGTGCAAGCTGCTCCGCGAGCAAGCAGAGCCCTGAG	1380
Db	1373	GAGAGAGACAGAACCCCGTGCCTGTGTGCAAGCTGCTCCGCGAGCAAGCAGAGCCCTGAG	1432
QY	1381	CAGGTGTACGCTTGTGTGGGAGCTGTGCTGCGCGGCTGTGTGCCCAAGGCTTGTGGGC	1440
Db	1433	CAGGTGTACGCTTGTGTGGGAGCTGTGCTGCGCGGCTGTGTGCCCAAGGCTTGTGGGC	1492
QY	1441	TCCAGGACCAAGAACGCGCTTCTTCAAGAAACCAAGAGTTATCTCCCTGGGGAAG	1500
Db	1493	TCCAGGACCAAGAACGCGCTTCTTCAAGAAACCAAGAGTTATCTCCCTGGGGAAG	1552
QY	1501	CATGCGAAGCTTCTCGCTGCAAGAGTGAACGTGGAAGATGAGCGTGTGGGACCTGTGG	1560
Db	1553	CATGCGAAGCTTCTCGCTGCAAGAGTGAACGTGGAAGATGAGCGTGTGGGACCTGTGG	1612


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Qy 2701 TTGGGGAAGACAGTGGTGAACCTCCCTGTAGAGAGAGAGCCCTGGGTGACAGGCTTTT 2760
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Db 3113 CCATTTTCATGAGAAAGTTTGGAAAGAACCCCACTTTTCTGAGGCTCATCTCTGAGCAGC 3172
Qy 3121 GCTCCCTCTGCTACTCTCACTCTGAAAGCCAAAGAGGAGTGTGAGGAGGAGGAGGAGGAG 3180
Db 3173 GCTCCCTCTGCTACTCTCACTCTGAAAGCCAAAGAGGAGTGTGAGGAGGAGGAGGAGGAG 3232
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Db 3233 GGGGCGGCGGCGGCTCTGCTCTGAGGCGGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAG 3292
Qy 3241 CTCAAGCTGACTGAGACAGGCTGTCACTTACGTGAGGCTCTGAGGAGTGTGAGGAGTGTGAG 3300
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Qy 3301 CAGAGCAGCTGAGTGTGAGAAAGTCTCCGAGGAGCAGAGCTGAGTGTGAGGAGCAGGAGC 3360
Db 3353 CAGAGCAGCTGAGTGTGAGAAAGTCTCCGAGGAGCAGAGCTGAGTGTGAGGAGCAGGAGC 3412
Qy 3361 AACCCGAGCAGTGTGAGAAAGTCTCAAGCTTCAAGACATCTGAGTGTGAGGAGCAGGAGC 3411
Db 3413 AACCCGAGCAGTGTGAGAAAGTCTCAAGCTTCAAGACATCTGAGTGTGAGGAGCAGGAGC 3463

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RESULT 6
PCT-US02-31635-1
; Sequence 1, Application PCT/US0231635
; GENERAL INFORMATION:
; APPLICANT: Boston University et al.
; TITLE OF INVENTION: PREADIPOTTE CELL STRAINS AND USES THEREFORE
; FILE REFERENCE: BUI-011PC
; CURRENT APPLICATION NUMBER: PCT/US02/31635
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327650
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/327651
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-31635-1

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Query Match 100.0%; Score 3411; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GAGGTGCTGCGGCTGCGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGG 120
Db 113 GAGGTGCTGCGGCTGCGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGG 172
Qy 121 CAGCGCGGAGACCCGAGCGCTTTTCCGCGCGCTGTGAGCCAGTGTGCTGTGTGAGTGTGAG 180
Db 173 CAGCGCGGAGACCCGAGCGCTTTTCCGCGCGCTGTGAGCCAGTGTGCTGTGTGAGTGTGAG 232
Qy 181 TTGGAGCGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 233 TTGGAGCGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 292
Qy 241 CTGAGTGCAGGAGTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 300
Db 293 CTGAGTGCAGGAGTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 352
Qy 301 GGGTTCGCGCTGCTGAGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 360
Db 353 GGGTTCGCGCTGCTGAGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 412
Qy 361 CGCAGTACTGCTGCGCAACAGGCTGAGCGAGCGAGCGAGGAGGAGGAGGAGGAGGAGGAGG 420
Db 413 CGCAGTACTGCTGCGCAACAGGCTGAGCGAGCGAGCGAGGAGGAGGAGGAGGAGGAGGAGG 472
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Db 473 CTGCTGCGCGCGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 532
Qy 481 GTGCTGAGTGTGCTCCAGCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
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Qy 661 GTGTGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
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RESULT 7
PCT-US02-33146-19
; Sequence 19, Application PC/TUS0233146
; GENERAL INFORMATION:
; APPLICANT: University of Rochester Medical Center
; APPLICANT: Rowley, Peter
; TITLE OF INVENTION: Telomerase Interference
; FILE REFERENCE: PP-71506-2/RPT/5RN
; CURRENT APPLICATION NUMBER: PCT/US02/33146
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-33146-19

Query Match 100.0%; Score 3411; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10

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PCT-US99-07097-1
; Sequence 1, Application PC/TUS9907097
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; TITLE OF INVENTION: Geron Corporation
; FILE REFERENCE: 015389-003310PC
; CURRENT APPLICATION NUMBER: PCT/US99/07097
; EARLIER APPLICATION NUMBER: US 09/052,864

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; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: US 09/126,354
; EARLIER FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT) cDNA
PCT-US99-07097-1

Query Match 100.0%; Score 3411; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12

US-08-974-549-1

Sequence 1, Application US/08974549

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 APPLICANT: Linsner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 726
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549
 FILING DATE: 18-NOV-1997
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4015 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 56..3454
 OTHER INFORMATION: /product= "hTERT"
 OTHER INFORMATION: /note= "human telomerase reverse
 transcriptase (hTERT) catalytic protein"
 OTHER INFORMATION: component"

Query Match 100.0%; Score 3411; DB 13; Length 4015;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 1, Application US/09052864
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; TITLE OF INVENTION: Variants
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,864
; FILING DATE: 31-MAR-1997
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
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; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
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; FILING DATE: 14-AUG-1997
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; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
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; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-003300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
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; OTHER INFORMATION: /product= "human telomerase reverse
; OTHER INFORMATION: transcriptase (hTRT)"
US-09-052-864-1

Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Freq. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 421 CTGCTGCGCGCGCTGAGGCGACGAGCTGCTGCTTCACTGCTGCGACGCTGCGCTTCTT 480
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OY	121	CAGGCGGAGGACCCCGGAGGCTTTCCGCGCGCTGATGACCTCACTGCTGATGATGCTGCC	180
Db	173	CAGGCGGAGGACCCCGGAGGCTTTCCGCGCGCTGATGATGACCTCACTGCTGATGATGCTGCC	232
OY	181	TGGAGCAGCAGGAGCGGCCCCCGCGCGGCGGCTCTCTTCGCGCAGATGCTCTGCTTAAGAG	240
Db	233	TGGAGCAGCAGGAGCGGCCCCCGCGCGGCGGCTCTCTTCGCGCAGATGCTCTGCTTAAGAG	292
OY	241	CTGGTGGCGCCGAGTGTGTGAGAGGCTGTGTGAGAGCGCGCGCGAGAAAGTATGCTGCTTC	300
Db	293	CTGGTGGCGCCGAGTGTGTGAGAGGCTGTGTGAGAGCGCGCGCGAGAAAGTATGCTGCTTC	352
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OY	361	CGCAGCTACCTGTCCCAACAGAGTGAACGAGACGTGTGCGGGGAGAGGAGGAGCTGTGGGGCTG	420
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OY	901	GAGCGCGCAGCAGCAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	960
Db	953	GAGCGCGCAGCAGCAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1011
OY	961	CCTGTGTCCCGGATGTATGCGGAGACCAAGCATCTTCTATCTGTGTGTGTGTGTGTGTGTGTGT	1021
Db	1013	CCTGTGTCCCGGATGTATGCGGAGACCAAGCATCTTCTATCTGTGTGTGTGTGTGTGTGTGTGT	1077
OY	1081	CTGCTGTGAGCATCTTTCTGTGGGTTTCTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG	1144
Db	1133	CTGCTGTGAGCATCTTTCTGTGGGTTTCTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG	1199
OY	1141	CCCGCGCTGCGCGCAGGCTACTGTGCAATGTGCGGCGGCTGTGTCTGTGAGCTGTGTGGAAC	1204
Db	1193	CCCGCGCTGCGCGCAGGCTACTGTGCAATGTGCGGCGGCGGCTGTGTCTGTGAGCTGTGTGGAAC	1254

QY	1201	CACGCGCAGTGCCTCCCTACGAGGATGCTCTCTCAAGACGCACTCCGCTACGACTGCGGCTC	1260
Db	1253	CACGCGCAGTGCCTCCCTACGAGGATGCTCTCTCAAGACGCACTCCGCTACGACTGCGGCTC	1312
QY	1261	ACCCGACGACCGGCTGTCTGTGCCCCGGAGAAAGCCCAAGGCTCTGTGGCGAGCCCCGAG	1320
Db	1313	ACCCGACGACCGGCTGTGTGTGCCGGAGAAAGCCCAAGGCTCTGTGTGGCGAGCCCCGAG	1372
QY	1321	GAGGAGACACAGAACCCCGCTGCTCCGTGTGAGCTGCTCCGCTACGACACAGGACGCCCTGAG	1380
Db	1373	GAGGAGACACAGAACCCCGCTGTGCTGTGTGAGCTGCTCCGCTACGACACAGGACGCCCTGAG	1432
QY	1381	CAGGTTTACGGCTTGTGTGGGGGCTGCTGCTGCGCGGCTGTGTGCCCAAGGCTCTGTGGGC	1440
Db	1433	CAGGTTTACGGCTTGTGTGGGGGCTGCTGCTGCGCGGCTGTGTGCCCAAGGCTCTGTGGGC	1492
QY	1441	TCCAGGCAACAAGAACCGCGCTTCTCTCAGAGAAACACAAGAGTTTCACTTCCCTGGGGAG	1500
Db	1493	TCCAGGCAACAAGAACCGCGCTTCTCTCAGAGAAACAACAAGAGTTTCACTTCCCTGGGGAG	1552
QY	1501	CATGCGCAAGCTTCTGCTGCAAGAGCTGACGTGAAAGATGACGTGTGGGGACTTGCGCTTGG	1560
Db	1553	CATGCGCAAGCTTCTGCTGCAAGAGCTGACGTGAAAGATGACGTGTGGGGACTTGCGCTTGG	1612
QY	1561	CTGCGCAGAGACCCAGAGGGTGTGGCTGTGTTCGCGCGCGACAGCAACCGTCTGCTGAGAG	1620
Db	1613	CTGCGCAGAGACCCAGAGGGTGTGGCTGTGTTCGCGCGCGACAGCAACCGTCTGCTGAGAG	1672
QY	1621	ATCTGGGCAAGTTCTTGCACTGGCTGATGATGTGTATCGTGTGACCTGCTCAAGTCT	1680
Db	1673	ATCTGGGCAAGTTCTTGCACTGGCTGATGATGTGTATCGTGTGACCTGCTCAAGTCT	1732
QY	1681	TTCTTTTATGTACAGAGACACACGTTTCAAAAAGAACAGGCTCTTTTCTACCGAGAGGT	1740
Db	1733	TTCTTTTATGTACAGAGACACACGTTTCAAAAAGAACAGGCTCTTTTCTACCGAGAGGT	1792
QY	1741	GTCGTGAGCAAGTTTCCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGG	1800
Db	1793	GTCGTGAGCAAGTTTCCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGG	1852
QY	1801	GAGCTGTGGAAGACAGAGTCAAGCACACATCGGAGAACACAGGCCCGGCTCTCAAGCTCC	1860
Db	1853	GAGCTGTGGAAGACAGAGTCAAGCACACATCGGAGAACACAGGCCCGGCTCTCAAGCTCC	1912
QY	1861	AGACTCCGCTTCAATCCCAAGCTGACGGGCTGCGGCCGATTGTGAACATGAACTTACGTC	1920
Db	1913	AGACTCCGCTTCAATCCCAAGCTGACGGGCTGCGGCCGATTGTGAACATGAACTTACGTC	1972
QY	1921	GTCGAGACCAAGACGTTTCCGACAGAAAGAGGCCGACAGCGTCACTCACTCAGAGGTGAAG	1980
Db	1973	GTCGAGACCAAGACGTTTCCGACAGAAAGAGGCCGACAGCGTCACTCACTCAGAGGTGAAG	2032
QY	1981	GCACTGTTTCAAGCTGTCTCAATTACGAGCGGGCGCGGCCCGGCTCTTGTGGCGCTCT	2040
Db	2033	GCACTGTTTCAAGCTGTCTCAATTACGAGCGGGCGCGGCCCGGCTCTTGTGGCGCTCT	2092
QY	2041	GTCGTGAGGCTCGACATATCCACAGGGGCTGGGCGCACCTTCGTGCTGCGGTGCTCGAGGC	2100
Db	2093	GTCGTGAGGCTCGACATATCCACAGGGGCTGGGCGCACCTTCGTGCTGCGGTGCTCGAGGC	2152
QY	2101	CAGGACCCGCGGCTTGAAGCTGTACTTGTCAAGGTGATGTGACGGGCGGTCACAGACCC	2160
Db	2153	CAGGACCCGCGGCTTGAAGCTGTACTTGTCAAGGTGATGTGACGGGCGGTCACAGACCC	2212
QY	2161	ATCCCCCAGACAGGCTCAAGAGGTCATCGCACATCATCAAAACCCAGAACACGTAC	2220
Db	2213	ATCCCCCAGACAGGCTCAAGAGGTCATCGCACATCATCAAAACCCAGAACACGTAC	2272
QY	2221	TGCGTGTGTGTGTATGCGCGGTGTTCAGAAAGCCGCCCATTTGGGCACTGTTCGCAAGGCTTC	2280
Db	2273	TGCGTGTGTGTGTATGCGCGGTGTTCAGAAAGCCGCCCATTTGGGCACTGTTCGCAAGGCTTC	2332

QY 2281 AAGAGCCAGCTCTCTACCTTGAAGAGCCTCCAGCCCTATGAGCAAGTTCTGCTGAC 2340
Db 2233 AAGAGCCAGCTCTCTACCTTGAAGAGCCTCCAGCCCTATGAGCAAGTTCTGCTGAC 2392
QY 2341 CTGAGAGAGAGCCAGCCCGCTGAGAGGATGCGCTGCTATGAGCAAGAGCTCTCTGAAT 2400
Db 2393 CTGAGAGAGAGCCAGCCCGCTGAGAGGATGCGCTGCTATGAGCAAGAGCTCTCTGAAT 2452
QY 2401 GAGAGCCAGAGTGGCTCTTTCAGAGCTCTTCTCTACGCTTATGAGCAAGAGCTCTCTGAAT 2460
Db 2453 GAGAGCCAGAGTGGCTCTTTCAGAGCTCTTCTCTACGCTTATGAGCAAGAGCTCTCTGAAT 2512
QY 2461 ATGAGAGAGAGAGCTCTACGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2520
Db 2513 ATGAGAGAGAGAGCTCTACGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2572
QY 2521 CTGCTCTGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2580
Db 2573 CTGCTCTGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2632
QY 2581 GAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2640
Db 2633 GAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2692
QY 2641 GCGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2700
Db 2693 GCGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2752
QY 2701 TTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2760
Db 2753 TTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2812
QY 2761 GTTCAAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2820
Db 2813 GTTCAAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2872
QY 2821 CTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2880
Db 2873 CTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2932
QY 2881 TTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2940
Db 2933 TTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 2992
QY 2941 CTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3000
Db 2993 CTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3052
QY 3001 AACATCTACAGAGTCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3060
Db 3053 AACATCTACAGAGTCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3112
QY 3061 CCATTTTCATGAGAGTCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3120
Db 3113 CCATTTTCATGAGAGTCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3172
QY 3121 GCTCTCTCTGAGAGTCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3180
Db 3173 GCTCTCTCTGAGAGTCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3232
QY 3181 GAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3240
Db 3233 GAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3292
QY 3241 CTGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3300
Db 3293 CTGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3352
QY 3301 CAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3360
Db 3353 CAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3412
QY 3361 AACCCGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3411

Db 3413 AACCCGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 3463

RESULT 15
US-09-601-645-10
; Sequence 10, Application US/09601645
; GENERAL INFORMATION:
; APPLICANT: Michael Dahm
; APPLICANT: Robert C. Phelps
; APPLICANT: Carsten Brockmeyer
; TITLE OF INVENTION: Method for the quantitative determination of tumor cells
; TITLE OF INVENTION: In a body fluid and test kits suitable therefor
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/601,645
; CURRENT FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: DE 198 04 372.4
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PADAT Sequenzmodul, Version 1.0
; SEQ ID NO 10
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-601-645-10

Query Match 100.0%; Score 3411; DB 25; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATATGCGAGAGGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 60
Db 53 GCATATGCGAGAGGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 112
QY 61 GAGGTGCTGCGCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 120
Db 113 GAGGTGCTGCGCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 172
QY 121 CAGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 180
Db 173 CAGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 232
QY 181 TGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 240
Db 233 TGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 292
QY 241 CTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 300
Db 293 CTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 352
QY 301 GAGGTGCTGCGCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 360
Db 353 GAGGTGCTGCGCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 412
QY 361 CGCAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 420
Db 413 CGCAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 472
QY 421 CTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 480
Db 473 CTGAGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 532
QY 481 GTGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 540
Db 533 GTGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 592
QY 541 GCTGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 600
Db 593 GCTGAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 652
QY 601 GAAAGAGAGAGCTCTGAGAGGCTCTGAGAGGATGCGCTGAGAGGCTCTCTCTGACG 660

[illegible]

Db	1733	TTCTTTATGTCACGGACACACGTTTGAAAGAAACAGCGCTCTTTTCTACCGAAGAGT	1732
Qy	1741	GTCCTGAGCAAGTTGCAAGATTTGGAATTCAGACAGCACTTGAAAGAGGTGACGTGCG	1800
Db	1793	GTCCTGAGCAAGTTGCAAGATTTGGAATTCAGACAGCACTTGAAAGAGGTGACGTGCG	1852
Qy	1801	GAGCTGTGGAAAGCAGAGGTCAAGCAGCATCGGAAGCCAGAGCCGCGCTCTGACGTCC	1866
Db	1853	GAGCTGTGGAAAGCAGAGGTCAAGCAGCATCGGAAGCCAGAGCCGCGCTCTGACGTCC	1912
Qy	1861	AGACTCCGCTTCATCCCAAGCCTGACGGGCTCGGGCCGATTGGAACTGGACTACGTC	1920
Db	1913	AGACTCCGCTTCATCCCAAGCCTGACGGGCTCGGGCCGATTGGAACTGGAATACGTC	1972
Qy	1921	GTGGAGCCAGAACCTTCCGACAGAAAGAGGACCAGAGCCTCACTCAGAGGTAAAG	1980
Db	1973	GTGGAGCCAGAACGTTCCGACAGAAAGAGGACCAGAGCCTCACTCAGAGGTAAAG	2032
Qy	1981	GCACTGTTCAAGGTGCTCACTAAGAGGGGCGGGGCCCCGGCCTTCGAGCGCTCT	2046
Db	2033	GCACTGTTCAAGGTGCTCACTAAGAGGGGCGGGGCCCCGGCCTTCGAGGGCGCTCT	2092
Qy	2041	GTGCTGGGCTTGACGATATCCAGAGGCTTGAGGCACTTTCGTGCTGCGTGGAGGC	2100
Db	2093	GTGCTGGGCTTGAGCGATATCCAGAGGCTTGAGGCACTTTCGTGCTGCGTGGAGGC	2152
Qy	2101	CAGGACCCGCGGCTGAGCTGTACTTGTCAAAGTGAATGTGATCGGGCGGTATGACACC	2160
Db	2153	CAGGACCCGCGGCTGAGCTGTACTTGTCAAAGTGAATGTGATCGGGCGGTATGACACC	2212
Qy	2161	ATCCCCCAGAGCAGAGCTCACAGAGGTATGCGCAGCATCATCAAAACCCAGAACGCTAC	2220
Db	2213	ATCCCCCAGAGCAGAGCTCACAGAGGTATGCGCAGCATCATCAAAACCCAGAACGCTAC	2272
Qy	2221	TGCGTGCGTGGATATGCGCGTGTGTCACAGAGGCCGCCCATAGGGACGTCGCCAGGCTTC	2280
Db	2273	TGCGTGCGTGGATATGCGCGTGTGTCACAGAGGCCGCCCATAGGGACGTCGCCAGGCTTC	2332
Qy	2281	AAGAGCCACGTCCTACCTTGACAGACCTCAGCGCGTACATGCGACAGTTGCGTGGCTAC	2340
Db	2333	AAGAGCCACGTCCTACCTTGACAGACCTCAGCGCGTACATGCGACAGTTGCGTGGCTAC	2392
Qy	2341	CTGACAGAGAACACACCCGCTGAGAGGATGCGGTGTCATCGACAGAGCTCCTCCCTGAT	2400
Db	2393	CTGACAGAGAACACACCCGCTGAGAGGATGCGGTGTCATCGACAGAGCTCCTCCCTGAT	2452
Qy	2401	GAGGCCAGCAAGTGGCTCTTCGACGTCCTTACGCTTCTACGCTTCAATGTCACACAGCCGCTGCGC	2460
Db	2453	GAGGCCAGCAAGTGGCTCTTCGACGTCCTTACGCTTCTACGCTTCAATGTCACAGCCGCTGCGC	2512
Qy	2461	ATCAGGGGGCAAGTCCCTAAGTCACAGTGGCCAGAGGATCCCGAGAGGCTCAATCTCTCAAG	2520
Db	2513	ATCAGGGGGCAAGTCCCTAAGTCACAGTGGCCAGAGGATCCCGAGAGGCTCAATCTCTCAAG	2572
Qy	2521	CTGCTCTGACAGCTGTGTCTACCGGCAATGAGAACAAAGCTGTTTGCGGGGATTCGCGCG	2580
Db	2573	CTGCTCTGACAGCTGTGTCTACCGGCAATGAGAACAAAGCTGTTTGCGGGGATTCGCGCG	2632
Qy	2581	GAGGGGCGTGCCTCCGCGGTTTGGTGAATGATTTCTTGTTGGTGAACCTCCACCTCACCCAC	2640
Db	2633	GAGGGGCGTGCCTCCGCGGTTTGGTGAATGATTTCTTGTTGGTGAACCTCCACCTCACCCAC	2692
Qy	2641	GCGAAAACTTCTCTCAGAGACCTTGATCCAGAGTGTCCCTGAGTATGAGCTGCGGTGAAC	2700
Db	2693	GCGAAAACTTCTCTCAGAGACCTTGATCCAGAGTGTCCCTGAGTATGAGCTGCGGTGAAC	2752
Qy	2701	TTTGCGAAGACAGTGTGGAACCTTCCCTGTAGAAAGAGGACCTCGGGGTGACAGGCTTTT	2760
Db	2753	TTTGCGAAGACAGTGTGGAACCTTCCCTGTAGAAAGAGGACCTCGGGGTGACAGGCTTTT	2812
Qy	2761	GTTTCAGATGCGGCGCCACGGGCTATTTCCCTGCTGGGCGCTGCTGCTGAATCCGAGACC	2820
Db	2813	GTTTCAGATGCGGCGCCACGGGCTATTTCCCTGCTGGGCGCTGCTGCTGAATCCGAGACC	2872

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OY 2821 CTGAGGTGACAGAGACTACTCCAGCTATGCCCGGACCTTCATCAAGCCAGCTTCACC 2880
DB 2873 CTGGAGGTGACAGAGACTACTCCAGCTATGCCCGGACCTTCATCAAGCCAGCTTCACC 2932
OY 2881 TTCAACCGCGGCTTCAAGGCTGGAGGAAACAATGCGTGCACAACTTTGGGGGTCTTGCGG 2940
DB 2933 TTCAACCGCGGCTTCAAGGCTGGAGGAAACAATGCGTGCACAACTTTGGGGGTCTTGCGG 2992
OY 2941 CTGAGGTGACAGAGCTGTCTGATTTGGAGGTGAACAGCTTCCAGACGATGTGCACC 3000
DB 2993 CTGAGGTGACAGAGCTGTCTGATTTGGAGGTGAACAGCTTCCAGACGATGTGCACC 3052
OY 3001 AACATCTACAGATCTCTCTGCTGACAGGCGTACAGATTTACAGCATGTGTGTCAGCTC 3060
DB 3053 AACATCTACAGATCTCTCTGCTGACAGGCGTACAGATTTACAGCATGTGTGTCAGCTC 3112
OY 3061 CCATTTTCATCAGCAAGTTGGAGAACCCACATTTTCTGCGCGTCACTCTGACACG 3120
DB 3113 CCATTTTCATCAGCAAGTTGGAGAACCCACATTTTCTGCGCGTCACTCTGACACG 3172
OY 3121 GCCTCCCTCTGCTACTCCATCTGTAAGCCAGAGAGATGTGCTGGGGGTCACTCAGAGACAGC 3180
DB 3173 GCCTCCCTCTGCTACTCCATCTGTAAGCCAGAGAGATGTGCTGGGGGTCACTCAGAGACAGC 3232
OY 3181 GGGCGCGCGGCGCTCTGCGCTCTCGAGGCGGTGCAAGTGTGTCACCAAGCATTCCTG 3240
DB 3233 GGGCGCGCGGCGCTCTGCGCTCTCGAGGCGGTGCAAGTGTGTCACCAAGCATTCCTG 3292
OY 3241 CTCAAGCTGACTGACACCGGTGACAGTACAGTGCACCTCTGGGGGTCACTCAGAGACAGC 3300
DB 3293 CTCAAGCTGACTGACACCGGTGACAGTACAGTGCACCTCTGGGGGTCACTCAGAGACAGC 3352
OY 3301 CAGACGAGCTGAGTGGAAAGCTCCGAGGACGACGCTGACTGCTGAGAGGCGGACAGC 3360
DB 3353 CAGACGAGCTGAGTGGAAAGCTCCGAGGACGACGCTGACTGCTGAGAGGCGGACAGC 3412
OY 3361 AACCAGGACATGCGCTCAGACTTGAAGCATCTGACTGATGGCCACCC 3411
DB 3413 AACCAGGACATGCGCTCAGACTTGAAGCATCTGACTGATGGCCACCC 3463
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Search completed: March 1, 2004, 22:57:54
Job time : 6924.41 secs

DB 425 C C C T G C G C G T C G A C C C G G C C C C C C C G T C C C C G C C G C G C G C G C G C G C C C C C C C C C C T C G C C A C 484

QY 66 GCTGCGGCTGAGCAAGTTGCGGCGGCGCTGAGGCGCCCAAGGCTGAGGCTGATGACAGC 125
DB 167 GCGGCTGACTACGCGGCGCGCGCGGAGCAAGCTGCGGCGGCGCGCGGCTGACAGC 226
QY 126 CGGAGGACCCGCGGCTTTCGCGCGCTGAGTGGCCAGTGGCTGAGTGGCTGAGTGG 185
DB 227 CTGGGGCGAGAGCGGCTGCGCGCGCATGACTTCAAGAGCTGGCATTCGAGTAAAGC 286
QY 186 CGGAGGCGCGGCG 245
DB 287 CTGCG 346
QY 246 GCGCGGAGTGTGAGAGGCTGAGTGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 303
DB 347 CGAGGCGCTTATGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 406
QY 304 TTGCGGCTGCTGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 363
DB 407 GTCCAGCG 466
QY 364 AGTACCTGCG 423
DB 467 GCGGCGCTTGCAGAGCG 526
QY 424 CTGCG 472
DB 527 CCGGAGTGAAGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 575

RESULT 5
US-10-767-701-30024
; Sequence 30024, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 30024
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURe:
; OTHER INFORMATION: Clone ID: 9848339
US-10-767-701-30024

Query Match 1.6%; Score 53.2; DB 6; Length 522;
Best Local Similarity 49.4%; Pred. No. 0.0033;
Matches 167; Conservative 0; Mismatches 168; Indels 3; Gaps 1;
QY 63 GGTGCTGCG 122
DB 56 GAGGCGGCTGCTGCG 115
QY 123 GCGGCGGAGCG 179
DB 116 GCGGCG 175
QY 180 CTGGGAGCGAGCG 239
DB 176 GCTGCTGCTGAGGCG 235
QY 240 GCTGCTGAGCG 299
DB 236 CATGCG 295
QY 300 CGGCTTGGCG 359
DB 296 CGAGCTGCGAGCG 355

QY 360 GCGGAGTACTTGTGCG 397
DB 356 GCTGTGAGCTGTCCCG 393

RESULT 6
US-10-767-701-8805
; Sequence 8805, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 8805
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURe:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUB56975_1
US-10-767-701-8805

Query Match 1.6%; Score 53.2; DB 6; Length 667;
Best Local Similarity 45.0%; Pred. No. 0.0035;
Matches 199; Conservative 0; Mismatches 243; Indels 0; Gaps 0;
QY 67 CTGCG 126
DB 23 CTCTCTGTGATGAGCGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 82
QY 127 GAGGAGCG 186
DB 83 CACCAAGCG 142
QY 187 GCAGCG 246
DB 143 GCGTGCCTGCG 202
QY 247 GCGGAGTGTGAGAGGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 306
DB 203 CCG 262
QY 307 GCGGCTGAGAGCG 366
DB 263 GCGGCG 322
QY 367 TACCTGCCAAGCGAGTGAAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 426
DB 323 GCG 382
QY 427 GCG 486
DB 383 GCG 442
QY 487 GTGAGTCCAGAGTGGCG 508
DB 443 CTTCG 464

RESULT 7
US-10-767-701-4466
; Sequence 4466, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 4466
LENGTH: 580
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS80039_1
US-10-767-701-4466

Query Match 1.5% Score 52.6; DB 6; Length 580;
Best Local Similarity 54.9%; Pred. No. 0.0046;
Matches 128; Conservative 0; Mismatches 99; Indels 6; Gaps 1;

QY 7 CCGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 66
DB 165 CCGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 224
QY 67 CTGCGCTGCGGACGCTTCGTCGCGCGCTGCGGACGCTGCGGACGCTGCGGACGCG 126
DB 225 CCGGCGGCTTCGCGGCTGCGGACGCTGCGGACGCTGCGGACGCTGCGGACGCG 284
QY 127 GGGGAGC-----CGGCGGCTTCGCGGCTGCGGACGCTGCGGACGCTGCGGACGCG 180
DB 285 TCGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 344
QY 181 TGGAGCGACGAGCG 233
DB 345 GTGGGCGGCG 397

RESULT 8
US-10-767-701-12235/c
Sequence 12235, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 12235
LENGTH: 1165
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS24569_1
US-10-767-701-12235

Query Match 1.5% Score 51.2; DB 6; Length 1165;
Best Local Similarity 50.4%; Pred. No. 0.011;
Matches 123; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 23 GCGGAGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 82
DB 591 GCTTGGGCGGAGCGCGCGCTTCGCTTCGCTTCGCGGAGCGCTTCGCGGAGCG 532
QY 83 TCGTGGCGGCGCTTCGCGGAGCGCTTCGCTTCGCGGAGCGCTTCGCGGAGCG 142
DB 531 TCTTGGGCGGCTTCGCGGAGCGCTTCGCTTCGCGGAGCGCTTCGCGGAGCG 472
QY 143 TCGGCGGCTTCGCGGAGCGCTTCGCTTCGCGGAGCGCTTCGCGGAGCG 202
DB 471 GGGGCGGCTTCGCGGAGCGCTTCGCTTCGCGGAGCGCTTCGCGGAGCG 412
QY 203 CCGGCGGCTTCGCGGAGCGCTTCGCTTCGCGGAGCGCTTCGCGGAGCG 262
DB 411 CGAGCTTCGCGGAGCGCTTCGCTTCGCGGAGCGCTTCGCGGAGCG 352

QY 263 GCGTGTGC 270
DB 351 GCTTCTCC 344

RESULT 9
US-10-767-701-2473

Sequence 2473, Application US/10767701

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 2473
LENGTH: 570
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
NAME/KEY: unsure
LOCATION: (1) (570)
OTHER INFORMATION: unsure at all n locations

OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41826_1
US-10-767-701-2473

Query Match 1.5% Score 51; DB 6; Length 570;
Best Local Similarity 50.4%; Pred. No. 0.01;
Matches 207; Conservative 0; Mismatches 195; Indels 9; Gaps 3;

QY 88 GCGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 147
DB 19 CCGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 77
QY 148 GCGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 207
DB 78 GCGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 137
QY 208 CCGTCTTCGCGGAGCGCTTCGCTTCGCGGAGCGCTTCGCGGAGCG 267
DB 138 CCGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 197
QY 268 TCGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 327
DB 198 CAGCGGCGGCTTCGCGGAGCGCTTCGCTTCGCGGAGCGCTTCGCGGAGCG 257
QY 328 GGGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 387
DB 258 CCGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGACGACCTACCGGAGAGTG 310
QY 388 GAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 447
DB 311 CCGGCGGCTCCCGCTCCGAGCCGTCGCTCCCTGCGGAGCGCTTCGCGGAGCG 369
QY 448 CTGCTTACGCTTCGCGGAGCGCTTCGCTTCGCGGAGCGCTTCGCGGAGCG 498
DB 370 CCGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420

RESULT 10
US-10-767-701-8767

Sequence 8767, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 8767
LENGTH: 1215
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS56207_1
US-10-767-701-8767

Query Match
Best Local Similarity 48.4%; Pred. No. 0.013;
Matches 170; Conservative 0; Mismatches 180; Indels 1; Gaps 1;

1 GCGATGCGCGCGCTCCCGCTGCGAGCCGCTGCTGCTGCGAGCACTACCG 60
Db GCGCGACCGCGCTGCTGCGAGCCGCTGCTGCTGCGAGCACTACCG 92
QY GAGGTGCTGCGCTGCGAGCACTGCTGCGAGCGCTGCGAGCGCTGCTG 120
Db GCG 152
QY 121 CAGCGCGCGAGCGCGCGCGCTTCCGCGCGCTGCTGCTGCTGCTG 180
Db 153 CTCG 212
QY 181 TGGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 213 GCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 272
QY 241 CTGCTGCGCGCGAGCTGCTGCGAGCGCTGCTGCGAGCGCGCGAG 300
Db 273 CAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 332
QY 301 GCGTTCGCGCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 351
Db 333 -TCTCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 382

RESULT 11
US-10-767-701-1482
Sequence 1482, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 1482
LENGTH: 963
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS5355_1
US-10-767-701-1482

Query Match
Best Local Similarity 1.5%; Score 50.8; DB 6; Length 963;
Matches 200; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

16 CCGCGCTGCGAGCGCTGCTGCTGCTGCGAGCACTACCGAGGCTGCG 75
Db 108 CTCTGCTGCGCGCGCGCTGCGCTGCGCTGCGCGAGCACTACCG 167
QY 76 GCGAGCTGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCTGCTGCG 132
Db 168 GAGCGCGCGCGAGCTGCGCGCTGCTGCGCGCGCTGCTGCGCG 227

QY 133 CCGCGCGCTTCCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCG 192
Db 228 TCG 287
QY 193 CCG 252
Db 288 GCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 347
QY 253 CTGCTGCGAGCGCTGCTGCGAGCGCGCGCGCGCGCGCGCGCG 312
Db 348 CTCTACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 407
QY 313 CTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 372
Db 408 CCGTCCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 467
QY 373 CCGACACGCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 432
Db 468 CGCGCGAGCGCTGCGCGAGCGCGCGCGCGCGCGCGCGCGCG 527
QY 433 GTGCGCGAGCG 442
Db 528 CAGCGCGTGC 537

RESULT 12
US-10-767-701-18773
Sequence 18773, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 18773
LENGTH: 571
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: LIB3478-056-Q6-K1-H7
US-10-767-701-18773

Query Match
Best Local Similarity 54.3%; Pred. No. 0.014;
Matches 102; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 90 GCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 149
Db 194 GCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 253
QY 150 GCTGATGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 209
Db 254 GCTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 313
QY 210 CTCTTCCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269
Db 314 CTCTTCCGCGAGAGCTGAGCGCGCGCGCGCGCGCGCGCGCG 373
QY 270 CGAGCGCG 277
Db 374 TGAAGAG 381

RESULT 13
US-10-767-701-10516/C
Sequence 10516, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 10516
LENGTH: 572
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1663_1
US-10-767-701-10516

Query Match 1.5%; Score 50.4; DB 6; Length 572;
Best Local Similarity 46.6%; Pred. No. 0.014;
Matches 194; Conservative 0; Mismatches 221; Indels 1; Gaps 1;

QY 120 GCAGCGGGGAGCCCGGCTTTCCGCGGCTGTGTGGCCCACTGCTGTGTGCTGC 179
DB 521 GCGCGGGGCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 462
QY 180 CTGGAGCAGCAGCG 239
DB 461 GCGCGGCTGT 402
QY 240 GCTGT 299
DB 401 GCAGGAGAGCG 342
QY 300 CGAGCTTCGCGCTGT 359
DB 341 GGGCTGT 283
QY 360 GCGCAGCTTCTGT 419
DB 282 GCG 223
QY 420 GCTGT 479
DB 222 ACTGT 163
QY 480 TGT 535
DB 162 CCAGCAGGT 107

RESULT 14

US-10-767-701-11623
Sequence 11623, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 11623
LENGTH: 584
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS70322_1
US-10-767-701-11623

Query Match 1.5%; Score 50.4; DB 6; Length 584;
Best Local Similarity 47.0%; Pred. No. 0.014;
Matches 156; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 67 CTGCGCTGTGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 126
DB 236 CTGCGCGAGCTGT 295
QY 127 GGGGACCCGGGCTTTTCCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 186
DB 296 CTGTCAAGCCGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 355
QY 187 GCAGCG 246
DB 356 TCCGACCG 415
QY 247 GCGCGAGCTGT 306
DB 416 GCGCGGAGGT 475
QY 307 GCGCTGT 366
DB 476 GCGAGCTGT 535
QY 367 TACCTGCCCAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 398
DB 536 CAGCTGCCCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 567

RESULT 15

US-10-767-701-14885
Sequence 14885, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 14885
LENGTH: 1854
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS810_1
US-10-767-701-14885

Query Match 1.5%; Score 50.4; DB 6; Length 1854;
Best Local Similarity 43.0%; Pred. No. 0.019;
Matches 356; Conservative 0; Mismatches 466; Indels 6; Gaps 2;

QY 134 CCGCGGCTTTCCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 193
DB 947 GCGCGT 1006
QY 194 CG 253
DB 1007 GCGCGGAGAGCTGT 1066
QY 254 TGTGTCAAGAGCTGT 311
DB 1067 GCGCGGAGAGAGCGGT 1126
QY 312 GCTGT 371
DB 1127 GCTGT 1186
QY 372 GCGCGAG 431
DB 1187 GCGCGGAG 1246
QY 432 GGT 491

Tue Mar 2 09:53:26 2004

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Page 7

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Db 1247 GGGGCGCGAGCCCGGGGCGCCCGCGGTCGCGCGAGCGAGCGAGCGCGCCCGCGCGC 1306
QY 492 TCCAGCTGCGCTTACCAAGGTGTGCGGGCGCGCTGTATACAGCTGAGCGCTGCACTCA 551
Db 1307 GGGGCGGGGCGCCCGACAGCTTCCCGCCCGCTCCGGGGTAGC----CGTGGCCCGGGCGC 1362
QY 552 GGGCGGGCGCGCGCAACAGCTGTAGGAGCGCGAGCGCTGTGGATGGAAAGGGCGCTG 611
Db 1363 GGGCGCGCGCGCGCGCGCTGAGCGCGAGCGAGCGCGCGGGGGGGGGGGCGCGC 1422
QY 612 GAACCATAGCGTCAAGGAGCGCGGGGTCCCGCTGGGCTGCGAGCGCGCGGTGCGAGAG 671
Db 1423 GGGCGCGCGCGAGACCGCGCCCTTCCCTCCCGCGCGCGCGCGCGCGCGCGCGC 1482
QY 672 GCGGCGGGGCGAGTGCAGCGCGAAGTGTGCGCCAGAGGCGCGAGCGCGCTGCG 731
Db 1483 CCGCGCGCGCGAGGGGGCGAGCGCGCGCATCTGCGCGCGAGCGGGCTGCGC 1542
QY 732 CCTGAGCGCGAGCGAGCGCGCTTGGAGAGGGGTCTGGGCCCAACCGGCGAGAGCGC 791
Db 1543 GCGCGCTCCAGCGCCCTGCGCGCGCGAGCGCGCGCGCGCGAGCGCGCGCGCGCGCG 1602
QY 792 TGGACCGAGTGAACCGTGTGTTCTGTGTGTGTACTGTGCAAGCGCGCGCGAGAGCGC 851
Db 1603 GGGCGCGAGCGCGCGAGCGCTGCGCGCTGCCGACAGCGCGCGCGCGCGCGCGCGC 1662
QY 852 CTCTTGGAGGATGCGCTCTGTGCAAGCGCGCACTCCACCCATCGGTGGCGCGCAGCA 911
Db 1663 CCCCAAGCGCGCGCGCGCGCGCTCTCTCGCGCTCACTTCCACTCCACAGTGGCGCGC 1722
QY 912 CCAAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 959
Db 1723 CACTACCGGAGACCATTCATTGCGCACACCGCGCGCGCGCGCGCGCGCGCGCGC 1770
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JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES

Location/Qualifiers

gene

1..1826
/organism="Homo sapiens"
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ORIGIN

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Query Match      46.4%; Score 1584; DB 29; Length 1826;
Best Local Similarity 86.7%; Pred. No. 3.2e-246;
Matches 1584; Conservative 0; Mismatches 242; Indels 0; Gaps 0;

QY 1577 GGGTTGCTGTGTTCCGGCCGACAGACACCGTCTGCTGAGAGATCTGGCCAAAGTTCC 1636
Db      1 GGGTTGCTGTGTTCCGGCCGACAGACACCGTCTGCTGAGAGATCTGGCCAAAGTTCC 60

QY 1637 TGCACTGGCTGATGATGTGTACGTCTGAGCTGCTCAAGTCTTTTATGTCACGG 1696
Db      61 TGCACTGGCTGATGATGTGTACGTCTGAGCTGCTCAAGTCTTTTATGTCACGG 120

QY 1697 AGACACAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAAGATGTCTGGAACAAGTTGC 1756
Db      121 AGACACAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAAGATGTCTGGAACAAGTTGC 180

QY 1757 AAAAGCATTTGAATCAGACAGCACTTAAAGAGGTGACGTGCGGAGCTGTGGAAGCAG 1816
Db      181 AAAAGCATTTGAATCAGACAGCACTTAAAGAGGTGACGTGCGGAGCTGTGGAAGCAG 240

QY 1817 AGGTGAGGACGATCGGGAAGACGAGCGCCCTGCTGACGTCCAAACATCCCGCTTATCC 1876
Db      241 AGGTGAGGACGATCGGGAAGACGAGCGCCCTGCTGACGTCCAAACATCCCGCTTATCC 300

QY 1877 CCAAGCCTGACGGGCTGCGGCCGATTTGTAAATGATGATGCTGTGGAGCCAGAAAGT 1936
Db      301 CCAAGCCTGACGGGCTGCGGCCGATTTGTAAATGATGATGCTGTGGAGCCAGAAAGT 360

QY 1937 TCCGAGAGAAAGAGGCGCGACGCTCACTCGAGGGTGAAGACCTGTTCAACGTC 1996
Db      361 TCCGAGAGAAAGAGGCGCGACGCTCACTCGAGGGTGAAGAGGACCTGTTCAACGTC 420

QY 1997 TCACTACGAGCGGCGCGCGCCCTGCTGAGGCGCTCTGTGTGCGCTGAGCG 2056
Db      421 TCACTACGAGCGGCGCGCGCCCTGCTGAGGCGCTCTGTGTGCGCTGAGCG 480

QY 2057 ATATCCACAGGCGCTGCGCCGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2116
Db      481 ATATCCACAGGCGCTGCGCCGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540

QY 2117 AGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACAGACCAATCCCCAGACAGGC 2176
Db      541 AGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACAGACCAATCCCCAGACAGGC 600

QY 2177 TCACGAGGTCAATCGCAGCATATCAACCCAGAACAGTATGCTGCTGCTGCTGCTG 2236
Db      601 TCACGAGGTCAATCGCAGCATATCAACCCAGAACAGTATGCTGCTGCTGCTGCTG 660

QY 2237 CCGTGTTCAGAGGCGCGCCCATGAGCAGTCCGACAGGCTTCAAGAGCCAGCTCTCTA 2296
Db      661 CCGTGTTCAGAGGCGCGCCCATGAGCAGTCCGACAGGCTTCAAGAGCCAGCTCTCTA 720

QY 2297 CCTTGACAGCTCCCGCCGCTGATATGCGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2356
Db      721 CCTTGACAGCTCCCGCCGCTGATATGCGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780

QY 2357 CGCTGAGGATGCGCTGCTCATGAGCAGAGCTCCTCTGATGAGGCGAGCAGTGGCC 2416
Db      781 CGCTGAGGATGCGCTGCTCATGAGCAGAGCTCCTCTGATGAGGCGAGCAGTGGCC 840

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QY 2417 TCTTCAGAGTCTTCTCAAGCTTATGTCACACGACGCGTGGCATGAGGGCAAGTCT 2476
Db      841 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 900

QY 2477 ACCTTCAGTGCAGAGGATCCCGAGGGCTTCATCTCTCCACGCTGCTGTGACGCTGT 2536
Db      901 ACCTTCAGTGCAGAGGATCCCGAGGGCTTCATCTCTCCACGCTGCTGTGACGCTGT 960

QY 2537 GCTACGCGCATGAGAGAACAGTGTGTCGGGGATTCGCGGGAGAGGCTGCTGCTGC 2596
Db      961 GCTACGCGCATGAGAGAACAGTGTGTCGGGGATTCGCGGGAGAGGCTGCTGCTGC 1020

QY 2597 GTTTGTGATGATTTCTTTGTGTGATGACCTCACTCACTCACTCACTCACTCACTCACTCA 2656
Db      1021 GTTTGTGATGATTTCTTTGTGTGATGACCTCACTCACTCACTCACTCACTCACTCACTCA 1080

QY 2657 GACACCTGATCCGAGGTGCTCCCTGATGATGAGCTGCGGTGATGATGATGATGATGATG 2716
Db      1081 GACACCTGATCCGAGGTGCTCCCTGATGATGAGCTGCGGTGATGATGATGATGATGATG 1140

QY 2717 TGAATCTTCCCTGTGAAAGACAGGCGCTGAGTGCACAGGCTTTTGTTCAGATGCCGCC 2776
Db      1141 TGAATCTTCCCTGTGAAAGACAGGCGCTGAGTGCACAGGCTTTTGTTCAGATGCCGCC 1200

QY 2777 ACGGCTATTCCTCGTGTGAGGCGCTGCTGCTGATACCCGGAACCTGGAGGTGACAGCG 2836
Db      1201 ACGGCTATTCCTCGTGTGAGGCGCTGCTGCTGATACCCGGAACCTGGAGGTGACAGCG 1260

QY 2837 ACTACTCAAGTATGCCCGACCTTCATACAGACCAAGTCACTCACTCACTCACTCACTCA 2896
Db      1261 ACTACTCAAGTATGCCCGACCTTCATACAGACCAAGTCACTCACTCACTCACTCACTCA 1320

QY 2897 AGGTGAGGAGAACATGCGTGGCAACTCTTTGGGGGTCTGGCGGTGAAGTGCACAGCC 2956
Db      1321 AGGTGAGGAGAACATGCGTGGCAACTCTTTGGGGGTCTGGCGGTGAAGTGCACAGCC 1380

QY 2957 TGTTCGTGATTTGACAGTAAACAGCTCCAGACGCTGTGACCAACATCTACAAAGTCC 3016
Db      1381 TGTTCGTGATTTGACAGTAAACAGCTCCAGACGCTGTGACCAACATCTACAAAGTCC 1440

QY 3017 TCCGTGACAGGAGTACAGTTTCAAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3076
Db      1441 TCCGTGACAGGAGTACAGTTTCAAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500

QY 3077 TTTGGAAGAACCCACATTTTCTGCGGCTCATCTGTGACAGGCGCTCCTCTGTACT 3136
Db      1501 TTTGGAAGAACCCACATTTTCTGCGGCTCATCTGTGACAGGCGCTCCTCTGTACT 1560

QY 3137 CCATCTGAAAGCCAAAGACGAGGATGTGCTGGGGGCTCAAGGGCGCTGCGGCTTC 3196
Db      1561 CCATCTGAAAGCCAAAGACGAGGATGTGCTGGGGGCTCAAGGGCGCTGCGGCTTC 1620

QY 3197 TGCCCTCGAGGCGCTGACAGTGTGCTGACCAACAACTTCTGCTCAAGTACTGAC 3256
Db      1621 TGCCCTCGAGGCGCTGACAGTGTGCTGACCAACAACTTCTGCTCAAGTACTGAC 1680

QY 3257 ACCGTGTCACTTACGTGCACTCTCTGGGCTCATCTGAGACGCGCAAGCAGCTGATC 3316
Db      1681 ACCGTGTCACTTACGTGCACTCTCTGGGCTCATCTGAGACGCGCAAGCAGCTGATC 1740

QY 3317 GGAAGCTCCCGGGGAGAGAGCTGACCTGAGAGGCGCAGCAACCCGAGCTGCTGCT 3376
Db      1741 GGAAGCTCCCGGGGAGAGAGCTGACCTGAGAGGCGCAGCAACCCGAGCTGCTGCTG 1800

QY 3377 CAGACTTCAAGACCATCTGAGTGA 3402
Db      1801 CAGACTTCAAGACCATCTGAGTGA 1826

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RESULT 2
AY407350
LOCUS

AY407350 1584 bp DNA linear GSS 15-DEC-2003

DEFINITION Pan troglodytes TERT gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY407350
VERSION AY407350.1 GI:39763321
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 1584)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.U.,
Adam,M.D. and Cargill,M.
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
AUTHORS 2 (bases 1 to 1584)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.U.,
Adam,M.D. and Cargill,M.
TITLE Direct Submissions
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN
Query Match 38.4%; Score 1308.6; DB 29; Length 1584;
Best Local Similarity 83.1%; Pred. No. 1.2e-201;
Matches 1317; Conservative 0; Mismatches 267; Indels 0; Gaps 0;
QY 1577 GGGTGGCTGTGTTCCGCGCCGAGACACCGTCTCGTGAGAGATCTGCGCAAGTTCC 1636
Db 1 GGGTGGCTGTGTTCCGCGCCGAGACACCGTCTCGTGAGAGATCTGCGCAAGTTCT 60
QY 1637 TGCACGTGCTGATGAGTGTGTCGTGTCGAGCTGCTCAGAGCTTTCTTTATGTCACGG 1696
Db 61 TGCACGTGCTGATGAGTGTGTCGTGTCGAGCTGCTCAGAGCTTTCTTTATGTCACGG 120
QY 1697 AGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTGAGCAAGTTGC 1756
Db 121 AGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTGAGCAAGTTGC 180
QY 1757 AAAGCATTTGATTCAGACGACTTGAGAGAGGTGTCAGCTCGGAGAGTGTGGAAGAG 1816
Db 181 AAAGCATTTGATTCAGACGACTTGAGAGAGGTGTCAGCTCGGAGAGTGTGGAAGAG 240
QY 1817 AGGTAGGACAGCATGCGAAGACGAGCCCGCTGCTGACGTCCAGACTCCGCTTCAATCC 1876
Db 241 AGGTAGGACAGCATGCGAAGACGAGCCCGCTGCTGACGTCCAGACTCCGCTTCAATCC 300
QY 1877 CCAAGCTGACGGGCTGCGGCGGATTTGAACTAGGACTAGCTGCGGAGCCAGAACT 1936
Db 301 CCAAGCTGACGGGCTGCGGCGGATTTGAACTAGGACTAGCTGCGGAGCCAGAACT 360
QY 1937 TCCGCAAGAAAGAGGCGCTGACCTCAGCTGAGGAGTGAAGCACTGTTTCAAGCGTGC 1996
Db 361 TCCGCAAGAAAGAGGCGCGGCTCAGCTCAGGAGTGAAGCACTGTTTCAAGCGTGC 420
QY 1997 TCAACTAGAGGCGGCGGCGCGCGCGCTCTGAGGAGCTCTGCTGAGGCTGAGACG 2056
Db 421 TCAANNACGAGCGGCGGCGCGCGCGCTCTGAGGAGCTCTGCTGAGGCTGAGACG 480

QY 2057 ATATCCAGAGGCGCTGCGGACCTTGCTGCTGTCGCGGCGCCAGAGACCCGCGCTG 2116
Db 481 ATATCCAGAGGCGCTGCGGACCTTGCTGCTGTCGTCGCGGCGCCAGAGACCCGCGCTG 540
QY 2117 AGCTGTACTTTGTCAAGTGAATGTGACGGGCGCTGACGACACCATCCCGAGAGACGCG 2176
Db 541 AGCTGTACTTTGTCAAGTGAATGTGACGGGCGCTGACGACACCATCCCGAGAGACGCG 600
QY 2177 TCAGGAGGTCATCGCCAGCATCATCAACCCAGAACAGTCTGCTGCTGATG 2236
Db 601 NNN 660
QY 2237 CCGTGTCCAGAAAGCGCCCATGCGGACGTCGCAAGGCGCTTCAAGAGCAGTCTCTA 2296
Db 661 NNN 720
QY 2297 CTTTGAAGACCTTCAGCCGTAATGCGAGACGTTCTGCTGCTCACTGCGAGAGACAGCC 2356
Db 721 CTTTGAAGACCTTCAGCCGTAATGCGAGACGTTCTGCTGCTCACTGCGAGAGACAGCC 780
QY 2357 CGCTGAGGATGCGCGTGCATGAGAGAGAGTCTCTCCCTGAATGAGGCGAGAGTGGCC 2416
Db 781 CACTGAGGATGCGCGTGCATGAGAGAGAGTCTCTCCCTGAATGAGGCGAGAGTGGCC 840
QY 2417 TCTTGCAGCTCTTCTCTACGCTTCAATGTCACACGCGCTGCGCATCAGGCGAGTCT 2476
Db 841 NNN 900
QY 2477 AGCTCAGTGCAGAGGATCCGCGAGGCTCCATCTCTCCAGGCTGCTGAGGCTGT 2536
Db 901 AGCTCAGTGCAGAGGATCCGCGAGGCTCCATCTCTCCAGGCTGCTGAGGCTGT 960
QY 2537 GCTACGCGCATGAGAACCAAGCTGTTGCGGAGATTCGCGCGGAGCGGCTGCTCTGC 2596
Db 961 GCTACGCGCATGAGAACCAAGCTGTTGCGGAGATTCGCGCGGAGCGGCTGCTCTGC 1020
QY 2597 GTTGTGATGATATTTCTGTTGATGACACCTCACTCCACCGGAAACCTTCTCTCA 2656
Db 1021 GTTGTGATGATATTTCTGTTGATGACACCTCACTCCACCGGAAACCTTCTCTCA 1080
QY 2657 GAAACCTGATCCAGAGTGTCTGATGATGCTGCTGCTGATGCTGCGAAGACAGTGG 2716
Db 1081 GAAACCTGATCCAGAGTGTCTGATGATGCTGCTGCTGATGCTGCGAAGACAGTGG 1140
QY 2717 TGAATTTCCCTGTAAGAACAGAGCCCTGGTGGCACGGCTTTTGTTCAGATGCGGCC 2776
Db 1141 TGAATTTCCCTGTAAGAACAGAGCCCTGGTGGCACGGCTTTTGTTCAGATGCGGCC 1200
QY 2777 ACCGCTATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2836
Db 1201 ACCGCTATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 2837 ACTATCTCAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2896
Db 1261 ACTATCTCAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
QY 2897 AGGCTGGAGAGAACAGTGCCTGCAAACTTTTGGGGCTTGTGGGGCTGAAAGTGTCAAGCC 2956
Db 1321 AGGCTGGAGAGAACAGTGCCTGCAAACTTTTGGGGCTTGTGGGGCTGAAAGTGTCAAGCC 1380
QY 2957 TGTTTTGTGATTTGCAAGTGAACAGCTTCAGACGCTGTCACCAATCTCAAAATCTC 3016
Db 1381 TGTTTTGTGATTTGCAAGTGAACAGCTTCAGACGCTGTCACCAATCTCAAAATCTC 1440
QY 3017 TCTGTGTGAGGCGTACAGGTTTCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3076
Db 1441 TCTGTGTGAGGCGTACAGGTTTCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 3077 TTTGAGAAACCCCAATTTTCTGCGGCTGATCTTGACACGAGCTCTCTCTACT 3136
Db 1501 TTTGAGAAACCCCAATTTTCTGCGGCTGATCTTGACACGAGCTCTCTCTACT 1560

QY 3010 AGATCTCTCTGCTGAGGCGTACAGGTTTACGACATGTGTGCTGAGCTCCATTTCAT 3069
 DB 1441 AAGATCTCTCTGCTGAGGCGTACAGGTTTACGACATGTGTGCTGAGCTCCATTTCAT 1500
 QY 3070 CAGCAGTTTGAAGAAACCCACATTTTCTGCGGCGTATCTGTACAGGCGCTCCCTC 3129
 DB 1501 CAGCAGTTTGAAGAAACCCACATTTTCTGCGGCGTATCTGTACAGGCGCTCCCTC 1560
 QY 3130 TGTACTTCATCTCTGAAAGCCAGAAAGGAGATGCTGAG--GGGCGAAGGCGCGC 3187
 DB 1561 TGTACTTCATCTCTGAAAGCCAGAAAGGAGATGCTGAG--GGGCGAAGGCGCGC 1620
 QY 3188 CCGGCGCTCTGCGCTCCGAGGCGCTGAGTGTGTGCGACCAAGATTTCTGCTCAAG 3247
 DB 1621 CTGCTCTCTCTCTCTGAAAGCCAGAAAGGAGATGCTGAG--GGGCGAAGGCGCGC 1680
 QY 3248 TGAATGACACCTGTCACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3307
 DB 1681 TGAATGACACCTGTCACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
 QY 3308 AGCTGAGTGGAGAGCTTCCGCGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3367
 DB 1741 TGTGTGCGGAGAGCTTCCGCGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
 QY 3368 CACTGCGCTGACGACTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3402
 DB 1801 CCTTAAAGCAGACCTTTCAGACCATTTTGAAGCTAA 1835

RESULT 4
 BM453198 925 bp mRNA linear EST 05-FEB-2002
 LOCUS AGENCOURT 638755 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5529840
 DEFINITION 5', mRNA sequence.
 ACCESSION BM453198
 VERSION BM453198.1 GI:18502238
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 925)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csabps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LLM12208 row: P column: 01
 High quality sequence step: 646.
 Location/Qualifiers
 1..925
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5529840"
 /issue_type="telomysarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_71"
 /note="Organ: uterus; Vector: pCMV-SPORT6; site: 1; Notif;
 site: 2; Sail; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.1 kb."

ORIGIN
 Query Match 23.6%; Score 806; DB 12; Length 925;
 Best Local Similarity 99.2%; Prid. No. 2.4e-120;
 Matches 821; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 2097 GGCCAGAGACCCGCGCTGAGCTGTAATTGTCAAGTGAATGAGCGGCGCTACGA 2156
 DB 2 GGCCAGAGACCCGCGCTGAGCTGTAATTGTCAAGTGAATGAGCGGCGCTACGA 61
 QY 2157 CACCATCCCCCAGAGACGCTTACAGAGTGTATGCGCATATCAAAACCCAGAAC 2216
 DB 62 CACCATCCCCCAGAGACGCTTACAGAGTGTATGCGCATATCAAAACCCAGAAC 121
 QY 2217 GTACTGCGTGTGTGTATGCGCATATGCGCATATGCGCATATGCGCATATGCGCATATGCGCATAT 2276
 DB 122 GTACTGCGTGTGTGTATGCGCATATGCGCATATGCGCATATGCGCATATGCGCATATGCGCATAT 181
 QY 2277 CTTCAAGAGCCAGCTTCTTACCTTGAAGACCTTCAAGCGTATGCGCATATGCGCATATGCGCATAT 2336
 DB 182 CTTCAAGAGCCAGCTTCTTACCTTGAAGACCTTCAAGCGTATGCGCATATGCGCATATGCGCATAT 241
 QY 2337 TCACCTGAGAGAGACGAGCGCGCTGAGAGAGAGCGGTGATGCGCATATGCGCATATGCGCATATGCGCATAT 2396
 DB 242 TCACCTGAGAGAGACGAGCGCGCTGAGAGAGAGCGGTGATGCGCATATGCGCATATGCGCATATGCGCATAT 301
 QY 2397 GAATGAGGCGAGAGTGGCTTTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTT 2456
 DB 302 GAATGAGGCGAGAGTGGCTTTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTT 361
 QY 2457 GCGGATGAGGCGAGAGTGGCTTTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTT 2516
 DB 362 GCGGATGAGGCGAGAGTGGCTTTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTTGAAGCTTCTT 421
 QY 2517 CACGCTCTCTGACGCTTGTCTACGCGGACATGAGAGACAGCTTTTGGGAGATTTCG 2576
 DB 422 CACGCTCTCTGACGCTTGTCTACGCGGACATGAGAGACAGCTTTTGGGAGATTTCG 481
 QY 2577 GCGGAGAGGCGTGTCTCTGCGTTTGTGTGATGATTTTGTGTGACACTTCACTTCACT 2636
 DB 482 GCGGAGAGGCGTGTCTCTGCGTTTGTGTGATGATTTTGTGTGACACTTCACTTCACT 541
 QY 2637 CCAAGCGGAGAGCTTCTCTGAGACCTTGTCTGAGAGTGTCTTGAAGTGTCTGAGTGTCTGAGTGTCT 2696
 DB 542 CCAAGCGGAGAGCTTCTCTGAGACCTTGTCTGAGAGTGTCTTGAAGTGTCTGAGTGTCTGAGTGTCT 601
 QY 2697 GAATTTGGGAGAGACAGTGTGTAACTTCTCTGAGAGAGAGAGGCTTGGTGTGACGCG 2756
 DB 602 GAATTTGGGAGAGACAGTGTGTAACTTCTCTGAGAGAGAGAGGCTTGGTGTGACGCG 661
 QY 2757 TTTTGTCAAGTGTGCGGCGGACGAGCTTATCCCTGTGTGCGGCTGTGTGATACCG 2816
 DB 662 TTTTGTCAAGTGTGCGGCGGACGAGCTTATCCCTGTGTGCGGCTGTGTGATACCG 721
 QY 2817 GACCTTGAAGTGTGAGAGGACATCTTCAAGCTTATCCCTGTGTGCGGCTGTGTGATACCG 2876
 DB 722 GACCTTGAAGTGTGAGAGGACATCTTCAAGCTTATCCCTGTGTGCGGCTGTGTGATACCG 781
 QY 2877 CACCTTGAAGTGTGAGAGGCTTCAAG--GGCTGGGAGAGACATGCTGTGCAAA 2922
 DB 782 CACCTTGAAGTGTGAGAGGCTTCAAGCTGTGAGAGACATGCTGTGCAAA 829

RESULT 5
 BU702370 851 bp mRNA linear EST 15-JUL-2003
 LOCUS BU702370
 DEFINITION U1-M-F10-byp-f-12-0-UT.r1 NIH_BMAP_F10 Mus musculus cDNA clone
 IMAGE:6400523 5', mRNA sequence.
 ACCESSION BU702370
 VERSION BU702370.1 GI:23627105
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 851)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

Site 2: Ncti; The S22SN06 library was contributed by the Soares laboratory and it was constructed as described by Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 13.0%; Score 445; DB 12; Length 492;
Best Local Similarity 100.0%; Pred. No. 5,3e-62;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2716 GTGAATCTCCCTGTGAAGACAGAGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGCC 2775
Db 1 GTGAATCTCCCTGTGAAGACAGAGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGCC 60

QY 2776 CACGAGCTATTCCTCGTGGTGGGCTGTGCTGATACCGGAGCCCTGGAGGTGCAGAGC 2835
Db 61 CACGAGCTATTCCTCGTGGTGGGCTGTGCTGATACCGGAGCCCTGGAGGTGCAGAGC 120

QY 2836 GACTACTCCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCACTTCAACCGCGGCTTC 2895
Db 121 GACTACTCCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCACTTCAACCGCGGCTTC 180

QY 2896 AAGGCTGGAGGAACATGCGTGGGAACTCTTTGGGGCTTGGGGCTGAAGTGCAGC 2955
Db 181 AAGGCTGGAGGAACATGCGTGGGAACTCTTTGGGGCTTGGGGCTGAAGTGCAGC 240

QY 2956 CTGTTTCTGATTTGACAGTGAACAGGCTCCAGACGCTGTGACCAACAATCTACAGATC 3015
Db 241 CTGTTTCTGATTTGACAGTGAACAGGCTCCAGACGCTGTGACCAACAATCTACAGATC 300

QY 3016 CTCTGCTGACAGGCTCAGGTTTTCAGCATGTGTGTGTGTGAGTCCCATTTATCAGCA 3075
Db 301 CTCTGCTGACAGGCTCAGGTTTTCAGCATGTGTGTGTGTGAGTCCCATTTATCAGCA 360

QY 3076 GTTTGGAAGAACCCCAATTTTCTGCGGCTCATCTGACAGGCTCCCTGCTGCTAC 3135
Db 361 GTTTGGAAGAACCCCAATTTTCTGCGGCTCATCTGACAGGCTCCCTGCTGCTAC 420

QY 3136 TCCATCTCTGAAGCCAGAACGACG 3160
Db 421 TCCATCTCTGAAGCCAGAACGACG 445

RESULT 7
Bg917907 851 bp mRNA 1linear EST 05-JUN-2001
LOCUS 602820830F1 NCT_CGAP_Mam6 Mus musculus cDNA clone IMAGE:494987 5',
DEFINITION mRNA sequence.
ACCESSION Bg917907
VERSION Bg917907.1 GI:14298383
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL0903 Row: K Column: 08

FEATURES
High quality sequence stop: 753.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:494987"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCT_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: Ncti; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

Query Match 12.3%; Score 419; DB 12; Length 851;
Best Local Similarity 71.9%; Pred. No. 1.1e-57;
Matches 579; Conservative 0; Mismatches 215; Indels 11; Gaps 2;

QY 2599 TTGGTGAATGATTTCTTGTGTGTGACACCTCACTCAACCCAGGAAACCTTCTCAGG 2658
Db 38 TTGGTGAATGATTTCTTGTGTGTGACACCTCACTCAACCCAGGAAACCTTCTCAGG 97

QY 2659 AACCCTGTCGAGGTGTCCTCGTGAATGCTGCGTGTGAACCTTGCGAAGACAGTGGTG 2718
Db 98 AACCCTGTCGAGGTGTCCTCGTGAATGCTGCGTGTGAACCTTGCGAAGACAGTGGTG 157

QY 2719 AACTCCCTGTAAGAAAGACGAGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGCCAC 2778
Db 158 AACTCCCTGTAAGAAAGACGAGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGCCAC 217

QY 2779 GACCTATTCCTGCTGTGGGCTGCTGTGTGATACCGGACCTGAGGTGCAGAGCAGC 2838
Db 218 GACCTATTCCTGCTGTGGGCTGCTGTGTGATACCGGACCTGAGGTGCAGAGCAGC 277

QY 2839 TACTCCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCACTTTCACACCGGCTTCAG 2898
Db 278 TACTCCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCACTTTCACACCGGCTTCAG 337

QY 2899 GCTGGAGGAACATGCGTCCGAACTCTTTGGGGCTTGGCGCTGAAGTGCAGAGCTG 2958
Db 338 GCTGGAGGAACATGCGTCCGAACTCTTTGGGGCTTGGCGCTGAAGTGCAGAGCTG 397

QY 2959 TTTCTGATTTGGCAGGTGAACAGGCTCCAGAGGTGTGCACCAATCTACAAATCTCTC 3018
Db 398 TTTCTGATTTGGCAGGTGAACAGGCTCCAGAGGTGTGCACCAATCTACAAATCTCTC 457

QY 3019 CTGCTGACAGGCGTACAGGTTTTCAGCATGTGTGTGTGACGCTCCCATTTCAAGCAAGT 3078
Db 458 CTGCTGACAGGCGTACAGGTTTTCAGCATGTGTGTGTGACGCTCCCATTTCAAGCAAGT 517

QY 3079 TGAAGAAGCCCAATTTTCTGCGGCTGATCTGTACAGAGGCTCTCTGTATCTCC 3138
Db 518 TGAAGAAGCCCAATTTTCTGCGGCTGATCTGTACAGAGGCTCTCTGTATCTCC 577

QY 3139 ATCTGAAGAGCAGAAAGCAGAGGATGCTGCTGGGAGGCGGCGGCGCTCTG 3198
Db 578 ATCTGAAGAGCAGAAAGCAGAGGATGCTGCTGGGAGGCGGCGGCGCTCTG 627

QY 3199 CCTTCGAGAGCGCTGCGAGTGTGTGTGTGCACCAAGCATTTCT -GTCAGCTGACTGCACA 3257
Db 628 CCTTCGAGAGCGCTGCGAGTGTGTGTGTGCACCAAGCATTTCT -GTCAGCTGACTGCACA 687

QY 3258 CCGGTGACCTAGGTGCACCTCTGGGGTGACTCAGAGCAGCCAGAGCGAGCTGAGTG 3317
Db 688 TTTGTGATATTCAGAAATGTCTCTGTGAGACCTCTGAGAGCAGCCCAAAACCGCTGTGCGG 747

QY 3318 GAAGCTCCCGGAGCAGAGCTGACTGCTGTGAGGCGGCGAGCCACCGGCACTGCGCTC 3377

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 664)

AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: J. Baker (Stanford University)
CDNA Library Arrayed by: The I.W.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Clone distribution: NCI-CCAP clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at: info@image.llnl.gov
MG1:1845958
Plate: LLAM2043 row: N column: 7
Seq primer: Sp6 primer.
Location/Qualifiers
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/clone="IMAGE:5409222"
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/dev_stage="embryo, 7.5 dpc"
/lab_host="XLI-Blue"
/clone_lib="Baker mouse embryo e7.5"
/note="Vector: PCS105; Site: NotI; Site 2: SalI; CDNA made by oligo-dT priming. Directionally cloned into SalI/NotI sites using the following 5' adaptor: 5'-TCGACCACGCGCTCG-3'. Size-selected for average insert size 1.8-1.9 kb. Library constructed by J. Baker (Stanford University)."

ORIGIN

Query Match 9.3%; Score 317.8; DB 13; Length 664;
Best Local Similarity 68.3%; Pred. No. 2.4e-41;
Matches 479; Conservative 0; Mismatches 177; Indels 45; Gaps 1;

1056 GCCCAGCTGAGCTGCGCTGCGAGCTGCGAGACATCTTCTGGGTTCCAGGCGCTG 1115
9 GCTTAAGTACTGAGCTGCGGCGCAGAGAGTGTGAGATCATCTTTCTGGGCTCAAGGCTTAC 68
1116 GATCCAGGAGACTCCCGCAGGTTGCGCCCTGCGCCAGCGCTAAGCAATGCGGCC 1175
69 GACATCAGAGACCACTGTGAGAGACACACCGTCTATGCGTCAATGCGATGCGAGATCGGCC 128
1176 CCTGTTTCTGAGCTGCTTGGAGACAGCGAGTGCCTTACGCGGCTGCTCTTAAGAC 1235
129 CCGTTTCCAAAGCTCTGTGTAACCATATGCAAGTGTCAAGTCTCTTCAAGGTC 188
1236 GCACTGCGCGCTGCGAGCTGCGGTCAACCCAGCAGCGGTGTCTGTGCCCGGAGAACCC 1295
189 ACATTGCAAGTTTCGAACAGCAACCAACAGAGTGAAGATGCTT----- 232
1296 CCAGGAGCTGTGGGCGGCCCGGAGAGAGAGACACAGACCCCGTCCGCTGTGCACT 1355
233 -----TGAACACAGCCCGCAGCCGCACTCAATGAGATT 263
1356 GCTCCGCCAGCAGCAGAGCCCTGTGAGGTGATGAGGCTTGTGCGGAGCTGCTGCGCG 1415
264 GCTCCGCCCTGACAGAGAGTCCCTGCGAGGTATATGTTTCTTGGGCTGCTCTTGCA 323
1416 GGTGGTGGCCCGCAGGCTGCTGGGCTCCAGCAGCAACAGAGCCGCTTCTCAAGAACAC 1475
324 GGTGGTGTGCTGATGTTCTTGGGAGTACAGGAGCAATGAGGCGGCTTCTTAAGAACTT 383
1476 CAAGAAGTTCAATCTCCCTGGGAGAACATGCCAAGCTCTGCTGACAGAGTGAAGTGAA 1535

Db 384 AAGAGTTCAATCTCTGTTGGGAAATACGAGACTTCACTGAGAACTGATGAGAA 443
1536 GATGAGCGTGGGAGACTGCGCTTGGCTGCGAGAGGCCAGAGGTTGCTGTCCGCG 1595
444 GATGAAGTAAAGATGATGCGACTGCTCCGAGAGCCAGGAGAACCGGTGTCCCGCG 503
1596 CGCAGAGACCGCTTGGTGAAGAGATCTTGGCCCAATTTCTGACCTGCTGATGAGTGT 1655
504 TGCGAGAGACCGCTTGAAGAGAGATCTTGGCTACGTTCTTCTGCTGATGAGAC 563
1656 GTACGCTGTGAGCTGCTGAGTCTTCTTCTTATGTCAGCAGAGACACGTTTCAAGAA 1715
564 ATACGTGTGATAGCTGCTGATGATGATCTTTCATCATCAGAGAGACATTCAGAA 623
1716 CAGGCTCTTCTTCAACCGAAGAGTGTCTGAGCAAGTTGC 1756
624 CAGGCTCTTCTTCAACCGAAGAGTGTCTGAGCAAGTTGC 664

RESULT 12
LOCUS BB618671
DEFINITION BB618671 RIKEN full-length enriched, 8 days embryo Mus musculus
ACCESSION BB618671
VERSION BB618671.1 GI:16458173
KEYWORDS EST.
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 599)

AUTHORS Arai, K., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sugabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M., and Hayashizaki, Y.

RIKEN Mouse ESTs (Arai, K., et al. 2001)
Unpublished (2001)
Contact: Yoshinori Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0445, Japan
Tel: 81-45-503-9226
Fax: 81-45-503-9226
Email: genome-resgsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayashizaki, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsui, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamazaki, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINTL at: image.lint.gov

Plate: LINCW94 row: c column: 03

High quality sequence stop: 634.

FEATURES

SOURCE

1. 715

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3621050"

/tissue_type="Burkitt lymphoma"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH MGC 8"

/note="Organ: lymph; Vector: Vector; Site: 1; XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAAGG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match

Best Local Similarity 7.4%; Score 252.2; DB 10; Length 715;

Matches 307; Conservative 0; Mismatches 13; Indels 7; Gaps 4;

QY	1575	AGGGGTTGGCTGTGTCGCGCCGACAGACCGCTGCTGAGAGAGATCTGACCAAGTT	1634
DB	372	AGGGGTTGGCTGTGTCGCGCCGACAGACCGCTGCTGAGAGATCTGACCAAGTT	431
QY	1635	CCTGCACTGGCTGATGATGTGTGACGTGTGAGCTGCTCAGGCTCTTTCTTT	1693
DB	432	CCTGCACTGGCTGATGATGTGTGACGTGTGAGCTGCTCAGGCTCTTTCTTTATATGTC	491
QY	1694	CGGAGACCAAGTTTCAAGAACAGGCTCTTTTCTACCGGAGAGAGTGTGAGCAAGT	1753
DB	492	CGGAGACCAAGTTTCAAGAACAGGCTCTTTTCTACCGGAGAGAGTGTGAGCAAGT	551
QY	1754	TGCAAGCATTTGATCAGACAGCACTTGAAGAGGTGACCTGCGGAGCT-GTGGAA	1812
DB	552	TGCAAGCATTTGATCAGACAGCACTTGAAGAGGTGACCTGCGGAGGTAGTGGAA	611
QY	1813	GCAGAGGTGAGGAGATCGGG--AAGCAGGCGCGCTGCTGATCTCCAGACTCCGCT	1870
DB	612	GCAGAGGTGAGGAGATCGGGAAAGCGGCGCTGCTGATCTCCAGACTCCGCT	668
QY	1871	TGATCCCAAGCCTGACGGGCTGCGGC	1897
DB	669	TTCATCCCAAGCTGAAGGCTGCGGC	695

Search completed: March 1, 2004, 03:42:19
Job time : 5409.07 secs

Db	173	CAGCGCGGGAAACCCCGGGGGCTTTCCGCGCGCGCTGTGTGGCCAGTGCCTGTGTGTGTGTGCC	232
QY	181	TGGGACGACAGAGGCGCGCCCCCGCGCGCCCCCTCTTCGCGCAGGTGTCTGTGCTGAAGAG	240
Db	233	TGGGACGACAGAGCGCGCCCCCGCGCGCCCCCTCTTCGCGCAGGTGTCTGTGCTGAAGAG	292
QY	241	CTGTGTGCGCCGAGTGTCTGACAGAGGCTGTGTGACGCGCGCGAGAAACGTGTGCGCTTC	300
Db	293	CTGTGTGCGCCGAGTGTCTGACAGAGGCTGTGTGACGCGCGCGAGAAACGTGTGCGCTTC	352
QY	301	GCGTTCCGCGGTGCTGACAGCGGGGCGCGCGGGGGCCCCCGGAGGCTTTCACACAGCTGTG	360
Db	353	GCGTTCCGCGGTGCTGACAGCGGGGCGCGCGGGGGCCCCCGGAGGCTTTCACACAGCTGTG	412
QY	361	CGCAGCTACCTGTGCGCAACACGTGTACCGACGCACTGTGCGGGAGAGCGGGGCGTGTGGAGCTG	420
Db	413	CGCAGCTACCTGTGCGCAACACGTGTACCGACGCACTGTGCGGGAGAGCGGGGCGTGTGGAGCTG	472
QY	421	CTGTGTGCGCGCGGTGGGCGACACAGTGTGTGTTCACGTGTGAGACGCTGTGCGCTTC	480
Db	473	CTGTGTGCGCGCGGTGGGCGACAGTGTGTGTTCACGTGTGAGACGCTGTGCGCTTC	532
QY	481	GTCGTGTGTGCTCCAGCTGTGCGCTTACACAGTGTGTGCGGCGCGCTGTACACACTGTGCG	540
Db	533	GTCGTGTGTGCTCCAGCTGTGCGCTTACACAGTGTGTGCGGCGCGCTGTACACACTGTGCG	592
QY	541	GCTGTGCACCTAGAGGCGCGGGCGCGCGCGCACACGTGTATGTGACCCCGAAGGCTGTGGATGC	600
Db	593	GCTGTGCACCTAGAGGCGCGGGCGCGCGCGCACACGTGTATGTGACCCCGAAGGCTGTGGATGC	652
QY	601	GAAACGGGCGTGGAACCATATAGCGTCAAGGAGAGCGGGGATCCCTCTGTGCGCTGTGCGACCG	660
Db	653	GAAACGGGCGTGGAACCATATAGCGTCAAGGAGAGCGGGGATCCCTCTGTGCGCTGTGCGACCG	712
QY	661	GATGTGAGAGAGAGCGCGGGGCGAGTGCAGCGCGAATCTGTGCGTGTGCCAAGAGGCCACAG	720
Db	713	GATGTGAGAGAGAGCGGGGCGAGTGCAGCGCGAATCTGTGCGTGTGCCAAGAGGCCACAG	772
QY	721	CGTGTGCGCTGCCCCCTTAGCGCGAGCGGAGCGCCGTTTGTGGCAGGGGATCTGTGGGCCACCG	780
Db	773	CGTGTGCGCTGCCCCCTTAGCGCGAGCGGAGCGCCGTTTGTGGCAGGGGATCTGTGGGCCACCG	832
QY	781	GGCAGAGACGCGTGTGACCGAGTGCAGGTGTTTCTGTGTGTGTGTGTACCTGTGCGACACCGCG	840
Db	833	GGCAGAGACGCGTGTGACCGAGTGCAGGTGTTTCTGTGTGTGTGTGTACCTGTGCGACACCGCG	892
QY	841	GAAAGAAAGCCACTCTTTTGGAGGGGTGCGCTCTCTGTGACGCGCACTTCCACCCATCCGTG	900
Db	893	GAAAGAAAGCCACTCTTTTGGAGGGGTGCGCTCTCTGTGACGCGCACTTCCACCCATCCGTG	952
QY	901	GGCGCGCAGAGACACGCGGGGGCCCCCATTCACATGTGGGGCGCACAGGTCCTGTGGACAG	960
Db	953	GGCGCGCAGAGACACGCGGGGGCCCCCATTCACATGTGGGGCGCACAGGTCCTGTGGACAG	1011
QY	961	CTTTGTCCCCCGGTGTACGCGCGACACCAAGCACTTCTGTACTCTTCAGGCGACAAAGAG	1020
Db	1013	CTTTGTCCCCCGGTGTACGCGCGACACCAAGCACTTCTCTTCTTCAGGCGACAAAGAG	1072
QY	1021	CAGGTGTGGGCGCTCTTTCTTACTCAGGCTGTGAGGGCCACGCTGTGATGTGTGCGAGG	1080
Db	1073	CAGGTGTGGGCGCTCTTTCTTACTCAGGCTGTGAGGGCCACGCTGTGATGTGTGCGAGG	1133
QY	1081	CTGTGTGAGACCATCTTTTCTGTGGTTTCAGGGCCCTGTGATGTGAGGAACTCCCGCGAGTTG	1144
Db	1133	CTGTGTGAGACCATCTTTTCTGTGGTTTCAGGGCCCTGTGATGTGAGGAACTCCCGCGAGTTG	1199
QY	1141	CCCGCGCTGTGCCAGGCTACTAGGAAATGTGGGCCCCCTGTCTTGTGTGAGCTGTGTGGAAAC	1200
Db	1193	CCCGCGCTGTGCCAGGCTACTAGGAAATGTGGGCCCCCTGTCTTGTGTGAGCTGTGTGGAAAC	1251
QY	1201	CAGCGCAGTGTCCCTTACGGGGTGTCTCTCAAGACGACTGTGCCGTGTGCGAGCTGTGCGTTC	1261

Dp	1253	CACGGCAGATGCCCTTACGAGGGGTGTCCTCAAGAAGACTGCGCCGCTGCAGACTGCGGCT	1312
Qy	1261	ACCCCAGATGCGGGTTCTGTGTCCCGGGAGAAAGCCCACAGGGCTCTGTGTGGCCCCCGAG	1320
Dp	1313	ACCCCAGAGCGGGTGTCGTGTGCCCGGAAGAACCCAGGGCTCTGTGTGGCCCCCGAG	1372
Qy	1321	GAGAGGACAAGAACCCCGCTCGCTGATGTGACGTGTCCGCAAGACAGACGCCCTTG	1380
Dp	1373	GAGAGGACAAGAACCCCGCTCGCTGATGTGACGTGTCCGCAAGACAGACGCCCTTG	1432
Qy	1381	CAGGTGTAACGGCTTCGTGTGGGGCTGCTGTGGCGCTGGTGTGGTCCCCAAGCTCTTGGGGC	1440
Dp	1433	CAGGTGTAACGGCTTCGTGTGGGGCTGCTGTGGCGCTGGTGTGGTCCCCAAGCTCTTGGGGC	1492
Qy	1441	TCCAGGCAACAAGACCGCGCTTCCCTCAGNACAACAAGAAATTCACTCCCTGGGAG	1500
Dp	1493	TCCAGGCAACAAGACCGCGCTTCCCTCAGNACAACAAGAAATTCACTCCCTGGGAG	1552
Qy	1501	CATGCGAAGCTCTGCTGTGCAAGSACSTACGCTGGAAGATGAGCGGTGGGAACTGCGCTTG	1560
Dp	1553	CATGCGAAGCTCTGCTGTGCAAGSACSTACGCTGGAAGATGAGCGGTGGGAACTGCGCTTG	1612
Qy	1561	CTGGCAGAGACCCAGAGGGTTGACTGTATTCGCGCGCAAGACAACGCTGTGCTGAGAG	1620
Dp	1613	CTGGCAGAGACCCAGAGGGTTGACTGTATTCGCGCGCAAGACAACGCTGTGCTGAGAG	1672
Qy	1621	ATCCGTGCGAAGTTCCTGTGCACTGGCTGTATGATGTATACGTCCGTGAGCTGTCCAGTCT	1680
Dp	1673	ATCCGTGCGAAGTTCCTGTGCACTGGCTGTATGATGTATACGTCCGTGAGCTGTCCAGTCT	1732
Qy	1681	TTCTTTTATGTACAGGAGACCAGCTTCAAAGAACAGGCTCTTTTCTACCCGAGAGT	1740
Dp	1733	TTCTTTTATGTACAGGAGACCAGCTTCAAAGAACAGGCTCTTTTCTACCCGAGAGT	1792
Qy	1741	GTCGTGAGCAAGTTGCAAGAGCATTTGAAATGACACAGACTTGAAGAAGGTGTGACCTCG	1800
Dp	1793	GTCGTGAGCAAGTTGCAAGAGCATTTGAAATGACACAGACTTGAAGAAGGTGTGACCTCG	1852
Qy	1801	GAGCTGTGGAAGCAGAGGTCAGGACCATTCGGAACCCAGGCCCGCTTGTGACGTCC	1860
Dp	1853	GAGCTGTGGAAGCAGAGGTCAGGACCATTCGGAACCCAGGCCCGCTTGTGACGTCC	1912
Qy	1861	AGACTCCGCTTCACTCCCAAGCCTGAGGGGTGGCGCATTTGGAACATGSACTAGTC	1920
Dp	1913	AGACTCCGCTTCACTCCCAAGCCTGAGGGGTGGCGCATTTGGAACATGSACTAGTC	1972
Qy	1921	GTGGAAGCAGAACGTTCCGAGAGAAAAGAGGCCGAGCGTTCACCTTGAGGGTGAAG	1980
Dp	1973	GTGGAAGCAGAACGTTCCGAGAGAAAAGAGGCCGAGCGTTCACCTTGAGGGTGAAG	2032
Qy	1981	GCACTGTTCAAGCGTGTCAACTYACGACGGGGCGGGGCCCGGCTCTGTGGGCGCTCT	2040
Dp	2033	GCACTGTTCAAGCGTGTCAACTYACGACGGGGCGGGGCCCGGCTCTGTGGGCGCTCT	2092
Qy	2041	GTGCTGGGCTTGAAGCATATCCACAGGGCCTGGCGCACTTCTGTGCTGTGTGGGGC	2100
Dp	2093	GTGCTGGGCTTGAAGCATATCCACAGGGCCTGGCGCACTTCTGTGCTGTGTGGGGC	2152
Qy	2101	CAGAACCCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACCC	2160
Dp	2153	CAGAACCCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACCC	2212
Qy	2161	ATCCCCCAGACAGGCTCACAGAGGTATATGCCACGATCATCAAAACCCAGAACAGTAC	2220
Dp	2213	ATCCCCCAGACAGGCTCACAGAGGTATATGCCACGATCATCAAAACCCAGAACAGTAC	2272
Qy	2221	TGCGTGTGCGTATGTGCGGTGTTCAGAAAGCGGCCCATGGGCACTGTCCCAAGCGCTTC	2280
Dp	2273	TGCGTGTGCGTATGTGCGGTGTTCAGAAAGCGGCCCATGGGCACTGTCCCAAGCGCTTC	2332
Qy	2281	AAAGGCCACGTCTTACCTTGAAGACACTTCAGCCGATCATTTGGAACAGTTCTGTGCTCAC	2340
Dp	2333	AAAGGCCACGTCTTACCTTGAAGACACTTCAGCCGATCATTTGGAACAGTTCTGTGCTCAC	2392

QY 2341 CTGAGAGAGACCAAGCCGCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2400
Db 2393 CTGAGAGAGACCAAGCCGCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2452
QY 2401 GAGGCGAGAGAGCTGCTCTTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2460
Db 2453 GAGGCGAGAGAGCTGCTCTTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2512
QY 2461 ATCAGAGAGAGAGCTGCTCTTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2520
Db 2513 ATCAGAGAGAGAGCTGCTCTTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2572
QY 2521 CTGCTCTGAGAGAGCTGCTCTTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2580
Db 2573 CTGCTCTGAGAGAGCTGCTCTTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2632
QY 2581 GACGAGAGAGAGCTGCTCTTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2640
Db 2633 GACGAGAGAGAGCTGCTCTTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2692
QY 2641 GCGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2700
Db 2693 GCGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2752
QY 2701 TTGCGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2760
Db 2753 TTGCGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2812
QY 2761 GTTCAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2820
Db 2813 GTTCAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2872
QY 2821 CTGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2880
Db 2873 CTGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2932
QY 2881 TTCAAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2940
Db 2933 TTCAAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 2992
QY 2941 CTGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3000
Db 2993 CTGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3052
QY 3001 AACATCTACAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3060
Db 3053 AACATCTACAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3112
QY 3061 CCAATCTACAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3120
Db 3113 CCAATCTACAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3172
QY 3121 GCTCTCTCTGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3180
Db 3173 GCTCTCTCTGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3232
QY 3181 GGGGCGCGCGCGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3240
Db 3233 GGGGCGCGCGCGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3292
QY 3241 CTGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3300
Db 3293 CTGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3352
QY 3301 CAGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3360
Db 3353 CAGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3412
QY 3361 AACCGGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3411
Db 3413 AACCGGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 3463

RESULT 2
US-09-990-080-1
; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/2586
; CURRENT APPLICATION NUMBER: US/09/990,080
; PRIORITY FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-990-080-1

Query Match 100.0%; Score 3411; DB 9; Length 4015;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 60
Db 53 GCGATGCGCGCGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 112
QY 61 GAGGTGCTGCGCTGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 120
Db 113 GAGGTGCTGCGCTGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 172
QY 121 CAGGCGGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 180
Db 173 CAGGCGGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 232
QY 181 TGGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 240
Db 233 TGGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 292
QY 241 CTGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 300
Db 293 CTGAGAGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 352
QY 301 GGGTCTGCGCTGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 360
Db 353 GGGTCTGCGCTGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 412
QY 361 CCGAGCTACCTGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 420
Db 413 CCGAGCTACCTGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 472
QY 421 CTGCTGCGCGCGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 480
Db 473 CTGCTGCGCGCGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 532
QY 481 GTGCTGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 540
Db 533 GTGCTGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 592
QY 541 GCTGCGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 600
Db 593 GCTGCGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 652
QY 601 GAGGCGGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 660
Db 653 GAGGCGGAGAGAGCTTCTCTGAGAGCTTCTCTGAGAGATGCCGTGCTCATCGAGAGAGCTTCTCTGAAT 712

QY	661	GGTGGCAGAGGAGCGCGGGGGCAGTGGCAGCGCAAGTCTCCGTTGGCCAAAGAGCCCAAG	720
Db	713	GGTGGCAGAGGAGCGCGGGGGCAGTGGCAGCGCAAGTCTCCGTTGGCCAAAGAGCCCAAG	772
QY	721	CGTGGCGCTGGCCCTTGAAGCCGGAAGCGCCGTTGGCAAGGAGTCTGGGCCCAACCG	780
Db	773	CGTGGCGCTGGCCCTTGAAGCCGGAAGCGCCGTTGGCAAGGAGTCTGGGCCCAACCG	832
QY	781	GGCAGGACGGGTGAGCCAGAGTGAACGTGGTTTCTGTGTGTGTCACTTCCAGACCCGGCC	840
Db	833	GGCAGGACGGGTGAGCCAGAGTGAACGTGGTTTCTGTGTGTGTCACTTCCAGACCCGGCC	892
QY	841	GAAGAAGCCACTCTTTTGAAGGGTGGCTCTTGACAGCGGCCACTCCACCATCCGTG	900
Db	893	GAAGAAGCCACTCTTTTGAAGGGTGGCTCTTGACAGCGGCCACTCCACCATCCGTG	952
QY	901	GGCCGCGCAGACCAACGCGGGGCCCCCATCAACATGGGGGCAACAGTCCCTGGGACAG	960
Db	953	GGCCGCGCAGACCAACGCGGGGCCCCCATCAACATGGGGGCAACAGTCCCTGGGACAG	1012
QY	961	CCTTGTCTCCCGGCTGAGCCCAAGCAACACTTCTTACTCTCAAGCGCAACAAGAG	1020
Db	1013	CCTTGTCTCCCGGCTGAGCCCAAGCAACACTTCTTACTCTCAAGCGCAACAAGAG	1072
QY	1021	CAGCTGCGGCGCTCTCTCTCTCACTCAAGCTGTCAAGGCCAGCTCATCTGGCGCTGGAG	1080
Db	1073	CAGCTGCGGCGCTCTCTCTCTCACTCAAGCTGTCAAGGCCAGCTCATCTGGCGCTGGAG	1132
QY	1081	CTGTGTGAGACCACTTTCTGGGTTTCAGGCCCTGTGATTCAGAGCACTCCCGCAGATTG	1140
Db	1133	CTGTGTGAGACCACTTTCTGGGTTTCAGGCCCTGTGATTCAGAGCACTCCCGCAGATTG	1192
QY	1141	CCCGCGCTGCCCGAGCGCTACTGGCAAAATGGCGCCCTGTTCTGAGAGCTGTTGGAGAC	1200
Db	1193	CCCGCGCTGCCCGAGCGCTACTGGCAAAATGGCGCCCTGTTCTGAGAGCTGTTGGAGAC	1252
QY	1201	CACGCGCAGTGCCTTACGAGGGTGTCTCTCAAGACGCACTGGCCGCTGCGAGCTCGGTC	1260
Db	1253	CACGCGCAGTGCCTTACGAGGGTGTCTCTCAAGACGCACTGGCCGCTGCGAGCTCGGTC	1312
QY	1261	ACCCGAGCAGCGCGGTGTCTGTGACCCGGGAGAGCCCGAGGCTCTGTGGCGGCCCCCGAG	1320
Db	1313	ACCCGAGCAGCGCGGTGTGTGACCCGGGAGAGCCCGAGGCTCTGTGGCGGCCCCCGAG	1372
QY	1321	GAGGAGGACACAGAACCCCGCTGCGCTGTGCACTTCCGACAGCAGCAGCCCTTGG	1380
Db	1373	GAGGAGGACACAGAACCCCGCTGCGCTGTGCACTTCCGACAGCAGCAGCCCTTGG	1432
QY	1381	CAGGTGTACGGCTTGTGTGGGGGCTGGCTGGCGCGCGGTGTGTGACCCCGAGCTCTGGGGC	1440
Db	1433	CAGGTGTACGGCTTGTGTGGGGGCTGGCTGGCGCGCGGTGTGTGACCCCGAGCTCTGGGGC	1492
QY	1441	TTCAGGCAACAAGAACCGCGCTTCTCTCAAGAACACCAAGATTATCTCCCTGGGGAAG	1500
Db	1493	TTCAGGCAACAAGAACCGCGCTTCTCTCAAGAACACCAAGATTATCTCCCTGGGGAAG	1552
QY	1501	CATGCGCAAGCTCTGCTGTGAGGAGGTGACGTGGAAGATGAGCGTGGCGGGAATGGCGCTTGG	1560
Db	1553	CATGCGCAAGCTCTGCTGTGAGGAGGTGACGTGGAAGATGAGCGTGGCGGGAATGGCGCTTGG	1612
QY	1561	CTGGCGCAGAGCCCAAGGGGTTGGCTGTGTTCCGGCCGACAGACACCTCTGCTGAGAG	1620
Db	1613	CTGGCGCAGAGCCCAAGGGGTTGGCTGTGTTCCGGCCGACAGACACCTCTGCTGAGAG	1672
QY	1621	ATCTGGCGCAAGTTCTCTGAGCTGGCTGATGATGTGTAACGTGTGAGACCTGTCAAGTCT	1680
Db	1673	ATCTGGCGCAAGTTCTCTGAGCTGGCTGATGATGTGTAACGTGTGAGACCTGTCAAGTCT	1732
QY	1681	TTCCTTTATGTCAACGAGACCACTGTTCAAAAAGAACAGGCTCTTTTCTTACCGAAGAGT	1740
Db	1733	TTCCTTTATGTCAACGAGACCACTGTTCAAAAAGAACAGGCTCTTTTCTTACCGAAGAGT	1792

QY	1741	GTCTGAGCAAGTTGCAAGATTTGAATCAGACGACTTGAAGAGGGTACGTGGC	1800
Db	1739	GTCTGAGCAAGTTGCAAGATTTGAATCAGACGACTTGAAGAGGGTACGTGGC	1852
QY	1801	GAGCTGTGGAAGCAGAGGTCAAGCAGATCGGAAAGCCAGGCGCCCTGTGACGTCC	1866
Db	1853	GAGCTGTGGAAGCAGAGGTCAAGCAGATCGGAAAGCCAGGCGCCCTGTGACGTCC	1912
QY	1861	AGACTCCGCTTCATCCCCAGCCTGACGAGGCTGGGGCGAATTGTGAACATGACATGTC	1920
Db	1913	AGACTCCGCTTCATCCCCAGCCTGACGAGGCTGGGGCGAATTGTGAACATGACATGTC	1972
QY	1921	GTGGAGCCAGAACGTTCCGACAGAGAAAGAGGCCGAGCGCTTCACCTCGAGGGTGAAG	1986
Db	1973	GTGGAGCCAGAACGTTCCGACAGAGAAAGAGGCCGAGCGCTTCACCTCGAGGGTGAAG	2032
QY	1981	GCACGTGTCAAGGTGTCAACTAAGAGAGGAGCGGCGCCCGGCGCTCTGTGGGCGCTCT	2040
Db	2033	GCACGTGTCAAGGTGTCAACTAAGAGAGGAGCGGCGCCCGGCGCTCTGTGGGCGCTCT	2092
QY	2041	GTGCTGGGCTCTGAGCATATTCACAGGGCCTTGCGCACCTTTCGTGTGCTGTGTGGGCGC	2100
Db	2093	GTGCTGGGCTCTGAGCATATTCACAGGGCCTTGCGCGACCTTTCGTGTGCTGTGTGGGCGC	2152
QY	2101	CAGGACCGGCGGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGGGCGGCTACAGACCC	2160
Db	2153	CAGGACCGGCGGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGGGCGGCTACAGACCC	2212
QY	2161	ATCCCCCAGAACAGGCTTCACGAGAGTCAATGCGCAGATCATCAAAATCCACAGAACGTAC	2220
Db	2213	ATCCCCCAGAACAGGCTTCACGAGAGTCAATGCGCAGATCATCAAAATCCACAGAACGTAC	2272
QY	2221	TGCGGTGCGTGGATATGCGGTGTATCAAGAAAGGCGCCCATGGGCAACGTCCGAAAGCCCTTC	2280
Db	2273	TGCGGTGCGTGGATATGCGGTGTATCAAGAAAGGCGCCCATGGGCAACGTCCGAAAGCCCTTC	2332
QY	2281	AAAGACCAAGTCTTACCTTGAACAGACCTCACGCTGCATATGCGACAGTTGTGGTCTCAC	2340
Db	2333	AAAGACCAAGTCTTACCTTGAACAGACCTCACGCTGCATATGCGACAGTTGTGGTCTCAC	2392
QY	2341	CTGACAGAGACACAGCCCGCTGAAGGAGAGCCGTCATTCAGACGAGACTCCTCCCTGAAT	2400
Db	2393	CTGACAGAGACACAGCCCGCTGAAGGAGAGCCGTCATTCAGACGAGACTCCTCCCTGAAT	2452
QY	2401	GAGGTCAGCAAGTGGCTCTTGCAGCTTCTTCAAGCTTCAATGTGCACACAGCCGTGTGC	2460
Db	2453	GAGGTCAGCAAGTGGCTCTTGCAGCTTCTTCAAGCTTCAATGTGCACACAGCCGTGTGC	2512
QY	2461	ATCAGGGGCAAGTCTTACGTGCAGGTGCAGAGGATCCCGAGAGGCTCAATCCTCTCAGC	2520
Db	2513	ATCAGGGGCAAGTCTTACGTGCAGGTGCAGAGGATCCCGAGAGGCTCAATCCTCTCAGC	2572
QY	2521	CTGCTCTGACAGCTGTGTACTACGGGCACATGAGAAACAAGCTGTTTGTGGGGAATTCGGCGG	2580
Db	2573	CTGCTCTGACAGCTGTGTACTACGGGCACATGAGAAACAAGCTGTTTGTGGGGAATTCGGCGG	2632
QY	2581	GACGAGGCTGCTCTGCTTTGTGTGATGATTTCTGTGTGTGACACTCACTCACTCACAC	2640
Db	2633	GACGAGGCTGCTCTGCTTTGTGTGATGATTTCTGTGTGTGACACTCACTCACTCACAC	2692
QY	2641	GCGAAACCTTCTCAGAGACCCGTGTCCAGAGGTGCCCTGAGATATGGCTGCGGTGTGAAC	2700
Db	2693	GCGAAACCTTCTCAGAGACCCGTGTCCAGAGGTGCCCTGAGATATGGCTGCGGTGTGAAC	2752
QY	2701	TTGGGGAAGACAGGTGTGAACCTTCCCTGTAGAAAGCAGAGGCCCTGTGGTGCACGGCTTTT	2760
Db	2753	TTGGGGAAGACAGGTGTGAACCTTCCCTGTGTAGAAAGCAGAGGCCCTGTGGTGCACGGCTTTT	2812
QY	2761	GTTCAAGATGCGCGGCCACCGGCTAATTCCTCGATGTGGGCGCCGTGTGTGTGATAACCGGAC	2820
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Db 2873 CTGAGGTGACAGGCGACTACTCCAGCTATGCCGAGCTCCATCAGAGCCACTCTACCC 2932
QY 2881 TTCAACCGCGGCTTTCAAGGCTGGAGAGAACATCGTCGCAAACTCTTTGGGGTCTTGGCG 2940
Db 2933 TTCAACCGCGGCTTTCAAGGCTGGAGAGAACATCGTCGCAAACTCTTTGGGGTCTTGGCG 2992
QY 2941 CTGAAGTGTACAGGCTGTGTTCTGATTTGGCAGGTGACAGGCTCCAGAGGCTGGAGC 3000
Db 2993 CTGAAGTGTACAGGCTGTGTTCTGATTTGGCAGGTGACAGGCTCCAGAGGCTGGAGC 3052
QY 3001 AACATCTACAAAGTCTCTCTGTCGACAGGCTGACAGGCTTTCAGCATGTGTGTGACGCTC 3060
Db 3053 AACATCTACAAAGTCTCTCTGTCGACAGGCTGACAGGCTTTCAGCATGTGTGTGACGCTC 3112
QY 3061 CCATTCATCAGAGGCTGGAGAGAACCCCACTTTTCTGCGGCTGATCTCTGACAGC 3120
Db 3113 CCATTCATCAGAGGCTGGAGAGAACCCCACTTTTCTGCGGCTGATCTCTGACAGC 3172
QY 3121 GCTCTCTCTGCTACTCTCACTCTGAAAGCCAAAGACGACAGGATGTGCTGGGGCCAAAG 3180
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RESULT 3
US-09-843-676-224
Sequence 224, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morlin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-843-676-224

Query Match 100.0%; Score 3411; DB 9; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCGCGGCGCTCCCGCTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db 53 GCATGCGCGGCGCTCCCGCTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 112
QY 61 GAGGTGCTGCGGCTGCGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 113 GAGGTGCTGCGGCTGCGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 172
QY 121 CAGCGCGGAGACCGCGGCTTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 173 CAGCGCGGAGACCGCGGCTTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 232
QY 181 TGGAGCGACGCGCGGCG 240
Db 233 TGGAGCGACG 292
QY 241 CTGCTGCGCGGAGTGTGCAAGAGCTGTGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 293 CTGCTGCGCGGAGTGTGCAAGAGCTGTGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GCGTTCGCGCTGTGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 353 GCGTTCGCGCTGTGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGCAGCTACCTGCGCAACGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 413 CGCAGCTACCTGCGCAACGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472
QY 421 CTGCTGCGCGGAGTGTGCAAGAGCTGTGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db 473 CTGCTGCGCGGAGTGTGCAAGAGCTGTGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 532
QY 481 GTGCTGTGAGCTCCAGCTGCGCTACGAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db 533 GTGCTGTGAGCTCCAGCTGCGCTACGAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 592
QY 541 GCTGCGACACGAGCG 600
Db 593 GCTGCGACACGAGCG 652

QY	601	GAAAGGAGCTGTGAAACCACTAAGCTCAAGAGAGGCGGGAGTCCCTCGTGGCTGACGACGCGCG	660
Db	653	GAAAGGAGCTGTGAAACCACTAAGCTCAAGAGAGGCGGGAGTCCCTCGTGGCTGACGACGCGCG	712
QY	661	GGTGTGAGAGAGCGCGGGGGCAAGTGTCCAGCCGAAGTCTTGCCTTGCCCAAGAGGCCAGG	720
Db	713	GGTGTGAGAGAGCGCGGGGGCAAGTGTCCAGCCGAAGTCTTGCCTTGCCCAAGAGGCCAGG	772
QY	721	CGTGGCCATCCCTCTGAGCGGAGCGGAGCGCCGCTTGGGCAAGGGAGTCTTGAGCCACCGG	780
Db	773	CGTGGCCATCCCTCTGAGCGGAGCGGAGCGCCGCTTGGGCAAGGGAGTCTTGAGCCACCGG	832
QY	781	GGCAGGACGCTGTGACCGAGTGAACGTGGTCTTGTGTGTGTCACTTGCCAGACCGCGC	840
Db	833	GGCAGGACGCTGTGACCGAGTGAACGTGGTCTTGTGTGTGTCACTTGCCAGACCGCGC	892
QY	841	GAAAGAACCACTCTTTTGGAGGGGTGGCTCTTGAGCAAGCCCACTCCACCCATCCGATG	900
Db	893	GAAAGAACCACTCTTTTGGAGGGGTGGCTCTTGAGCAAGCCCACTCCACCCATCCGATG	952
QY	901	GGCGCGCAGACCAACGCGGGGCCCCCATTCACATGTCCGACCAACAGTCCCTGTGGACAG	960
Db	953	GGCGCGCAGACCAACGCGGGGCCCCCATTCACATGTCCGACCAACAGTCCCTGTGGACAG	1011
QY	961	CCTTGTCCCCGGGTGTATACGCCAGACCAAGACCTTCCTATCTCTCAGGCGACAAAGAG	1021
Db	1013	CCTTGTCCCCGGGTGTATACGCCAGACCAAGACCTTCCTATCTCTCAGGCGACAAAGAG	1077
QY	1021	CAGTGTGGGCTTCTCTTCTCACTCAAGCTCTTGAGGCCCAAGCTGACTGGGCTGTGGAGG	1086
Db	1073	CAGTGTGGGCTTCTCTTCTCACTCAAGCTCTTGAGGCCCAAGCTGACTGGGCTGTGGAGG	1133
QY	1081	CTGTGTGAGACCATCTTTCTGGGATTCAGAGCCCTTGAGATGCGAGAGGATCCCGCCAGATTG	1141
Db	1133	CTGTGTGAGACCATCTTTCTGGGATTCAGAGCCCTTGAGATGCGAGAGGATCCCGCCAGATTG	1197
QY	1141	CCCCGCTGTCCCAAGGCTCATCTGGCAATATGCGGCCCTCTGTTCTTGAGACTCTTGGGAAC	1200
Db	1193	CCCCGCTGTCCCAAGGCTCATCTGGCAATATGCGGCCCTCTGTTCTTGAGACTCTTGGGAAC	1255
QY	1201	CAGCGCAGTGCCTCTACCGGGGTGTCTCTCAAGAGACGACGTGGCGCGCTGAGCTGTGGTGC	1266
Db	1253	CAGCGCAGTGCCTCTACCGGGGTGTCTCTCAAGAGACGACGTGGCGCGCTGAGCTGTGGTGC	1311
QY	1261	ACCCCAAGCAAGCCGAGTCTGTGTCCCGGAGAAAGCCCAAGGCTCTGTGTGCGGCCCCGAG	1320
Db	1313	ACCCCAAGCAAGCCGAGTCTGTGTCCCGGAGAAAGCCCAAGGCTCTGTGTGCGGCCCCGAG	1377
QY	1321	GAGAGAGACACAGACCCCGCTGCTGTGTGTGACCTGTCCGACAGACACAGACCCCTGAG	1386
Db	1373	GAGAGAGACACAGACCCCGCTGCTGTGTGTGACCTGTCCGACAGACACAGACCCCTGAG	1433
QY	1381	CAGGTGAAGGCTTGTGTGTGGGGCTGTGCTGTGGCGCGCTGGTGTCCCAAGGCTCTTGGGCG	1440
Db	1433	CAGGTGAAGGCTTGTGTGTGGGGCTGTGCTGTGGCGCGCTGGTGTCCCAAGGCTCTTGGGCG	1492
QY	1441	TCCAGGACACAGAACGCGCTTCTCAGAGAACCAAGAAATTCATCTCCCTGGGGAGAG	1500
Db	1493	TCCAGGACACAGAACGCGCTTCTCAGAGAACCAAGAAATTCATCTCCCTGGGGAGAG	1555
QY	1501	CATGCCAAGCTCTCGCTGAGAGAGTTACGTGTGAAGATGAGCGTGTGGGAGCTTGCGCTTGG	1566
Db	1553	CATGCCAAGCTCTCGCTGAGAGAGTTACGTGTGAAGATGAGCGTGTGGGAGCTTGCGCTTGG	1612
QY	1561	CTGCGCAGAGCCCAAGGGTTGGCTGTGTTTCCCGGCCCAAGAGACCGTCTGTGTGAGAGG	1620
Db	1613	CTGCGCAGAGCCCAAGGGTTGGCTGTGTTTCCCGGCCCAAGAGACCGTCTGTGTGAGAGG	1677
QY	1621	ATCTGTGGCCAAATTCCTGTGACATGAGCTGTATGAGAGTGTATACGTGTGAGAGCTGTCAAGTCT	1688
Db	1673	ATCTGTGGCCAAATTCCTGTGACATGAGCTGTATGAGAGTGTATACGTGTGAGAGCTGTCAAGTCT	1732

QY	1681	TTCTTTTATGTACACGAGAACACAGTTTCAAAAAGAACAGGCTCTTTTCTTACACGGAAGAGT	1740
Dp	1733	TTCTTTTATGTACAGGAGACCAAGTTTCAAAAAGAACAGGCTCTTTTCTTACACGGAAGAGT	1792
QY	1741	GTCTGAGACGAACTTTCAGAAAGCATTTGGATTCAGACAGCATTTGAAAGGGGTGACGTGGCG	1800
Dp	1793	GTCTGAGACGAACTTTCAGAAAGCATTTGGAAATCAGACAGCATTTGAAAGGGGTGACGTGGCG	1852
QY	1801	GAGCTGTGCGAAGCAGAGAGTCAAGCAGCATGGGAAAGCAGAGCCCGCCTCTCTGACGTCC	1860
Dp	1853	GAGCTGTGCGAAGCAGAGAGTCAAGCAGCATGGGAAAGCAGAGCCCGCCTCTCTGACGTCC	1912
QY	1861	AACATCCCGCTTCATCCCGAACGCTGACGGGCTGGCGCGAATTGTGAACATGGAATTAAGTC	1920
Dp	1913	AACATCCCGCTTCATCCCGAACGCTGACGGGCTGGCGCGAATTGTGAACATGGAATTAAGTC	1972
QY	1921	GTGGAGCCAGAACCGTTCCGACAGAAAGAGGGCCGAGACGCTCAACCTCGAGGGTGAAG	1980
Dp	1973	GTGGAGCCAGAACCGTTCCGACAGAAAGAGGGCCGAGACGCTCAACCTCGAGGGTGAAG	2032
QY	1981	GCACCTGTTCACGCGTCTCACTTACGAGGGGGCGGGCGCCCGCCTCTCTGGCGCTCT	2040
Dp	2033	GCACCTGTTCACGCGTCTCACTTACGAGGGGGCGGGCGCCCGCCTCTCTGGCGCGCTCT	2092
QY	2041	GTGCTGGGCTTGACGATATCCAGAGGCTTGCGGACACTTCGTGCTGCGGTGCGGAGC	2100
Dp	2093	GTGCTGGGCTTGACGATATCCAGAGGCTTGCGGACACTTCGTGCTGCGGTGCGGAGC	2152
QY	2101	CAGGACCCGCGCGCTGAGCTGTACTTTGTCAAAGTGGATGTGACGGGCGGTACGACAC	2160
Dp	2153	CAGGACCCGCGCGCTGAGCTGTACTTTGTCAAAGTGGATGTGACGGGCGGTACGACAC	2212
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Dp	2213	ATCCCCCAGAGCAGAGCTTCACGAGAGTATCGCCAGCATCATCAACCCCAAGAACGTAC	2272
QY	2221	TGCGTGGCTCGGTATGCGCGTGTCTCAAGAGGCCGCCCATGGGACGTCGCCAGAGCCTTC	2280
Dp	2273	TGCGTGGCTCGGTATGCGCGTGTCTCAAGAGGCCGCCCATGGGACGTCGCCAGAGCCTTC	2332
QY	2281	AAGAGCCACGTCTCTACTTGAACAGACCTCCAGCGCGTACATGCGACAGTTCGTGGCTCAC	2340
Dp	2333	AAGAGCCACGTCTCTACTTGAACAGACCTCCAGCGCGTACATGCGACAGTTCGTGGCTCAC	2392
QY	2341	CTGCAAGAGAGACCAACCCCGCTGAGGGAGTGCCTGTCTTCGACAGAGACTCTCTCCCTGAAT	2400
Dp	2393	CTGCAAGAGAGACCAACCCCGCTGAGGGAGTGCCTGTCTTCGACAGAGACTCTCTCCCTGAAT	2452
QY	2401	GAGGCGACGATGGCTCTTTCGACAGTCTTCGACGCTTCGACATGTGCGCACACGCGCGTGGCG	2460
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QY	2521	CTGCTCTGACGCTGTGTCTACCGGAGCATGAGAACAAAGCTGTTTGGGAGGATTCGGCGG	2580
Dp	2573	CTGCTCTGACGCTGTGTCTACCGGAGCATGAGAACAAAGCTGTTTGGGAGGATTCGGCGG	2632
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Dp	2693	GCGAAAAACCTTCTCAAGAACCTTGTCGAGGTGCTCCCTGAGTATGAGCTGCGGTGAAC	2752
QY	2701	TTGGGAGAAAGCAGTGTGTGAACCTTCCCTGTGAGAGAGAGGCCCTCGAGTGTGACAGGCTTTT	2760
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Db 2513 ATGAGGGGCAAGTCTTCACTGAGTGGCAGGGGATCCCGAGGCTTCATCTCTCCACG 2572
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Db 2573 CTGCTCTGACGCTGTGCTAGCGGCAACAGAGAGAAAGAGCTGTTTCCGCGGATTCGGCGG 2632
Qy 2581 GACGGGCTGCTCTGCTAGCTTGTGATGATTTCTTGTGTGTGACACTTCACTCACTCCAC 2640
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Db 2693 GCGAAAACCTTCTCTGAGAACCTTCCCTGTAGAGAGAGGCGCTGAGTATGCTGCTGAAC 2752
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Db 2753 TTGGGAGAGACAGTGTGAGAACCTTCCCTGTAGAGAGAGGCGCTGAGTATGCTGCTGAAC 2812
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Qy 3001 AACATCTACAGATCTCTCTGCTGAGCGGTACAGGTTTCAAGATGTGTGCTGAGCTC 3060
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RESULT 5

US-10-053-758-224

; Sequence 224, Application US/10053758

; Publication No. US20030032075A1

; GENERAL INFORMATION:

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; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
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transcriptase (hTRT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224
Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGATGCGGCGGCTCTCCGCTCCGAGCCGAGCGCTCTCTGCTGCGAGCACTACCGC 60
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Db 353 GAGCTTGTGAGTGTGACAGAGGCTGTGTGAGCGCGGAGCGCGGAGCGCTTCACACAGCGTG 412
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Db 413 CGAGAGTGTGAGTGTGACAGAGGCTGTGTGAGCGCGGAGCGCGGAGCGCTTCACACAGCGTG 472
Qy 421 CTGCTGTGAGCGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAGCGCTTCCTTT 480
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Db 593 GCTGTGAGTGTGAGCGCGGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAGCGCTTCCTTT 652
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Qy 841 GAAAGAGCGAGCTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAGCGCTTCCTTT 900
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Db 953 GGTGTGAGAGGAGCGCGGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAGCGCTTCCTTT 1012
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Db 1073 GGTGTGAGAGGAGCGCGGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAGCGCTTCCTTT 1132
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Db 1253 GGTGTGAGAGGAGCGCGGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAGCGCTTCCTTT 1312
Qy 1261 GGTGTGAGAGGAGCGCGGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAGCGCTTCCTTT 1320
Db 1313 GGTGTGAGAGGAGCGCGGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAGCGCTTCCTTT 1372

Qy 1321 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1380
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Db 1433 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1492
Qy 1441 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1500
Db 1493 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1552
Qy 1501 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1560
Db 1553 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1612
Qy 1561 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1620
Db 1613 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1672
Qy 1621 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1680
Db 1673 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1732
Qy 1681 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1740
Db 1733 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1792
Qy 1741 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1800
Db 1793 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1852
Qy 1801 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1860
Db 1853 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1912
Qy 1861 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1920
Db 1913 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1972
Qy 1921 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 1980
Db 1973 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2032
Qy 1981 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2040
Db 2033 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2092
Qy 2041 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2100
Db 2093 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2152
Qy 2101 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2160
Db 2153 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2212
Qy 2161 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2220
Db 2213 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2272
Qy 2221 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2280
Db 2273 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2332
Qy 2281 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2340
Db 2333 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2392
Qy 2341 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2400
Db 2393 GAGAGAGACACAGACCCCGGCTGTGTGAGCGAGCGAGTGTGTGACCTGTGCTGAGCGAG 2452

QY	661	GGTGGCAGAGAGGCGCGGAGGAGTCCAGAGCCGAAGCTGCGGTGGCCAGAGAGCCACAG	722
Dp	713	GGTGGCAGAGAGGCGCGGAGGAGTCCAGAGCCGAAGCTGCGGTGGCCAGAGAGCCACAG	772
QY	721	CTGGGCGCTGCCCCCTGAGACCGGAGCGGACGCCCGTTGGGCAAGGGTCTGGGCTCCACCCG	780
Dp	773	CGTGGGCTGCCCCCTGAGAGCCGAGAGCGGACGCCCGTTGGGCAAGGGTCTGGGCTCCACCCG	832
QY	781	GGCAGAGACGGTGGACCCAGGTGACCGTGGATTCTGTGGGTGTAACCTGGCACAACCGGC	840
Dp	833	GGCAGAGACGGTGGACCCAGGTGACCGTGGATTCTGTGGGTGTAACCTGGCACAACCGGC	892
QY	841	GAAGAAACCACCTCTTTGGAGGGTGCCTCTTGGCAGACGGGCCATTCACCCATCCGTG	900
Dp	893	GAAGAAACCACCTCTTTGGAGGGTGCCTCTTGGCAGACGGGCCATTCACCCATCCGTG	952
QY	901	GGCGGCGCAGACCAAGCGGGGGCCCCCATTCACATTCGGGGGACCAACAGTCCCTGGGACAG	960
Dp	953	GGCGGCGCAGACCAAGCGGGGGCCCCCATTCACATTCGGGGGACCAACAGTCCCTGGGACAG	1012
QY	961	CCTTGTCCCCGGGTGACGCGCAGACCAAGCACTTCTCTTACTCTTACGCGACAGAGAG	1020
Dp	1013	CCTTGTCCCCGGGTGACGCGCAGACCAAGCACTTCTCTTACTCTTACGCGACAGAGAG	1072
QY	1021	CACCTGCGGCGCTTCTCTTCTTACTTACGCTCTTGAGAGCCACGCTGACTGGCGCTGGAGG	1080
Dp	1073	CACCTGCGGCGCTTCTCTTCTTACTTACGCTCTTGAGAGCCACGCTGACTGGCGCTGGAGG	1133
QY	1081	CTGTGGAGAACATCTTTCTGGGTTCCAGGCCCTGGATGACAGGACCTCCCGCAGATTG	1140
Dp	1133	CTGTGGAGAACATCTTTCTGGGTTCCAGGCCCTGGATGACAGGACCTCCCGCAGATTG	1192
QY	1141	CCCCGCGTCCCCCAGGCGTACACGCGAATGGCGGCCCTGTGTTCTGGAGCGTCTTGGGAAC	1200
Dp	1193	CCCCGCGTCCCCCAGGCGTACACGCGAATGGCGGCCCTGTGTTCTGGAGCGTCTTGGGAAC	1252
QY	1201	CACGCGCAGTGGCCCTTACCGGAGTGTCTCTCAAGACGCACTGCCGTGCAGGTGGGTC	1260
Dp	1253	CACGCGCAGTGGCCCTTACCGGAGTGTCTCTCAAGACGCACTGCCGTGCAGGAGTGGGTC	1312
QY	1261	ACCCGACGACCGGAGTCTGTGTGCTCCGGGAGAAAGCCCAAGGCTTGTGTGGCGTCCCGAG	1320
Dp	1313	ACCCGACGACCGGAGTCTGTGTGCTCCGGGAGAAAGCCCAAGGCTTGTGTGGCGTCCCGAG	1372
QY	1321	GAGAGAGACACAGACCCCGCTGCGCTGTGTGACCTGCTCCGACGACACAGACGCCCTGG	1380
Dp	1373	GAGAGAGACACAGACCCCGCTGCGCTGTGTGACCTGCTCCGACGACACAGACGCCCTGG	1432
QY	1381	CAGGTGTACGGCTTGTGTGGGAGCTGCTGTGCGCGGCTGGTGCCGCCAGGCTCTTGGAGC	1440
Dp	1433	CAGGTGTACGGCTTGTGTGGGAGCTGCTGTGCGCGGCTGGTGCCGCCAGGCTCTTGGAGC	1492
QY	1441	TCCAGGACACAGAACGCGCTTCTCTAGGAACACCAAGAAATTCACTCCCTGGGGAAG	1500
Dp	1493	TCCAGGACACAGAACGCGCTTCTCTAGGAACACCAAGAAATTCACTCCCTGGGGAAG	1552
QY	1501	CATGCCAAGCTCTCGCTGACGAGAGCTGAGTGAAGTGAAGCTGCGGAGCTGCGCTTGG	1560
Dp	1553	CATGCCAAGCTCTCGCTGACGAGAGCTGAGTGAAGTGAAGCTGCGGAGCTGCGCTTGG	1612
QY	1561	CTGCGCAGAGAGCCAGGGGTTGGCTGTGCTTCGGGCGCACAAGACCGTCTGGGTGAGAG	1620
Dp	1613	CTGCGCAGAGAGCCAGGGGTTGGCTGTGCTTCGGGCGCACAAGACCGTCTGGGTGAGAG	1672
QY	1621	ATCTGCGCAAGTCTCTGACCTGAGTGAATGAGTGTAGTGTGCTGTGACAGTCTCAGTCT	1680
Dp	1673	ATCTGCGCAAGTCTCTGACCTGAGTGAATGAGTGTAGTGTGCTGTGACAGTCTCAGTCT	1732
QY	1681	TTCCTTTATGTACGAGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTACGAGGAAGAT	1740
Dp	1733	TTCCTTTATGTACGAGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTACGAGGAAGAT	1792

QY	1741	GTCTGGAGCAAGTTGGCAAAGCATTTGAATCAGACAGACATTTGAAAGAGGTGACCTGGG	1800
Db	1793	GTCTGGAGCAAGTTGGCAAAGCATTTGAATCAGACAGACATTTGAAAGAGGTGACCTGGG	1852
QY	1801	GAGCTGTCCGAAAGCAGAGGTCAGGCGACATCCGGAGCCAGCCCGCTCGTCAAGCTCC	1860
Db	1853	GAGCTGTCCGAAAGCAGAGGTCAGGCGACATCCGGAGCCAGCCCGCTCGTCAAGCTCC	1912
QY	1861	AGACTCGGCTTCATCCCAAGCCTGAGAGGCGCTGGGCGCATTTGTGAACTATGACTAGTCC	1920
Db	1913	AGACTCGGCTTCATCCCAAGCCTGAGAGGCGCTGGGCGCATTTGTGAACTATGACTAGTCC	1972
QY	1921	GTGGGAACCCAGAAAGCTTCCGACAGAAAAGAGGCGCAGAGCTCTCACTCGAGGGTGAAG	1980
Db	1973	GTGGGAACCCAGAAAGCTTCCGAGAAAAGAGGCGCAGAGGCTCTCACTCGAGGGTGAAG	2032
QY	1981	GCACTGTTCAGAGCTGCTCAACTACAGAGCGGCGCGGCCCGCCCTCGTGGCGGCTCT	2040
Db	2033	GCACTGTTCAGAGCTGCTCAACTACAGAGCGGCGCGGCCCGCCCTCGTGGCGGCTCT	2092
QY	2041	GTGCTGGGAGCTGAGACGATATCCACAGGGGCTGGCGCACCTTGTGCTGCTGTGCGGGCC	2100
Db	2093	GTGCTGGGAGCTGAGACGATATCCACAGGGGCTGGCGCACCTTGTGCTGCTGTGCGGGCC	2152
QY	2101	CAGACACCCGCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGATACAGCAC	2160
Db	2153	CAGACACCCGCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGATACAGCAC	2212
QY	2161	ATCCCCCAGAGCAGGCTCACAGGAGTATATGCCAGCATCAATCAAACTCCAGAACAGTAC	2220
Db	2213	ATCCCCCAGAGCAGGCTCACAGGAGTATATGCCAGCATCAATCAAACTCCAGAACAGTAC	2272
QY	2221	TGCGTGGCGGTATGCGGTGATCCAGAAAGCGCGCCCATGGGCACTGCCCAAGGCGCTTC	2280
Db	2273	TGCGTGGCGGTATGCGGTGATCCAGAAAGCGCGCCCATGGGCACTGCCCAAGGCGCTTC	2332
QY	2281	AAGAGCCACGCTCTTACTTGTGACAGACCTCCAGCCGATCATATGGACAGCTTCGTGGCTCAC	2340
Db	2333	AAGAGCCACGCTCTTACTTGTGACAGACCTCCAGCCGATCATATGGACAGCTTCGTGGCTCAC	2392
QY	2341	CTGCAGAGAGACAGACCCGCTGAGGAGATGCCGTGTCATCCAGACAGAGCTCTCCCTGAAT	2400
Db	2393	CTGCAGAGAGACAGACCCGCTGAGGAGATGCCGTGTCATCCAGACAGAGCTCTCCCTGAAT	2452
QY	2401	GAGGCGAGCAGTGGGCTCTTCAGAGCTTCTCTAGAGCTTCAATATGGGCCACAGCGGCTGGCG	2460
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QY	2461	ATCAGGGGCAAGTCTCACTGTCAGAGTGCAGAGGATCCCGAGGAGCTTCATCTCTCCAGC	2520
Db	2513	ATCAGGGGCAAGTCTCACTGTCAGAGTGCAGAGGATCCCGAGGAGCTTCATCTCTCCAGC	2572
QY	2521	CTGCTCTGCAAGCCTGTGCTACAGCGGACATATGAGAAACAAGCTGTTTGGGGGGATTTCCGCGG	2580
Db	2573	CTGCTCTGCAAGCCTGTGCTACAGCGGACATATGAGAAACAAGCTGTTTGGGGGGATTTCCGCGG	2632
QY	2581	GACGGGCTGCTCTCGCTTTGTGTGATGATTTCTTGTGTGTGACACCTCACTCACTCAC	2640
Db	2633	GACGGGCTGCTCTCGCTTTGTGTGATGATTTCTTGTGTGTGACACCTCACTCACTCAC	2692
QY	2641	GCGAAAACCTTCTCAAGAACCTCGATCCAGAGGTCCCTGAGATATGGCTGAGGTGTAAC	2700
Db	2693	GCGAAAACCTTCTCAAGAACCTCGATCCAGAGGTCCCTGAGATATGGCTGAGGTGTAAC	2752
QY	2701	TTGCGAAGAGCAGGTGTGAACCTTCCCTGTAGAAAGCAGAGGCGCTGGGTGACGAGCTTTT	2760
Db	2753	TTGCGAAGAGCAGGTGTGAACCTTCCCTGTAGAAAGCAGAGGCGCTGGGTGACGAGCTTTT	2812
QY	2761	GTTTCAGATGCGCGGCCACAGGCGCTATTCCTCGGTGTGGCGGCGCTGCTGTGATACCCGGAC	2820
Db	2813	GTTTCAGATGCGCGGCCACAGGCGCTATTCCTCGGTGTGGCGGCGCTGCTGTGATACCCGGAC	2872
QY	2821	CTGAGAGTGCAGAGCGACTACTCCAGCTATGCCCGAGCTTCATCAAGAGCGACTTTCACC	2880

Db 2813 GTTCAGATGCGGCGCCAGGCGCTATTCCCTGATGCGGCGCTGCTGATGATCCCGAGCC 2872
Qy 2821 CTGAGAGTGCAGAGCGACTATCTCAGCTATGCGCGAGCTCCATCAGAGCCAGCTCTCACC 2880
Db 2873 CTGAGAGTGCAGAGCGACTATCTCAGCTATGCGCGAGCTCCATCAGAGCCAGCTCTCACC 2932
Qy 2881 TTGACCGCGGCTTCAAGGCTGGAGAGAACATGCGCTGCAAACTCTTTGGGCTTTGGCG 2940
Db 2933 TTGACCGCGGCTTCAAGGCTGGAGAGAACATGCGCTGCAAACTCTTTGGGCTTTGGCG 2992
Qy 2941 CTGAGAGTGCAGAGCTGTTTCTGATTTGCAAGTGAAGAGCTCCAGAGCTGTCACC 3000
Db 2993 CTGAGAGTGCAGAGCTGTTTCTGATTTGCAAGTGAAGAGCTCCAGAGCTGTCACC 3052
Qy 3001 AACATCTACAAAGTCTCTCTGCTGCAAGGCTGACAGGTTTCAAGCATGTGTGCTGCACTC 3060
Db 3053 AACATCTACAAAGTCTCTCTGCTGCAAGGCTGACAGGTTTCAAGCATGTGTGCTGCACTC 3112
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Qy 3121 GCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180
Db 3173 GCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3232
Qy 3181 GGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
Db 3233 GGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3292
Qy 3241 CTGAGAGTGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
Db 3293 CTGAGAGTGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3352
Qy 3301 CAGAGAGAGTGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
Db 3353 CAGAGAGAGTGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3412
Qy 3361 AACCCGCGACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3411
Db 3413 AACCCGCGACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3463

RESULT 8
US-10-054-611-224
Sequence 224, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product="hTERT"
/note="human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-611-224
Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db 53 GCGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 112
Qy 61 GAGGTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 113 GAGGTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 172
Qy 121 CAGCGCGGAGACCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 173 CAGCGCGGAGACCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 232
Qy 181 TGGAGCGCAGCG 240
Db 233 TGGAGCGCAGCG 292
Qy 241 CTGCTGCGCGAGTGTGCAAGAGCTGTGCAAGAGCTGTGCAAGAGCTGTGCAAGAGCTGTGCA 300
Db 293 CTGCTGCGCGAGTGTGCAAGAGCTGTGCAAGAGCTGTGCAAGAGCTGTGCAAGAGCTGTGCA 352
Qy 301 GGTCTGCGCGCTGCTGCAAGAGCTGTGCAAGAGCTGTGCAAGAGCTGTGCAAGAGCTGTGCA 360
Db 353 GGTCTGCGCGCTGCTGCAAGAGCTGTGCAAGAGCTGTGCAAGAGCTGTGCAAGAGCTGTGCA 412
Qy 361 GCGAGCTACTGCGCGCAACAGCTGACCGCAGCAGCTGCGCGGAGAGCGGAGCGGAGCGGAGCTG 420
Db 413 GCGAGCTACTGCGCGCAACAGCTGACCGCAGCAGCTGCGCGGAGAGCGGAGCGGAGCGGAGCTG 472
Qy 421 CTGCTGCGCGCGCTGCGCGCAACAGCTGACCGCAGCAGCTGCGCGGAGAGCGGAGCGGAGCTG 480
Db 473 CTGCTGCGCGCGCTGCGCGCAACAGCTGACCGCAGCAGCTGCGCGGAGAGCGGAGCGGAGCTG 532
Qy 481 GTGCTGAGTGTGCTGCGCGCAACAGCTGACCGCAGCAGCTGCGCGGAGAGCGGAGCGGAGCTG 540
Db 533 GTGCTGAGTGTGCTGCGCGCAACAGCTGACCGCAGCAGCTGCGCGGAGAGCGGAGCGGAGCTG 592

Db 2753 TTGGGAAGACAGTGGTGAACCTCCCTGTGAAGAGAGAGCCCTGGGTGGACGGCTTTT 2812
Qy 2761 GTTCAGATGCGCGGCCACCGGCCATATCCCTGGTGGGCGCTGTGTGATACCCGGACC 2820
Db 2813 GTTCAGATGCGCGGCCACCGGCCATATCCCTGGTGGGCGCTGTGTGATACCCGGACC 2872
Qy 2821 CTGAGAGTGCAGAGCGCACTACTCAGATATGCCCGACCTCCATCAGAGCCAGTCTACC 2880
Db 2873 CTGAGAGTGCAGAGCGCACTACTCAGATATGCCCGACCTCCATCAGAGCCAGTCTACC 2932
Qy 2881 TTCAACCGCGGCTTCAAGGCTGGAGAGAACATCGTGCAGAACTCTTTGAGGTCTTGGG 2940
Db 2933 TTCAACCGCGGCTTCAAGGCTGGAGAGAACATCGTGCAGAACTCTTTGAGGTCTTGGG 2992
Qy 2941 CTGAGAGTGCAGAGCGCTGTTCGTGATTTGAGATGAGAGCGCTCCAGAGGAGTGCACC 3000
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Db 3053 AACATCTACAAAGATTCCTCTCTGTGAGAGCGGTACAGGTTTCAAGCATGTGTGTGACGTC 3112
Qy 3061 CCATTTCATGAGAGATTTGAGAGAACCCCAATTTTCTGTGGGCTCATCTTGTACAGC 3120
Db 3113 CCATTTCATGAGAGATTTGAGAGAACCCCAATTTTCTGTGGGCTCATCTTGTACAGC 3172
Qy 3121 GCTTCCTCTGTACTCTCATCTGAAAGCCAGAGACGAGAGTGTGTGGGAGCCAG 3180
Db 3173 GCTTCCTCTGTACTCTCATCTGAAAGCCAGAGACGAGAGTGTGTGGGAGCCAG 3232
Qy 3181 GGGGCGCGGCGGCTCTGTGCTTCGAGGCGGTGCAAGTGTGTGCTGCAACAGATTTCTG 3240
Db 3233 GGGGCGCGGCGGCTCTGTGCTTCGAGGCGGTGCAAGTGTGTGCTGCAACAGATTTCTG 3292
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Db 3293 CTCAAGCTGACTGACAGCAGCGTGTCACTTACAGTGCCTCTGTGGGCTCACTCAGAGCAGCC 3352
Qy 3301 CAGAGCGAGTGTGAGAAAGCTCCCGGAGACGAGCGTGTGAGTGTGTGAGGCGCAGCC 3360
Db 3353 CAGAGCGAGTGTGAGAAAGCTCCCGGAGACGAGCGTGTGAGTGTGTGAGGCGCAGCC 3412
Qy 3361 AACCGGCGACTGCGCTCAGACTTCAAGACCATCTGTGAGCTGATGGCCAGCC 3411
Db 3413 AACCGGCGACTGCGCTCAGACTTCAAGACCATCTGTGAGCTGATGGCCAGCC 3463

RESULT 9
US-10-105-963-1
; Sequence 1, Application US/10105963
; Publication No. US20030068818A1
GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Deming, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schief, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; TITLE OF INVENTION: Recombination
; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

LOCATION: (56) ..(3454)
; OTHER INFORMATION:
US-10-105-963-1
Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGATGCGGCGGCGTCCCGCTGCGAGCGGTGCGTCCCTGTGCGCAGACGATACCGC 60
Db 53 GCGATGCGGCGGCGTCCCGCTGCGAGCGGTGCGTCCCTGTGCGCAGACGATACCGC 112
Qy 61 GAGGTGCTCCGCTGAGCAGCTTGTGAGGCGCTGTGAGGCGCAGGCTGAGCTGATG 120
Db 113 GAGGTGCTCCGCTGAGCAGCTTGTGAGGCGCTGTGAGGCGCAGGCTGAGCTGATG 172
Qy 121 CAGGCGGAGGACCCGCGGCTTTTCCGCGCTGTGTGAGCCAGTGTGCTGTGTGCTCC 180
Db 173 CAGGCGGAGGACCCGCGGCTTTTCCGCGCTGTGTGAGCCAGTGTGCTGTGTGCTCC 232
Qy 181 TGGAGCGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 233 TGGAGCGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 292
Qy 241 CTGTGTGCGCGAGTGTGTGAGAGGCTGTGTGAGGCGGCGGCGGCGGCGGCGGCGGCGG 300
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Db 353 GCGTTGCGGCTGTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 412
Qy 361 CGCAGTACTCTGCGCAGCAGCGTGTGAGAGCGCAGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 413 CGCAGTACTCTGCGCAGCAGCGTGTGAGAGCGCAGTGTGTGTGTGTGTGTGTGTGTGT 472
Qy 421 CTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 473 CTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 532
Qy 481 GT 540
Db 533 GT 592
Qy 541 GCTGCGACTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
Db 593 GCTGCGACTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 652
Qy 601 GAAAGGCGCTGGAACCATAGCGTCAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
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Qy 661 GGTGCGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
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Db 773 CGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 832
Qy 781 GCGAGAGCGGTGAGACCGAGTGAACGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 833 GCGAGAGCGGTGAGACCGAGTGAACGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 892
Qy 841 GAAAGAGCAGCTCTTTTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 893 GAAAGAGCAGCTCTTTTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 952
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QY 3241 CTCAGACTGACTGAGACAGCTGTGACCTTACGTGCTGCTGCTGCTGCTGCTGCTG 3300
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RESULT 10
US-10-044-692-1
Sequence 1, Application US/10044692
Publication No. US20030096344A1

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
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Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
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COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

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REFERENCE/DOCKET NUMBER: 015389-002600US
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TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-692-1

Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTTCCCGCTGCGCGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
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QY 61 GAGGTGCTGCGCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCT 120
DB 113 GAGGTGCTGCGCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCT 172
QY 121 CAGCGCGGAGACCGCGCGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTG 180
DB 173 CAGCGCGGAGACCGCGCGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTG 232
QY 181 TGGAGCCAGCG 240
DB 233 TGGAGCCAGCG 292
QY 241 CTGCTGCGCGAGCTGCTGAGAGCTGCTGAGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 300
DB 293 CTGCTGCGCGAGCTGCTGAGAGCTGCTGAGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 352
QY 301 GCGTTGCGCGCTGCTGAGAGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCT 360
DB 353 GCGTTGCGCGCTGCTGAGAGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCT 412
QY 361 GCGAGCTGCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTG 420
DB 413 GCGAGCTGCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTGCGCGAGCTTCTG 472
QY 421 CTGCTGCGCGAGCTTCTGAGAGCTTCTGAGAGCTTCTGAGAGCTTCTGAGAGCTTCTG 480
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QY 721 GTCGTGCTGCTGCGCGAGCTTCTGAGAGCTTCTGAGAGCTTCTGAGAGCTTCTGAGAG 780
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QY	481	GAAGAAGCACA	CTCTTTTGAAGGGTGCAGCTCTGTGGACGGCGCACATCCACCAATCCGTTG	900
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QY	901	GGCGGCGCAC	ACACGACGCGGGCCCCCATTCACATCGCGGCCACACGTCCTTGAGACG	960
Db	953	GGCGGCGCGCAC	ACACGACGCGGGCCCCCATTCACATCGCGGCCACACGTCCTTGAGACG	1012
QY	961	CCTTGTCCCGGGTATAG	CCCGAGACCAAGCACTTCCTCTACTCTCCAGGGGCAAAAGAG	1022
Db	1013	CCTTGTCCCGGGTATAG	CCCGAGAGCAAGCACTTCCTCTACTCTCCAGGGGCAAAAGAG	1072
QY	1021	CAGCTGCGG	CCCTCTCTACTCACTCAAGCTCTCTGAGGCCAGCCTGACTGAGCTTGAGAG	1086
Db	1073	CAGCTGCGG	CCCTCTCTCTACTCACTCAAGCTCTCTGAGGCCAGCCTGACTGAGCTTGAGAG	1132
QY	1081	CTCTGTGAGAC	CACTTTTCTGGGTTTCAGGCGCTTGGATGCCAGGGACCTCCCGCAGGTTG	1140
Db	1133	CTCTGTGAGAC	CACTTTTCTGGGTTTCAGGCGCTTGGATGCCAGGGACCTCCCGCAGGTTG	1192
QY	1141	CCCCGCTG	CCCCAGCGCTACTGAGAAATGCGAGCCCTGTTTCTGAGCTGCTTGAGAAC	1200
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QY	1201	CACGCGCAGT	CCCCCTTACCGGGTGTCTCTCAAGAGCAGCTGCGCCCTGAGCTGCGGTC	1312
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QY	1261	ACCCAGAGAG	CCGGTCTGTGACCCGGGAGAAAGCCCGAGGCTGTGTGAGCGGCCCCCGAG	1320
Db	1313	ACCCAGAGAG	CCGGTCTGTGACCCGGGAGAAAGCCCGAGGCTGTGTGAGCGGCCCCCGAG	1372
QY	1321	GAGAGAGAC	ACAGACCCCGTGTGCTGTGACGCTCTCCGACACACAGACGCCCTTG	1380
Db	1373	GAGAGAGAC	ACAGACCCCGTGTGCTGTGACGCTCTCCGACACACAGACGCCCTTG	1432
QY	1381	CAGGTGTAC	GGTTGTGTGGCGGCTGTGCGCGCGGCTGTGTGCGCCCGAGGCTCTGTGGGC	1440
Db	1433	CAGGTGTAC	GGTTGTGTGTGGCGGCTGTGCGCGCGGCTGTGTGCGCCCGAGGCTCTGTGGGC	1492
QY	1441	TCCAGGACAA	CGAAGCGCGCTCTCTCAGAGAACACAGAAAGTTATCTCCCTGGGAGAG	1500
Db	1493	TCCAGGACAA	CGAAGCGCGCTCTCTCAGAGAACACAGAAAGTTATCTCCCTGGGAGAG	1552
QY	1501	CATGCGAAG	CTCTGCTGACAGAGCTGACGTGAGAGATGAGGTGTGCGGACCTGCGTTGG	1560
Db	1553	CATGCGAAG	CTCTGCTGACAGAGCTGACGTGAGAGATGAGGTGTGCGGACCTGCGTTGG	1612
QY	1561	CTGACGAGAG	CCCGAGGGTGTGTGTCCGAGCGGACAGACCGTCTGCGTGAAGGAG	1620
Db	1613	CTGACGAGAG	CCCGAGGGTGTGTGTCCGAGCGGACAGACCGTCTGCGTGAAGGAG	1672
QY	1621	ATCTGTGAC	CAAGTTCTGTGACTGTGATGAGTGTGACGTGTGAGCTGTCAAGTCT	1680
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Db	1733	TTCTTTTAT	GTGACGGAGACACGTTTAAAGAAAGAGGCTCTTTTCTACCGAAGAGT	1792
QY	1741	GTCTTGACAA	ATTGCAATGCAAGCACTTGAAAGAGGTTGAAAGAGGTTGAGCTGCGG	1800
Db	1793	GTCTTGACAA	ATTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG	1852
QY	1801	GAGCTGTGGA	AGAGAGTCAAGATGCGGAAAGCGCAGGAGGCGCGCTGTGACGTTC	1860
Db	1853	GAGCTGTGGA	AGAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGT	1912
QY	1861	AGACTCCGCT	CATCCCAAGGCTGACGGGCTGCGCGGATTTGTGAACATGAGACTACGTC	1920
Db	1913	AGACTCCGCT	CATCCCAAGGCTGACGGGCTGCGCGGATTTGTGAACATGAGACTACGTC	1972
QY	1921	GTGGAGGCG	CAACGTTCCGACAGAGAAAGAGGCGCGAGCTCTCACTCGAGGTTGAG	1980

Db	1793	GTGGAGGCCGAACGTTTCCGAGAGAAAAGGCCCCAGACGCTTCACCTCGAGGGTGAAG	20322
Oy	1981	GCACGTGTTACAGCGTGTCAACTACAGACCGGAGCGGCCCCGGACCTCTGGAGCGCTCT	20408
Db	2033	GCACTGTTACAGCGTGTCAACTACAGACCGGAGCGGCCCCGGACCTCTGGAGCGCTCT	20522
Oy	2041	GTGCTGGAGCCCTGAGCAGATATCCACAAGGCGCTGGAGCAGCTTCGATGCGTGGCGGCGC	21000
Db	2093	GTGCTGGAGCCCTGAGCAGATATCCACAAGGCGCTGGAGCAGCTTCGATGCGTGGCGGCGC	21522
Oy	2101	CAGAACCCCGCGCGCTGAGCTGTACTTTGTGCAAGGTGATGTGACGGCGCGTACAGAACCC	21600
Db	2153	CAGAACCCCGCGCGCTGAGCTGTACTTTGTGCAAGGTGATGTGACGGCGCGTACAGAACCC	22122
Oy	2161	ATCCCCCAGAGCAGGCTTCACGGAGGTATATGCCACGATCATCAAAACCCCAAGAACGTAC	22200
Db	2213	ATCCCCCAGAGCAGGCTTCACGGAGGTATATGCCACGATCATCAAAACCCCAAGAACGTAC	22722
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Db	2273	TGCGTGGCTCGATATGCGGTGATCCAGAAAGGCGCCCATGGGAGCATCTCCGAAAGGCTTC	23322
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Db	2333	AAGAGCCACGTCTCTACTTGAACAGACCTCCACGCTGCATATGCGACATTTGTGTCTCAC	23922
Oy	2341	CTGACAGAGAACCAAGCCGAGTGGAGGATGGCGGTGCATTCAGACAGACCTCCGCTGAAT	24000
Db	2393	CTGACAGAGAACCAAGCCGAGTGGAGGATGGCGGTGCATTCAGACAGACCTCCGCTGAAT	24522
Oy	2401	GAGGCGACAGATGGAGCTTTTGAAGCTTTCAGCTTCATATGTGCAACAGACCGGTGCGC	24600
Db	2453	GAGGCGACAGATGGAGCTTTTGAAGCTTTCAGCTTCATATGTGCAACAGACCGGTGCGC	25122
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Oy	2521	CTGCTCTGCAGACCTGTGCTACAGGAGCATGAGAACAGCTGTTGCGGGATTCGAGCGG	25800
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Oy	2581	GACGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGTGACCTCACCTTACCCAC	26400
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Oy	2641	GCGAAAACCTTCCCTCAGAGACCCGTGGATCGAGAGTGCCTCGATATGCTGGTGGTGAAC	27000
Db	2693	GCGAAAACCTTCCCTCAGAGACCCGTGGATCGAGAGTGCCTCGATATGCTGGTGGTGAAC	27522
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Db	2753	TTGCGGAAGACAGATGATGAACCTTCCTGTAGAAACAGAGGCCCTGGGTGACGCGCTTTT	28122
Oy	2761	GTTTCAGATGCGCGGCCACAGGCGCTATTCCTCCGTGGGCGGCGCTGCTGCTGATACCGGAGC	28200
Db	2813	GTTTCAGATGCGCGGCCACAGGCGCTATTCCTCCGTGGGCGGCGCTGCTGCTGATACCGGAGC	28722
Oy	2821	CTGAGAGTGCAGAGCAGACTACCCAGCTATGCCCGAGCTTCATCAGAGCCAGTCTCAC	28800
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Db 3053 AACATCTACAAGATCTCTGCTGACAGCGCTACAGGTTTCAAGCATGTGCTGACAGTC 3112
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RESULT 11
US-10-044-539-1
; Sequence 1, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingenf, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00260005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
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transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-539-1

Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCGATGCGCGCGCTGCTCCCGCTGCGAGCGCTGCTCCCTGCTGCGAGCACTACCGC 60
Db 53 GCGATGCGCGCGCTGCTCCCGCTGCGAGCGCTGCTCCCTGCTGCGAGCACTACCGC 112
QY 61 GAGGTGCTGCGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTG 120
Db 113 GAGGTGCTGCGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTG 172
QY 121 CAGCGCGAGGACCGCGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTG 180
Db 173 CAGCGCGAGGACCGCGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTG 232
QY 181 TGGAGCGAGCGCGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTG 240
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QY 241 CTGCTGCGCGAGGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAG 300
Db 293 CTGCTGCGCGAGGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAG 352
QY 301 GCGTTCGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAG 360
Db 353 GCGTTCGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAG 412
QY 361 GCGAGCTACTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAG 420
Db 413 GCGAGCTACTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAG 472
QY 421 CTGCTGCGCGCGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAGCGCTGCTGCGAG 480
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Db 593 GCGGCGCTGAGGCG 652
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Db 713 GGGGCGAGGAGGCG 772

QY 721 CTTGGGCTGCTCCCTGAGCCGAGAGCCGAGCCGCTTGGGAGAGGCTCTGGGAGCCG 780
Db 773 CTTGGGCTGCTCCCTGAGCCGAGAGCCGAGCCGCTTGGGAGAGGCTCTGGGAGCCG 832
QY 781 GGCAGAGCCGCTGAGCCGAGAGCCGAGAGCCGCTTGGGAGAGGCTCTGGGAGCCG 840
Db 833 GGCAGAGCCGCTGAGCCGAGAGCCGAGAGCCGCTTGGGAGAGGCTCTGGGAGCCG 892
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Db 1553 CAGGAGAGCTCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1612
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QY 1801 GAGCTGTGAGAGCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAG 1860
Db 1853 GAGCTGTGAGAGCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAG 1912
QY 1861 AGACTCGCTTCAATCCCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCT 1920
Db 1913 AGACTCGCTTCAATCCCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCT 1972
QY 1921 GTGAGAGCCGAAAGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1973 GTGAGAGCCGAAAGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2032
QY 1981 GCACTGTGAGGCTCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Db 2033 GCACTGTGAGGCTCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2092
QY 2041 GTGCTGAGGCTGAGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
Db 2093 GTGCTGAGGCTGAGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2152
QY 2101 CAGGAGCCGCTGAGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Db 2153 CAGGAGCCGCTGAGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2212
QY 2161 ATCCCGAGAGAGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Db 2213 ATCCCGAGAGAGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2272
QY 2221 TGGCTGAGGCTGAG 2280
Db 2273 TGGCTGAGGCTGAG 2332
QY 2281 AAGAGCCAGCTCTCAATCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Db 2333 AAGAGCCAGCTCTCAATCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2392
QY 2341 CTTGAGAGAGCAAGCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Db 2393 CTTGAGAGAGCAAGCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2452
QY 2401 GAGGAGAGCAAGGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
Db 2453 GAGGAGAGCAAGGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2512
QY 2461 ATCAGGAGAGCAAGGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
Db 2513 ATCAGGAGAGCAAGGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2572
QY 2521 CTTGCTGAGAGCAAGGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
Db 2573 CTTGCTGAGAGCAAGGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2632
QY 2581 GAGGAGCTGCTCTGAG 2640
Db 2633 GAGGAGCTGCTCTGAG 2692
QY 2641 GCGAGAGAGCTTCTCAAG 2700
Db 2693 GCGAGAGAGCTTCTCAAG 2752
QY 2701 TTTGCGAG 2760
Db 2753 TTTGCGAG 2812
QY 2761 GTTCAAG 2820
Db 2813 GTTCAAG 2872
QY 2821 CTTGAG 2880
Db 2873 CTTGAG 2932
QY 2881 TTTCAAG 2940

Db 2933 TTCAACGCGGCTTCAAGGCTGGAGAGACATGCTGCGAACTCTTTGGGGCTTGGCG 2992
Qy 2941 CTGAAGTGTACAGACCTCTTTTGTGATTTGTGAGTGAACGCTCCAGAGGTTGACACC 3000
Db 2993 CTGAAGTGTACAGACCTCTTTTGTGATTTGTGAGTGAACGCTCCAGAGGTTGACACC 3052
Qy 3001 AACATCTACAGAGTCTCTCTGCTGACAGGCTTACAGGTTTACGATGTGTGTGACAGTC 3060
Db 3053 AACATCTACAGAGTCTCTCTGCTGACAGGCTTACAGGTTTACGATGTGTGTGACAGTC 3112
Qy 3061 CCATTTCATCAGCAGGTTTGAAGAACCCCACTTTTCTGCGCTCATCTTGAACAG 3120
Db 3113 CCATTTCATCAGCAGGTTTGAAGAACCCCACTTTTCTGCGCTCATCTTGAACAG 3172
Qy 3121 GCCTCCCTGCTACTCATCTCTGAAAGCCAGAGGATGTGCTGGGGGCGCAAG 3180
Db 3173 GCCTCCCTGCTACTCATCTCTGAAAGCCAGAGGATGTGCTGGGGGCGCAAG 3232
Qy 3181 GGGCGCGCGGCTCTGCTCTCTGAGGCGCTGCAAGTGTGTGCAACCAAGCATTTCTG 3240
Db 3233 GGGCGCGCGGCTCTGCTCTCTGAGGCGCTGCAAGTGTGTGCAACCAAGCATTTCTG 3292
Qy 3241 CTGAAGTGTACAGCAGGTTTGAAGAACCCCACTTTTCTGCGCTCATCTTGAACAG 3300
Db 3293 CTGAAGTGTACAGCAGGTTTGAAGAACCCCACTTTTCTGCGCTCATCTTGAACAG 3352
Qy 3301 CAGACGAGCTGAGTGTGAAAGCTCCGAGGACAGACGCTGACTGCTGAGGCGCGAGCC 3360
Db 3353 CAGACGAGCTGAGTGTGAAAGCTCCGAGGACAGACGCTGACTGCTGAGGCGCGAGCC 3412
Qy 3361 AACCGGCACTGGCCCTCAGACTTCAAGACCATCTGAGTGTGAGGCGCGAGCC 3411
Db 3413 AACCGGCACTGGCCCTCAGACTTCAAGACCATCTGAGTGTGAGGCGCGAGCC 3463

RESULT 12
US-10-385-882-1
; Sequence 1, Application US/10385882
; Publication No. US20030232409A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA
; APPLICANT: FARRIS, James
; APPLICANT: FOSTER, Douglas
; APPLICANT: O'GRADY, Scott
; TITLE OF INVENTION: IMMORTAL PORCINE CELLS
; FILE REFERENCE: 110.01700101
; CURRENT APPLICATION NUMBER: US/10/385,882
; PRIORITY FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/363,129
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4027
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding telomerase reverse transcriptase
US-10-385-882-1

Query Match 99.9%; Score 3407.8; DB 15; Length 4027;
Best Local Similarity 99.9%; P-Id. No. 0;
Matches 3409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCGATGCGGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGAGCCACTACCGC 60
Db 54 GCGATGCGGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGAGCCACTACCGC 113
Qy 61 GAGGTGCTGCGCTGCGAGCGGTGCGAGCGGTGCGAGCGGTGCGAGCGGTGCGAGCG 120
Db 114 GAGGTGCTGCGCTGCGAGCGGTGCGAGCGGTGCGAGCGGTGCGAGCGGTGCGAGCG 173

Qy 121 CAGCGCGGGGACCCGCGCGCTTTCCGCGCGCTGAGTGTGAGTGTGAGTGTGAGTGTG 180
Db 174 CAGCGCGGGGACCCGCGCGCTTTCCGCGCGCTGAGTGTGAGTGTGAGTGTGAGTGTG 233
Qy 181 TGGAGCGAGCG 240
Db 234 TGGAGCGAGCG 293
Qy 241 CTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 300
Db 294 CTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 353
Qy 301 GAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 360
Db 354 GAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 413
Qy 361 GCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 420
Db 414 GCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 473
Qy 421 CTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 480
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Qy 481 GTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540
Db 534 GTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 593
Qy 541 GCTGCACTGAGGCG 600
Db 594 GCTGCACTGAGGCG 653
Qy 601 GAAAGGCGTGTGAAACCATAGGCTGAGGAGCGCGGAGTCCCGCTGAGGCTGCGAGCC 660
Db 654 GAAAGGCGTGTGAAACCATAGGCTGAGGAGCGCGGAGTCCCGCTGAGGCTGCGAGCC 713
Qy 661 GGTGCGAGGAGGCG 720
Db 714 GGTGCGAGGAGGCG 773
Qy 721 CGTGGCGTGGCCCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 774 CGTGGCGTGGCCCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 833
Qy 781 GCGAGAGCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 840
Db 834 GCGAGAGCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 893
Qy 841 GAAAGAGCACTCTTTGAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 900
Db 894 GAAAGAGCACTCTTTGAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 953
Qy 901 GGGCGCGAGCAACAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Db 954 GGGCGCGAGCAACAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1013
Qy 961 CTTGTCCCGGAGTGTGAGCGCGAGAGCACTCTCTACTCTCTACTCTCTACTCTCTACT 1020
Db 1014 CTTGTCCCGGAGTGTGAGCGCGAGAGCACTCTCTACTCTCTACTCTCTACTCTCTACT 1073
Qy 1021 CAGCTGCGGCGCT 1080
Db 1074 CAGCTGCGGCGCT 1133
Qy 1081 CTGCTGAGAGCACTCTTTTGGGTTCCAGGCGCTGAGTGTGAGTGTGAGTGTGAGTGTG 1140
Db 1134 CTGCTGAGAGCACTCTTTTGGGTTCCAGGCGCTGAGTGTGAGTGTGAGTGTGAGTGTG 1193
Qy 1141 CCGCGCTGCGCGAGCGCTACTGCAATGCGGCGCGCTGTTTCTGAGAGTGTGAGAGAC 1200
Db 1194 CCGCGCTGCGCGAGCGCTACTGCAATGCGGCGCGCTGTTTCTGAGAGTGTGAGAGAC 1253
Qy 1201 CAGCGGAGTGTGCGCGCTTACGCGGAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1260

Db	1254	CACGCGAAGGCCCTTACGGGGTGTCTTCAAGACGACTGCGCGAGTGTGGCTC	1313
Qy	1261	ACCCGACAGCCGGGTGTCTGTGCTCCGGGAGAGGCCCTTGTGCGGCCCCGAG	1320
Db	1314	ACCCGACAGCCGGGTGTCTGTGCTCCGGGAGAGGCCCTTGTGCGGCCCCGAG	1373
Qy	1321	GAGAGAGACAGACCCCGCTGCTGGTGTGAGCTGTCCGACAGACAGACCCCTGAG	1380
Db	1374	GAGAGAGACAGACCCCGCTGCTGGTGTGAGCTGTCCGACAGACAGACCCCTGAG	1433
Qy	1381	CAGGTGTAAGGCTTGTGTGCGGAGCTGTGCTGCGCGGCTGTGTGCCCTTGTGGGC	1440
Db	1434	CAGGTGTAAGGCTTGTGTGCGGAGCTGTGCTGCGCGGCTGTGTGCCCTTGTGGGC	1493
Qy	1441	TCCAGGACACAGGAGCGCGCTTCTCAGGAAACCAAGAAAGTCACTCCCTGGGGAAG	1500
Db	1494	TCCAGGACACAGGAGCGCGCTTCTCAGGAAACCAAGAAAGTCACTCCCTGGGGAAG	1555
Qy	1501	CATGCCAAGCTCTGCTGACGAGAGCTGACGTGGAAGATGAGCGTGGGGAATTGCGCTTGG	1566
Db	1554	CATGCCAAGCTCTGCTGACGAGAGCTGACGTGGAAGATGAGCGTGGGGAATTGCGCTTGG	1613
Qy	1561	CTGCGACAGAGCCCAAGGGGTGGCTGTGTTTCCGCGCGACAGACCGTCTGCTGAGAG	1620
Db	1614	CTGCGAGAGAGCCCAAGGGGTGGCTGTGTTTCCGCGCGACAGACCGTCTGCTGAGAG	1673
Qy	1621	ATCCTGAGCAAGTTCCTGCACTGAGCTGATGAGTGTACGTGCGAGCTCAAGTGT	1680
Db	1674	ATCCTGAGCAAGTTCCTGCACTGAGCTGATGAGTGTACGTGCGAGCTCAAGTGT	1733
Qy	1681	TTCCTTTATGTCAAGAGACCAAGTTCGAAAGAACAGGCTCTTTTCTAACCGGAAGAT	1740
Db	1734	TTCCTTTATGTCAAGAGACCAAGTTCGAAAGAACAGGCTCTTTTCTAACCGGAAGAT	1793
Qy	1741	GTCGTGAGCAAGTTCGAAAGATTGGAATTCAGACAGCACTGGAAGGGGTCAGCGTGGG	1800
Db	1794	GTCGTGAGCAAGTTCGAAAGATTGGAATTCAGACAGCACTTGAAGGGGTCAGCGTGGG	1855
Qy	1801	GACCTGTGGAAGCAGAGGTCAAGGCAAGCATCGGGAACCAAGGCCGCTGTGTAAGTCC	1866
Db	1854	GACCTGTGGAAGCAGAGGTCAAGGCAAGCATCGGGAACCAAGGCCGCTGTGTAAGTCC	1919
Qy	1861	AGACTCCGCTTCAATCCCAAGCTTACAGGGCTGGCGGCCAATTGTGAACATGACATACGT	1922
Db	1914	AGACTCCGCTTCAATCCCAAGCTTACAGGGCTGGCGGCCAATTGTGAACATGACATACGT	1973
Qy	1921	GTCGAGCCAGAAAGTTCGACAGAGAAAGAGGGCCAGAGGCTCTCACTCGAGGGTGAAG	1980
Db	1974	GTCGAGCCAGAAAGTTCGACAGAGAAAGAGGGCCAGAGGCTCTCACTCGAGGGTGAAG	2033
Qy	1981	GCACTGTTCAGCGTGTCACTACAGAGCGGGCGGGCGCCCTCGGAGCTCTTGTGGGCGCTCT	2040
Db	2034	GCACTGTTCAGCGTGTCACTACAGAGCGGGCGGGCGCCCTCGGAGCTCTTGTGGGCGCTCT	2093
Qy	2041	GTCCTGGGCTTGAAGCATATCCACAGGGCCCTGGGACACTTCGTGTGCTGTGGGGGCG	2100
Db	2094	GTCCTGGGCTTGAAGCATATCCACAGGGCCCTGGGACACTTCGTGTGCTGTGGGGGCG	2155
Qy	2101	CAGAACCCGCGCTGAGCTGTACTTTTGTCAAGGTGATGTGACGGAGCGGTACAGACAC	2166
Db	2154	CAGAACCCGCGCTGAGCTGTACTTTTGTCAAGGTGATGTGACGGAGCGGTACAGACAC	2219
Qy	2161	ATCCCCCAGAGCAGGCTCACAGAGGTCACTGCGCAGCATCAATCAACCCAGAACAGTAC	2222
Db	2214	ATCCCCCAGAGCAGGCTCACAGAGGTCACTGCGCAGCATCAATCAACCCAGAACAGTAC	2273
Qy	2221	TGCGTGTGCTGATATGCGGTGTACAGAGGCCCCCATGGAGCAGTCCGCAAGGCGCTTC	2280
Db	2274	TGCGTGTGCTGATATGCGGTGTACAGAGGCCCCCATGGAGCAGTCCGCAAGGCGCTTC	2333
Qy	2281	AAGAGCAAGTCTTCACTTGAAGACCTCCAGCCGTACATGCGACAGTTGCTGTGCTAC	2340

Db	2334	AAAGGCCACGGCTCTACCTTGACAGACCTCCAGCCGTAACATATGACGACAGTTGCTGCTCAC	2393
QY	2341	CTGACAGAGAACCAACCCCGCTGAGGGATGCGCTGTCATTCAGACAGAGCTCTCTCTCAAT	2400
Db	2394	CTGACAGAGAACCAACCCCGCTGAGGGATGCGCTGTCATTCAGACAGAGCTCTCTCTCAAT	2453
QY	2401	GAGCCACAGAGTGCCTCTTCGACGTCCTTCCTACGCTTCATATGATGCACACAGCCGCTGCG	2460
Db	2454	GAGCCACAGAGTGCCTCTTCGACGTCCTTCCTACGCTTCATATGATGCACACAGCCGCTGCG	2513
QY	2461	ATCAGGGGCAAGTCTTAAGTCAAGTCCAGAGGATCCCGCAGGGCTCATCTCTCCACG	2520
Db	2514	ATCAGGGGCAAGTCTTAAGTCAAGTCCAGAGGATCCCGCAGGGCTCATCTCTCCACG	2573
QY	2521	CTGCTCTGACGCCGTGTCACGGGACATGAGAAACAAGCTGTTGGCGGGATTCGGCGG	2580
Db	2574	CTGCTCTGACGCCGTGTCACGGGACATGAGAAACAAGCTGTTGGCGGGATTCGGCGG	2633
QY	2581	GACGGGCTGCTCTGACCTTGTGGATGATTTCTTGTGTGACACCTCACTCAGCCAC	2640
Db	2634	GACGGGCTGCTCTGACCTTGTGGATGATTTCTTGTGTGACACCTCACTCAGCCAC	2693
QY	2641	GCGAAACCTTCTCTCAGACCTCTGCTCCGAGGTCTCCTCAAGTATGCTGTGCTGAAC	2700
Db	2694	GCGAAACCTTCTCTCAGACCTCTGCTCCGAGGTCTCCTCAAGTATGCTGTGCTGAAC	2753
QY	2701	TTGGGAAAGACAGTGTGTGAACCTTCCCTGTAAACACAGAGCCCTGGGTGACACGGCTTT	2760
Db	2754	TTGGGAAAGACAGTGTGTGAACCTTCCCTGTAAACACAGAGCCCTGGGTGACACGGCTTT	2813
QY	2761	GTTCAAGATGCCGGCCACACGGCTTAATCCCTGTGCGGCTGCTGCTGAATACCGGAC	2820
Db	2814	GTTCAAGATGCCGGCCACACGGCTTAATCCCTGTGCGGCTGCTGCTGAATACCGGAC	2873
QY	2821	CTGACAGGTGACAGACGACCTACTCCAGGTATGCCCGGACCTTCATCAGAGCCAGTCTCAC	2880
Db	2874	CTGACAGGTGACAGACGACCTACTCCAGGTATGCCCGGACCTTCATCAGAGCCAGTCTCAC	2933
QY	2881	TTCAACCGCGGCTTCAAGGCTGGAGGAAACATGCGTGCACAACTTTTGGGGTCTTGCGG	2940
Db	2934	TTCAACCGCGGCTTCAAGGCTGGAGGAAACATGCGTGCACAACTTTTGGGGTCTTGCGG	2993
QY	2941	CTGAAAGTGCACACCCGTTTCTGGAATTTGAGGTGAACAGCCCTCCAGACGCTGTGACG	3000
Db	2994	CTGAAAGTGCACACCCGTTTCTGGAATTTGAGGTGAACAGCCCTCCAGACGCTGTGACG	3053
QY	3001	AACATCTACAGATCTCTCTGCTGACAGCGTACAGTGTTCACGCAATGTGCTCAGCTC	3060
Db	3054	AACATCTACAGATCTCTCTGCTGACAGCGTACAGTGTTCACGCAATGTGCTCAGCTC	3113
QY	3061	CCATTTCAACAGCAAGTTTGGAGAACCCCAATTTTCTGCGCGTCATCTTGAACAG	3120
Db	3114	CCATTTCAACAGCAAGTTTGGAGAACCCCAATTTTCTGCGCGTCATCTTGAACAG	3173
QY	3121	GCTTCCTCTGCTACTCCATCTGTAAGACCAAGACCAAGGATGTGCTGGGAGCCCAAG	3180
Db	3174	GCTTCCTCTGCTACTCCATCTGTAAGACCAAGACCAAGGATGTGCTGGGAGCCCAAG	3233
QY	3181	GCGCGCGCGGCGCTCTGCTCTCGAGGCGGTGACGTGCTGTGCAACAAGCATCTCTG	3240
Db	3234	GCGCGCGCGGCGCTCTGCTCTCGAGGCGGTGACGTGCTGTGCAACAAGCATCTCTG	3293
QY	3241	CTCAAGCTGACTGACACCGGTGACCTTAAGTGCATCTCTGGGGGTACCTCAGGACAGCC	3300
Db	3294	CTCAAGCTGACTGACACCGGTGACCTTAAGTGCATCTCTGGGGGTACCTCAGGACAGCC	3353
QY	3301	CAGACGCAAGCTGATCGGAAGCTCCCGGGACGACGCTGACTGCTGAGACCGCAGCC	3360
Db	3354	CAGACGCAAGCTGATCGGAAGCTCCCGGGACGACGCTGACTGCTGAGACCGCAGCC	3413
QY	3361	AACTCCGCACTGCTCTCAAGATTTCAAGACCATCTGCACTGATGAGCCACCC	3411
Db	3414	AACTCCGCACTGCTCTCAAGATTTCAAGACCATCTGCACTGATGAGCCACCC	3464

Db 3987 CCAATGCGGCGGCTCCCGCTGCGGAGCGGTGCTCCCTGCTGCGGAGCACTACCGG 4046
QY 62 AGGTGCTGCGCTGAGCAAGTTGTGTCGCGGCTGTGAGCCCAAGGCTGAGCGCTGTGTC 121
Db 4047 AGGTGCTGCGCTGAGCAAGTTGTGTCGCGGCTGTGAGCCCAAGGCTGAGCGCTGTGTC 4106
QY 122 AGGCGGAGGAGCCCGGCGGCTTTTCCGCGCGCTGTGAGCCCAAGGCTGTGAGCGCTGTGTC 181
Db 4107 AGGCGGAGGAGCCCGGCGGCTTTTCCGCGCGCTGTGAGCCCAAGGCTGTGAGCGCTGTGTC 4166
QY 182 GGGAGCGACG 241
Db 4167 GGGAGCGACG 4226
QY 242 TGGTGGCGCGAGTGTGTCGAGAGGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 301
Db 4227 TGGTGGCGCGAGTGTGTCGAGAGGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4286
QY 302 GCTTCGCGCTGAGCAAGGAGCG 361
Db 4287 GCTTCGCGCTGAGCAAGGAGCG 4346
QY 362 GCAAGTACTTGTCCCAACAGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 421
Db 4347 GCAAGTACTTGTCCCAACAGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4406
QY 422 TGGTGGCGCGAGTGTGTCGAGAGGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481
Db 4407 TGGTGGCGCGAGTGTGTCGAGAGGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4466
QY 482 TGGTGGCGCTCCAGCTGCGCTTACAGGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 541
Db 4467 TGGTGGCGCTCCAGCTGCGCTTACAGGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 4526
QY 542 CTGCGCACTAGGCG 601
Db 4527 CTGCGCACTAGGCG 4586
QY 602 AACGGGCTTGAACCAATAGCGTGAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 661
Db 4587 AACGGGCTTGAACCAATAGCGTGAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4646
QY 662 GTTCCGAGAGGCG 721
Db 4647 GTTCCGAGAGGCG 4706
QY 722 GTGCGCTGCGCTTGAAGCGGAGCG 781
Db 4707 GTGCGCTGCGCTTGAAGCGGAGCG 4766
QY 782 GCGAGAGCGGTGAGCGAGTGAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 841
Db 4767 GCGAGAGCGGTGAGCGAGTGAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4826
QY 842 AAGAGGCACTCTTTGAGAGGAGT 901
Db 4827 AAGAGGCACTCTTTGAGAGGAGT 4886
QY 902 GCGCGCAAGCAAGCGGAGCG 961
Db 4887 GCGCGCAAGCAAGCGGAGCG 4946
QY 962 CTGTCGCGCGGAGT 1021
Db 4947 CTGTCGCGCGGAGT 5006
QY 1022 AGCTGCGCGCTCTCTTCTACTAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1081
Db 5007 AGCTGCGCGCTCTCTTCTACTAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5066
QY 1082 TCGTGGAGACATCTTTCTGTGGGTTCAAGGCGGTGATGCGAGGAGCTCCCGCGAGGTTGC 1141

Db 5067 TCGTGGAGACATCTTTCTGTGGGTTCAAGGCGGTGATGCGAGGAGCTCCCGCGAGGTTGC 5126
QY 1142 CCCGCTGCGCGAGCGCTACTGGAATATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1201
Db 5127 CCCGCTGCGCGAGCGCTACTGGAATATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5186
QY 1202 ACGCGAGTGCCTCTAGCGGAGTGTCTCAAGAGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1261
Db 5187 ACGCGAGTGCCTCTAGCGGAGTGTCTCAAGAGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5246
QY 1262 CCCGAGAGCGGCTGT 1321
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QY 1382 AGGTGTACGGCTTGT 1441
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Db 5547 TGGCGAGAGCGCGAGGCTGT 5606
QY 1622 TCGTGGCGAAGTTCTGCACTGAGT 1681
Db 5607 TCGTGGCGAAGTTCTGCACTGAGT 5666
QY 1682 TCTTTTATGTCAAGGAGACCAAGTTCAAAAGAACAGGCTCTTTTGTACCGGCGAGTG 1741
Db 5667 TCTTTTATGTCAAGGAGACCAAGTTCAAAAGAACAGGCTCTTTTGTACCGGCGAGTG 5726
QY 1742 TCTGAGCAAGTTGCAAGAGATGAGATGAGACAGCACTTGAAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1801
Db 5727 TCTGAGCAAGTTGCAAGAGATGAGATGAGACAGCACTTGAAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5786
QY 1802 AGCTGTGGAAGCAGAGGTCAGGCAAGTCAGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1861
Db 5787 AGCTGTGGAAGCAGAGGTCAGGCAAGTCAGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5846
QY 1862 GACTCCGCTTCAATCCCAAGCTTGAAGCGGCTGT 1921
Db 5847 GACTCCGCTTCAATCCCAAGCTTGAAGCGGCTGT 5906
QY 1922 TGGAGAGCAAGACCTTCCGAGAGAAAGAGGAGCGGAGCGCTTCACTCGAGGAGTGAAG 1981
Db 5907 TGGAGAGCAAGACCTTCCGAGAGAAAGAGGAGCGGAGCGCTTCACTCGAGGAGTGAAG 5966
QY 1982 CACTGTTCAGGTGTCTAATCTAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2041
Db 5967 CACTGTTCAGGTGTCTAATCTAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6026
QY 2042 TGTGAGGCTGTGAGATATCAAGGAGCTGTGAGCACTTGT 2101
Db 6027 TGTGAGGCTGTGAGATATCAAGGAGCTGTGAGCACTTGT 6086
QY 2102 AGGACCGCGCGCTGAGCTGTCTTTGTCAAGT 2161
Db 6087 AGGACCGCGCGCTGAGCTGTCTTTGTCAAGT 6146
QY 2162 TCCCGCAGAGCAGGCTGAGGAGT 2221
Db 6147 TCCCGCAGAGCAGGCTGAGGAGT 6206

2222 GCGGCGCTGGTATGCGGTGCTCAGAGAGCGCCCATGGGAGCGTCCGCAAGGCTTCA 2281
Db 6207 GCGTGGCTGGTATGCGGTGCTCAGAGAGCGCCCATGGGAGCGTCCGCAAGGCTTCA 6266
QY 2282 AGAGCCAGCTCTGTACCTTGAAGAGAGCGTCCGCAAGGCTTCA 2341
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Db 6387 AGAGCCAGCTCTGTACCTTGAAGAGAGCGTCCGCAAGGCTTCA 6446
QY 2462 TCGAGGAGAGAGCTCTGTACCTTGAAGAGAGCGTCCGCAAGGCTTCA 2521
Db 6447 TCGAGGAGAGAGCTCTGTACCTTGAAGAGAGCGTCCGCAAGGCTTCA 6506
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QY 2582 AGAGGAGAGAGAGCTCTGTACCTTGAAGAGAGCGTCCGCAAGGCTTCA 2641
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RESULT 15
US-09-749-728B-32
Sequence 32, Application US/09749728B
Patent No. US20020142457A1
GENERAL INFORMATION:
APPLICANT: Umezawa, Akihito
APPLICANT: Hata, Jun-ichi
APPLICANT: Fukuda, Keiichi
APPLICANT: Ogawa, Satoshi
APPLICANT: Sakurada, Kazuhiro
APPLICANT: Gojo, Satoshi
APPLICANT: Yamada, Yoichi
TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMYOCYTE

PRIOR REFERENCE: 00766.000043
CURRENT APPLICATION NUMBER: US/09/749,728B
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: H11-372826
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: PCT-JP00-01148
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT-JP00-07741
PRIOR FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patent Ver.2.0
SEQ ID NO 32
LENGTH: 3396
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: CDS
OTHER INFORMATION: (1)...(3399)
US-09-749-728B-32

Query Match 99.6%; Score 3396; DB 9; Length 3396;
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